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(54) Title: GENES FOR MODIFYING PLANT TRAITS IV

(57) Abstract: The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a reference plant. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

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## GENES FOR MODIFYING PLANT TRAITS IV

This application claims priority benefit of: prior U.S application entitled "Plant Trait Modification III," serial no. 60/227,439, filed August 22, 2000; prior U.S. application entitled "Genes for Modifying Plant Traits," attorney docket number MBI-0022, serial no. \_\_\_\_\_, filed November 16, 2000; and prior U.S. application entitled "Genes for Modifying Plant Traits II," serial no. 09/837,944, filed April 18, 2001. The entire content of each of these applications is hereby incorporated by reference.

### 10 Field of the Invention and Introduction

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

A plant's traits, such as its biochemical, developmental, or phenotypic characteristics, can be controlled through a number of cellular processes. One important way to manipulate that control is through transcription factors - proteins that influence the expression of a particular gene or sets of genes. Transgenic plants that comprise cells having altered levels of at least one selected transcription factor, for example, possess advantageous or desirable traits. Strategies for manipulating traits by altering a plant cell's transcription factor content can therefore result in plants and crops with commercially valuable properties. Applicants have identified polynucleotides encoding transcription factors, developed numerous transgenic plants using these polynucleotides, and have analyzed the plants for a variety of important traits. In so doing, applicants have identified important polynucleotide and polypeptide sequences for producing commercially valuable plants and crops as well as the methods for making them and using them. Other aspects and embodiments of the invention are described below and can be derived from the teachings of this disclosure as a whole.

### Background of the Invention

Transcription factors can modulate gene expression, either increasing or decreasing (inducing or repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an



organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways.

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### Summary of the Invention

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from: (a) a nucleotide sequence of the Sequence Listing, or SEQ ID Nos.: 2N-1 where N=1-232, preferably where N=1-232, or a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from those of the Sequence Listing, or SEQ ID Nos: 2N where N=1-232, or a complementary nucleotide sequence of any of these; (b) a nucleotide sequence encoding a polypeptide comprising a variant of a polypeptide of (a) or a variant having one or more, or between 1 and about 5, or between 1 and about 10, or between 1 and about 30, conservative amino acid substitutions; (c) a nucleotide sequence comprising a sequence selected from SEQ ID Nos.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence that hybridizes under stringent conditions, high stringent conditions, ultra-high stringent conditions, or ultra-ultra-high stringent conditions over substantially the entire length of a nucleotide sequence of one or more of (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides of a sequence of any of (a)-(e), or at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides outside of a region encoding a conserved domain of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's characteristic, functions as a transcription factor, results in ectopic expression or altered expression in a transgenic plant, or alters the level of transcription of a gene or transgene in a cell; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60%, or at least 70 %, or at least 80 %, or at least 90 %, or at least 95 % sequence identity to a nucleotide sequence of any of (a)-(g) or a 10 or 15 nucleotide, or at least about 20, or at least about 30 nucleotide region of a sequence of (a)-



(g) that is outside of a region encoding a conserved domain; (j) a nucleotide sequence that encodes a polypeptide having at least 31% sequence identity to a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232; (k) a nucleotide sequence that encodes a polypeptide having at least 60%, or at least 70 %, or at least 80%, or at least 90 %, or at least 95 % sequence identity to a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232; and (l) a nucleotide sequence that encodes a conserved domain of a polypeptide having at least 85%, or at least 90%, or at least 95%, or at least 98% sequence identity to a conserved domain of a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232. A recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-specific promoter operably linked to a nucleotide sequence listed above. The invention also relates to compositions comprising at least two of the above-described polynucleotides.

In a second aspect, the invention comprises an isolated or recombinant polypeptide having an amino acid sequence of the Sequence Listing, or SEQ ID Nos.: 2N-1 where N=1-232, or a polypeptide comprising a subsequence of at least about 10, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above, or comprising a subsequence of at least about 8, or at least about 12, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids outside of a conserved domain.

In another aspect, the invention is a transgenic plant comprising one or more of the above-described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a nucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any appropriate plant, including, but not limited to, *Arabidopsis*, mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, sugarbeet, canola, peanut, rosaceous fruits, vegetable brassicas, and mint or other labiates.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.



In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase, a polymerase and a primer, a cloning vector, or with a cell.

5 Furthermore, the invention relates to a method for producing a plant having a modified trait. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for a modified trait.

10 In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the  
15 polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity  
20 or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in a cell of the plant, the expression level of the polypeptide in a cell of the plant, and the modulation of an activity of the polypeptide in a cell of the plant.

25 In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a sequence of the Sequence Listing, SEQ ID Nos.: 1-464, to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium  
30 may comprise a link between one or more sequence strings to a modified plant trait.

In yet another aspect, the invention is a method for identifying a sequence similar to or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database, and  
35 querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides, such as those of SEQ ID Nos.: 1-464,



to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences. Such a method may also be a method of identifying a homolog sequence from a database, where the database comprises a plurality of known plant sequences. These sequences can be ESTs, cDNA, or genomic  
5 fragments. The database may contain sequences that are not "known" in addition to the known sequences, in that sequences may not be assigned or linked to a function or particular characteristic, yet the sequence itself is known. The method of identifying a homolog comprises inputting sequence information selected from one or more of SEQ ID Nos. 1-464; and querying the database to identify a homolog sequence. In this way, homolog sequences from any number  
10 of plant species, cultivars, or strains can be identified from the information of an inputted sequence or a fragment of the sequence. For these methods and for the sequence information, a computer readable medium having stored sequence information of one or more of SEQ ID Nos.: 1-464, or 1-37, or any one particular SEQ ID No., or any group of SEQ ID Nos. in between 1 and 464, can be used. The computer readable medium may include, for example, a floppy disc, a  
15 hard drive, random access memory (RAM), read only memory (ROM), and/or CD-ROM.

A method of the invention may comprise linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant phenotype.

## 20 **Brief Description of the Sequence Listing and the Appendices**

The Sequence Listing provides exemplary polynucleotide (SEQ ID Nos.: 2N-1 where N=1-232) and polypeptide (SEQ ID Nos.: 2N where N=1-232) sequences of the invention. The traits associated with the use of the sequences are included in the Examples or the Appendices.

25 The Tables of the Appendices include homologous sequences and homologs of specific polynucleotides and polypeptides, specific information about those sequences, and data concerning exemplary transgenic plants of the invention. The data and sequence information can be prepared according to the methods of the Examples or those known in the art. The Appendices  
30 include the Tables of this Appendix and those in the files of the Appendices of the priority documents.

Table 3 in the Appendix is a list of: the first 332 sequences from the Sequence Listing; the corresponding GID number (i.e. G28) used throughout to refer to both the cDNA and protein  
35 sequence of a particular transcription factor, and referred to or used in the Appendices of the U.S.



priority documents; and the identification of conserved amino acid domain start and stop sites (conserved domain) within the protein sequence.

5 Table 4 in the Appendix is a list of: selected sequences from the Sequence Listing; their corresponding GID number; the type of transgenic plant produced to determine ectopic expression, altered expression, or trait (either Knockout of overexpressor as in the Examples); and general descriptions and specific characteristics of the transgenic plant's traits as compared to a wild type, reference, or control plant.

10 Table 5 of the Appendix is a list of: selected sequences from the Sequence Listing; their corresponding GID number; the identification of the one or more homolog sequences and the corresponding GID numbers; the type of sequence of the particular SEQ ID No.; and the identification of conserved amino acid domain start and stop sites (conserved domain) within the protein sequence.

15 Table 6 of the Appendix is a list of selected homologs identified from genomic, EST, or other database, as referred to in the Examples. Table 6 includes: the particular SEQ ID No. in the Sequence Listing used to identify exemplary homologs; the corresponding GID number of the SEQ ID No. sequence; the Genbank NID reference number associated with the exemplary  
20 homolog identified (from which one of skill in the art can produce a genomic, cDNA, and/or EST sequence and corresponding polynucleotide); the P-value related to the particular, exemplary homolog comparison to the GID sequence; the percent identity between the GID sequence and the homolog; and the species the exemplary homolog sequence is derived from. All of the sequences referred to in the Table, as well as fragments or parts of these sequences,  
25 can be used in accordance with this invention, for example to produce transgenic plants with ectopic expression or altered expression.

#### Detailed Description of Exemplary Embodiments

In an important aspect, the present invention relates to polynucleotides and polypeptides, e.g. for  
30 modifying phenotypes of plants. Throughout this disclosure, various information sources are referred to and/or are specifically incorporated. The information sources include scientific journal articles, patent documents, textbooks, and web pages, for example. While the reference to these information sources clearly indicates that they can be used by one of skill in the art, applicants specifically incorporate each and every one of the information sources cited herein, in  
35 their entirety, whether or not a specific mention of "incorporation by reference" is noted. The



contents and teachings of each and every one of the information sources can be relied on and used to make and use embodiments of the invention.

The polynucleotides of the invention encode plant transcription factors or fragments of them.

- 5 As one of ordinary skill in the art recognizes, transcription factors can be identified by the presence of a region or domain of structural similarity or identity to a specific consensus sequence or the presence of a specific consensus DNA-binding site (*see, for example*, Riechmann *et al.*, *Science* 290: 2105-2110 (2000)). The plant transcription factors may belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family
- 10 (Riechmann and Meyerowitz (1998) *Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang *et al.* (1992) *Plant Cell* 4:1575-1588); the zinc finger protein (Z)
- 15 family (Klug and Schwabe (1995) *FASEB J.* 9: 597-604); the homeobox (HB) protein family (Duboule (1994) *Guidebook to the Homeobox Genes*, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein *et al.* (1996) *Mol. Gen. Genet.* 250:7-16); the NAM protein family (Souer *et al.* (1996) *Cell* 85:159-170); the IAA/AUX proteins (Rouse *et al.* (1998) *Science* 279:1371-1373); the HLH/MYC protein family (Littlewood *et al.* (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker *et al.* (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster *et al.* (1994) *FASEB J.* 8:192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva *et al.* (1993) *Plant J.* 4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl.*
- 25 *Acids Res. Mol. Biol.* 54:35-100); the scarecrow (SCR) family (Di Laurenzio *et al.* (1996) *Cell* 86:423-433); the GF14 family (Wu *et al.* (1997) *Plant Physiol.* 114:1421-1431); the polycomb (PCOMB) family (Kennison (1995) *Annu. Rev. Genet.* 29:289-303); the teosinte branched (TEO) family (Luo *et al.* (1996) *Nature* 383:794-799); the ABI3 family (Giraudat *et al.* (1992) *Plant Cell* 4:1251-1261); the triple helix (TH) family (Dehesh *et al.* (1990) *Science* 250:1397-1399); the
- 30 EIL family (Chao *et al.* (1997) *Cell* 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) *Journal of Biological Chemistry* 265:8573-8582); the SIFA family (Zhou *et al.* (1995) *Nucleic Acids Res.* 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109:723); the YABBY family (Bowman *et al.* (1999) *Development* 126:2387-96); the PAZ family (Bohmert *et al.* (1998) *EMBO J.* 17:170-80); a family of miscellaneous (MISC)
- 35 transcription factors including the DPBF family (Kim *et al.* (1997) *Plant J.* 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the golden



- (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936), the TUBBY family (Boggin et al, (1999) *Science* 286:2119-2125), the heat shock family (Wu C (1995) *Annu Rev Cell Dev Biol* 11:441-469), the ENBP family (Christiansen et al (1996) *Plant Mol Biol* 32:809-821), the RING-zinc family (Jensen et al. (1998) *FEBS letters* 436:283-287), the PDBP family (Janik et al
- 5 *Virology*. (1989) 168:320-329), the PCF family (Cubas P, et al. *Plant J.* (1999) 18:215-22), the SRS (SHI-related) family (Fridborg et al *Plant Cell* (1999) 11:1019-1032), the CPP (cysteine-rich polycomb-like) family (Cvitanich et al *Proc. Natl. Acad. Sci. U S A.* (2000) 97:8163-8168), the ARF (auxin response factor) family (Ulmasov, et al. (1999) *Proc. Natl. Acad. Sci. USA* 96: 5844-5849), the SWI/SNF family (Collingwood et al *J. Mol. End.* 23:255-275), the ACBF
- 10 family (Seguin et al *Plant Mol Biol.* (1997) 35:281-291), PCGL (CG-1 like) family (*Plant Mol Biol.* (1994) 25:921-924) the ARID family (Vazquez et al *Development.* (1999) 126: 733-42), the Jumonji family, Balciunas et al (*Trends Biochem Sci.* (2000) 25: 274-276), the bZIP-NIN family (Schauser et al *Nature.* (1999) 402: 191-195), the E2F family Kaelin et al (1992) *Cell* 70: 351-364) and the GRF-like family (Knaap et al (2000) *Plant Physiol.* 122: 695-704. As indicated by
- 15 any part of the list above and as known in the art, transcription factors have been sometimes categorized by class, family, and sub-family according to their structural content and consensus DNA-binding site, for example. All of the classes and many of the families and sub-families are listed here. However, the inclusion of one sub-family and not another, or the inclusion of one family and not another, does not mean that the invention does not encompass polynucleotides or
- 20 polypeptides of a certain family or sub-family. The list provided here is merely an example of the types of transcription factors and the knowledge available concerning the consensus sequences and DNA-binding site motifs that help define them (each of the references noted above are specifically incorporated herein by reference).
- 25 In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e, expression) of proteins; as regulators of plant gene expression; as diagnostic probes for the presence of complementary or partially complementary nucleic acids
- 30 (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like; as substrates for cloning e.g., including digestion or ligation reactions; and/or for identifying exogenous or endogenous modulators of the transcription factors.
- 35 A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least



about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

10

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid. A recombinant polynucleotide of the invention can be a cDNA or cDNA-derived polynucleotide that contains the entire coding region of a protein but does not contain the introns of genomic DNA. A recombinant polynucleotide of the invention can also be, or be derived from, a fragment of an isolated genomic DNA that is a full length coding region in that it contains the start of translation of a particular protein through the termination of translation of that same protein, where the start and termination sites are known.

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An "isolated polynucleotide" is a polynucleotide or nucleic acid molecule, whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

25

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the

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isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

5 The term "transgenic plant" refers to a plant that contains genetic material not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation, but any method can be used as one of skill in the art  
10 recognizes.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the  
15 expression of the polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cell or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

20 The phrase "ectopic expression or altered expression," or the terms "ectopic expression" or "altered expression" in reference to a polynucleotide or polypeptide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or  
25 polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression  
30 patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the phrase "ectopic expression or altered expression," or the terms "ectopic expression" or altered expression" may further relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous  
35 modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.



The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain is a subsequence of the polypeptide that performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding site or domain that binds to a DNA promoter region, an activation domain, or a domain for protein-protein interaction. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically of at least about 15 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein. A fragment or domain can be referred to as outside a consensus sequence or outside a consensus DNA-binding site that is known to exist or that exists for a particular transcription factor class, family, or sub-family. In this case, the fragment or domain will not include the exact amino acids of a consensus sequence or consensus DNA-binding site of a transcription factor class, family or sub-family, or the exact amino acids of a particular transcription factor consensus sequence or consensus DNA-binding site. Furthermore, a particular fragment, region, or domain of a polypeptide, or a polynucleotide encoding a polypeptide, can be "outside a conserved domain" if all the amino acids of the fragment, region, or domain fall outside of a defined conserved domain(s) for a polypeptide or protein. The conserved domains for polypeptides of the Sequence Listing are listed in the Tables of the Appendices. Also, many of the polypeptides of the Appendices have conserved domains specifically indicated by start and stop sites. A comparison of the regions of the polypeptides in the Sequence Listing, or of those in the Appendices, allows one of skill in the art to identify conserved domain(s) for any of the polypeptides listed or referred to in this disclosure, including those in the Appendices and homologs from other species, strains, or cultivars.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch or oil content of seed or leaves, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance. Any technique can be used to measure the



amount of, comparative level of, or difference in any selected chemical compound or macromolecule in the transgenic plants, however.

- “Trait modification” refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.
- Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyl lipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.



### Polynucleotides and Polypeptides of the Invention

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides and homologue polypeptide-encoding polynucleotides (homologs), and isolated or recombinant polynucleotides encoding the polypeptides, or novel variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here. These polypeptides and polynucleotides may be employed to modify one or more of a plant's characteristics or traits.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor or knockout plants and the changes in the characteristic(s) or trait(s) of the plants observed. Therefore, the polynucleotides and polypeptides can be employed to improve the characteristics of plants.

### Producing Polypeptides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides



can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed., and 3<sup>rd</sup> Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, ("Sambrook"); Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2001) ("Ausubel"); and Current Protocols in Cell Biology, Bonifacino, J.S. et al. (eds.) 2001 John Wiley & Sons, Inc.

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, *all supra*.



Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically  
5 ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized,  
10 purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

#### Homologous Sequences

Sequences homologous, i.e., that share significant sequence identity or similarity, to those  
15 provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as  
20 banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype  
25 can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such  
30 pine, poplar and eucalyptus, or mint or other labiates.

Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity, or at least about 30% amino acid sequence identity outside of a known consensus sequence or consensus DNA-binding site. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75%  
35 or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences, or with the listed sequences but excluding or outside a known consensus sequence or



consensus DNA-binding site, or with the listed sequences excluding or outside one or all conserved domain. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences, or to the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site or outside one or all conserved domain. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences, or to a listed sequence but excluding or outside a known consensus sequence or consensus DNA-binding site, or outside one or all conserved domain. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity. Transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence identity over the entire length of the polypeptide or the homolog.

20

#### Identifying Polynucleotides or Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH)



at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C. For example, high stringency is about 0.2 x SSC, 0.1% SDS at 65° C. Ultra-high stringency will be the same conditions except the wash temperature is raised about 3 or about 5° C, and ultra-ultra-high stringency will be the same conditions except the wash temperature is raised about 6 or about 9°C. For identification of less closely related homologs, washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC, as known in the art.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radioactive label, or the like.

Alternatively, transcription factor homolog polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homolog nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it



is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

#### Sequence Variations

- 5 It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences is capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

10

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid - serine. Accordingly, at each position in the sequence where there is a codon for serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

15

**Table 1**

Amino acid			Possible Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGA	GGC	GGG	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATA	ATC	ATT			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCA	CCC	CCG	CCT		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT



Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide. These conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.



**Table 2**

<b>Residue</b>	<b>Conservative Substitutions</b>
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

5

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The

10 substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side



chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

#### 5    **Further Modifying Sequences of the Invention – Mutation/Forced Evolution**

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to  
10    change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution  
15    methods are described, e.g., by Stemmer (1994) Nature 370:389-391, and Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751, and U.S. Patents 5,811,238; 5,811,654; 6,251,604; and 6,177,263. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

20    Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These  
25    modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the  
30    products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant  
35    RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be



modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

- 5 The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to  
10 change codon preference, to introduce splice sites, etc.

- Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived  
15 from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from  
20 bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

#### Expression and Modification of Polypeptides

- Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or  
25 RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

- 30 The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been  
35 inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably



linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

- General texts that describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.
- Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).
- Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

- Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see*, e.g., Odel et al. (1985) Nature 313:810); the nopaline



synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).



Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

#### Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acid, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be an eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York)



pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA  
5 plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

10 The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants, which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

15 For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the  
20 vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

#### 25 Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during  
30 recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated  
35 amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature.



#### Identification of Additional Factors

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homolog of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins:



one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be performed.

#### 15 Identification of Modulators

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northern, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998, and supplements through 2001). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator



composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

- 5 In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.
- 10
- A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.
- 15
- Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.
- 20
- 25
- 30 In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of
- 35



modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

5 Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

10

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of  
15 relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is,  
20 known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators that inhibit transcriptional activation or transcriptional  
25 repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test  
30 compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In  
35 some cases, an alteration in a plant phenotype can be detected following contact of a plant (or



plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

#### Subsequences

5 Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like,  
10 according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18  
15 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologs of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended  
20 along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a  
25 subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

30

#### Production of Transgenic Plants

##### Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve  
35 the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or



transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved characteristics, by altering expression levels of a particular transcription factor is described further in the Examples.

5

#### **Antisense and Cosuppression Approaches**

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.



Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer

5 RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue

10 cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with

15 antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences

20 comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene

25 silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor

30 homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a

35 transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).



A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the  
5 intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the  
10 endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery  
15 in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057, which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

20 The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the  
25 polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue  
30 of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover,  
35 etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.),



*Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

5

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence into a plant in a manner to cause stable or transient expression of the sequence.

15

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

20

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

25

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

30

35 **Integrated Systems – Sequence Identity**



Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link  
5 certain functional benefits, such improved characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public  
10 sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of  
15 Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence  
20 similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods for determining sequence relationships can be used, including manual  
25 alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill:

30 One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length  
35 W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the



- neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters
- 5 M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring
- 10 residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62
- 15 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915). Unless otherwise indicated, "sequence identity" here refers to the % sequence identity generated from a tblastx using the NCBI version of the algorithm at the default settings using gapped alignments with the filter "off" (<http://www.ncbi.nlm.nih.gov/>).
- 20 In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For
- 25 example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using
- 30 progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character

35 strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity.



The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element, which displays an alignment produced by the alignment instruction set.

- 5 The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may be implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in  
10 certain preferred embodiments, the computers may be components of an intranet or an internet.

- Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant  
15 phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

- Any sequence herein can be entered into the database, before or after querying the database.  
20 This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a  
25 remote terminal or computer across an internet or intranet.

### Examples

The following examples are intended to illustrate, but not limit, the scope of the present invention.

30

#### Example I: Full Length Gene Identification and Cloning

- Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower,  
35 depending on the length of the query sequence. Putative transcription factor sequence hits were



then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60°C) and labeled with <sup>32</sup>P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO<sub>4</sub> pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60°C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

#### Example II: Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with Sall and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were



ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

5

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

#### Example III: Transformation of *Agrobacterium* with the Expression Vector

- 10 After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance ( $A_{600}$ ) of 0.5 – 1.0 was reached.
- 15 Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl
- 20 aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

- Agrobacterium* cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of
- 25 *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100
- 30 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

- 35 **Example IV: Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector**



- After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance ( $A_{600}$ ) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044  $\mu$ M benzylamino purine (Sigma), 200  $\mu$ L/L Silwet L-77 (Lehle Seeds) until an absorbance ( $A_{600}$ ) of 0.8 was reached.
- 10 Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75  $\mu$ E/m<sup>2</sup>/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After
- 15 flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat

20 surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

#### 25 **Example V: Identification of *Arabidopsis* Primary Transformants**

- Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H<sub>2</sub>O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second
- 30 wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H<sub>2</sub>O. The
- 35 seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH),



1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75  $\mu\text{E}/\text{m}^2/\text{sec}$ ) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants ( $T_1$  generation) were visible and obtained. These seedlings were transferred first to fresh selection  
 5 plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds ( $T_2$ ) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant  
 10 polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

#### **Example VI: Identification of *Arabidopsis* Plants with Transcription Factor Gene**

##### **15 Knockouts**

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to  
 20 each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the  
 25 genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

#### **30 Example VII: Identification of Modified Phenotypes in Overexpression or Gene Knockout Plants**

Experiments were performed to identify those transformants or knockouts that exhibited modified biochemical characteristics. Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; prenol lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or  
 35 alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0, 18:3 (linolenic



acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmasterol or the like, glucosinolates, protein or oil levels.

- 5 Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H<sub>2</sub>SO<sub>4</sub> and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H<sub>2</sub>SO<sub>4</sub> (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were  
10 analyzed with a Supelco SP-2330 column.

- Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes,  
15 the extraction solvent is applied to a DEAE Sephadex column which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

- For wax alkanes, samples were extracted using an identical method as fatty acids and extracts  
20 were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographed on a J&W DB35 mass spectrometer (J&W Scientific).

- To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol  
25 determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x  
30 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in  
35 hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2% methylene chloride in hexane



and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25  $\mu$ m phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al., Plant  
5 Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers  
found in *Arabidopsis* leaves. Soluble sugars were separated from sugar polymers by extracting  
leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides  
was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated  
by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH<sub>4</sub>, then  
10 were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID.  
Identity of the peaks was determined by comparing the retention times of known sugars  
converted to the corresponding alditol acetates with the retention times of peaks from wild-type  
plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x  
250  $\mu$ m x 0.2  $\mu$ m) using a temperature program beginning at 180° C for 2 minutes followed by an  
15 increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is  
increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to  
room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2  
20 progeny plants were subjected to analysis by Near Infrared Reflectance (NIR) using a Foss  
NirSystems Model 6500 with a spinning cup transport system.

Experiments were performed to identify those transformants or knockouts that exhibited an  
improved pathogen tolerance. For such studies, the transformants were exposed to biotrophic  
25 fungal pathogens, such as *Erysiphe orontii*, and necrotrophic fungal pathogens, such as *Fusarium*  
*oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various  
annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-  
Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri  
dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was  
30 prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato  
dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the  
plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown  
overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant  
tissue was harvested and frozen in liquid nitrogen 48 hours post infection.

35



*Erysiphe orontii* is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

*Botrytis cinerea* is a necrotrophic pathogen. *Botrytis cinerea* was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (-sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens *Pseudomonas syringae* pv *maculicola* strain 4326 and pv *maculicola* strain 4326 was performed by hand inoculation at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease scoring occurred at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

In some instances, expression patterns of the pathogen-induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Meth. in Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and



Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagen software purchased from BioDiscovery (Los Angeles, CA).

5 Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8° C ), heat stress (6 hour exposure to 32-37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour  
10 exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (Nitrogen: all components of MS medium remained constant except N was reduced to 20mg/L of  $\text{NH}_4\text{NO}_3$ , or Phosphate: All components of MS medium except  $\text{KH}_2\text{PO}_4$ , which was replaced by  $\text{K}_2\text{SO}_4$ , Potassium: All components of MS medium except removal of  $\text{KNO}_3$  and  $\text{KH}_2\text{PO}_4$ , which were replaced by  $\text{NaH}_2\text{PO}_4$ ).

15 Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

20 Experiments were performed to identify those transformants or knockouts that exhibited modified sugar-sensing. For such studies, seeds from transformants were germinated on media containing 5% glucose or 9.4% sucrose which normally partially restrict hypocotyl elongation. Plants with altered sugar sensing may have either longer or shorter hypocotyls than normal plants  
25 when grown on this media. Additionally, other plant traits may be varied such as root mass.

Flowering time was measured by the number of rosette leaves present when a visible inflorescence of approximately 3 cm is apparent. Rosette and total leaf number on the progeny stem are tightly correlated with the timing of flowering (Koornneef et al (1991) *Mol. Gen. Genet*  
30 229:57-66). The vernalization response was measured. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside plates containing freshly sown non-vernalized controls. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent.

35



Modified phenotypes observed for particular overexpressor or knockout plants are provided in Table 4 of the Appendix and the Appendices of the priority documents. For a particular overexpressor that shows a less beneficial characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

The sequences of the Sequence Listing SEQ ID Nos. 1-464 or those disclosed here can be used to prepare transgenic plants and plants with altered traits. The specific transgenic plants listed below are produced from the sequences of the Sequence Listing, as noted. The Tables of the Appendix and the Appendices of the priority documents provide exemplary polynucleotide (cDNA) and polypeptide (protein) sequences of the invention. The Tables include SEQ ID Nos., the corresponding reference number (GID), and/or the identification of the start and stop residues of any conserved domain in the polypeptide sequence.

The transgenic plants of the invention display an ectopic expression or altered expression of one or more polypeptides encoded by the full length coding regions in the Sequence Listing, the homologs and/or fragments of the Tables of the Appendices, and/or another polypeptide described in this document, when the transgenic plant is compared to a wild type, control, or reference plant. As a result, the transgenic plants possess advantageous traits, as detailed by the limited and exemplary discussion of comparison data below.

Some of the polypeptides encoded by the full length coding regions in the Sequence Listing and the homologs and fragments of them noted in the Tables of the Appendices modulate a plant's defense response and even confer multipathogen resistance. These traits are extremely useful in many commercial crops and plants. For example, plants overexpressing G28 (SEQ ID NO.: 1 and 2) are more tolerant to infection by fungal pathogens, such as *Erysiphe orontii*, *Sclerotinia sclerotiorum*, or *Botrytis cinerea*. Similarly, plants overexpressing G1792 (SEQ ID NO.: 5 and 6) are more tolerant to infection by necrotrophic fungal pathogens, such as *Fusarium oxysporum* or *Botrytis cinerea*, and display increased resistance to fungal pathogens and to *Erysiphe orontii*. Increased tolerance to infection by *Fusarium oxysporum* is observed in G1047 (SEQ ID NO.: 23 and 24) and G1363 (SEQ ID NO.: 29 and 30) overexpressing plants. Knockout mutants also demonstrate the particular polypeptide's involvement in a defense response. A G1880 (SEQ ID NO.: 435 and 436) knockout mutant is more tolerant to *Botrytis cinerea*. G1196 (SEQ ID NO.: 27 and 28) knockout mutant plants show increased susceptibility to *Botrytis cinerea*. Manipulating the content or expression of any of these polypeptides, or fragments or homologs



of them, can therefore improve a plant's defense response, tolerance, or susceptibility to pathogens and infection.

- A number of the polypeptides encoded by the full length coding regions in the Sequence Listing, and homologs and fragments of them noted in the Tables of the Appendices, regulate the transition from vegetative to reproductive growth. These traits can be useful in crops and plants where fruit or seed is commercially valuable, for example. Overexpression of G180 (SEQ ID NO.: 53 and 54), G227 (SEQ ID NO.: 313 and 314), G1841 (SEQ ID NO.: 455 and 456), and G2347 (SEQ ID NO.: 477 and 478) results in an early flowering phenotype, whereas overexpression of G748 (SEQ ID NO.: 125 and 126) or G2007 (SEQ ID NO.: 457 and 458) results in late flowering. Other polypeptides and polynucleotides for modulating flowering time include G590 (SEQ ID NO.: 107 and 108), G1760 (SEQ ID NO.: 31 and 32), G1820 (SEQ ID NO.: 33 and 34), and G2010 (SEQ ID NO.: 37 and 38).
- The response to a variety of abiotic or environmental stresses is modified by an additional set of polypeptides encoded by the full length coding regions of the Sequence Listing and the homologs and fragments listed in the Tables of the Appendices. These traits can be useful in manipulating the growth medium or environment for plants, for example. G226 overexpressing plants are more tolerant to low nitrogen and high salt stress. G2130 (SEQ ID NO.: 417 and 418) overexpressors show improved heat stress tolerance in a germination assay. G867 (SEQ ID NO.: 15 and 16) and G1930 (SEQ ID NO.: 35 and 36) overexpressing plants show increased seedling vigor in germination assays on both high salt and high sucrose containing media. G912 (SEQ ID NO.: 19 and 20) is a member of the AP2 family related to the CBF1, CBF2 and CBF3 genes. Plants overexpressing G912 (SEQ ID NO.: 19 and 20) exhibit increased freezing and drought tolerance. Additional polypeptides and polynucleotides modifying stress responses include G175 (SEQ ID NO.: 9 and 10), G926 (SEQ ID NO.: 459 and 460), and G1820 (SEQ ID NO.: 33 and 34).
- Several transcription factors have been identified that can affect metabolic processes. These plants can be used to optimize or improve production of various plants extracts used for commercial products including, for example, foodstuffs, paper and paper-related products, edible plants, fruits and vegetables with improved properties, organic compounds, oils and alcohols, additives and binders for pharmaceutical or cosmetic products, and industrial products. For instance, plants overexpressing G1750 (SEQ ID NO.: 395 and 396) produce seed with increased seed oil content. Overexpression of G280 (SEQ ID NO.: 461 and 462) results in an increase in gamma and delta tocopherol in leaves. G663 (SEQ ID NO.: 13 and 14) overexpressors exhibit



constitutive anthocyanin production in seeds, leaves and roots. In contrast, seeds of G156 (SEQ ID NO.: 7 and 8) knockout mutant plants exhibit a colorless phenotype indicative of the involvement of the gene in the regulation of the anthocyanin pathway.

- 5 Also of particular interest are polypeptides involved in plant growth and development. The following polypeptides encoded by the full length coding regions of the Sequence Listing and the homologs and fragments listed in the Tables of the Appendices are some examples. Transgenic plants overexpressing G1073 exhibit a substantial increase in size. An increase in size is also observed in G189 (SEQ ID NO.: 11 and 12) overexpressing plants. Transgenic plants
- 10 overexpressing G634 (SEQ ID NO.: 3 and 4) exhibit a substantial increase in trichome number. Null mutations in G374 (SEQ ID NO.: 463 and 464) and in G877 (SEQ ID NO.: 17 and 18) result in embryo lethality. A G979 (SEQ ID NO.: 153 and 154) knockout mutation results in delayed seed ripening.
- 15 G987 (SEQ ID NO.: 21 and 22) knockout mutant plants can only be grown on sucrose-containing medium. In addition, G987 appears to control an aspect of thylakoid membrane development and the tocopherol, carotenoid, and/or chlorophyll content of the plant is altered. Since the compounds represented by these groups are commercially important in a number of industries, including use as dietary supplements, a transgenic plant's altered tocopherol,
- 20 carotenoid, and/or chlorophyll content is an advantageous and valuable trait.

**G634 (SEQ ID. Nos 3 and 4), G1841 (SEQ ID. Nos 455 and 456), G979 (SEQ ID. Nos 153 and 154): modified plant development**

- 25 **G634:** Overexpression of G634 produced an increase in trichome density on later arising rosette leaves, cauline leaves, inflorescence stems and sepals. Trichomes of 35S::G634 plants also appeared slightly larger than those of wild type, and stem trichomes were more highly branched. These effects were not apparent in young seedlings and became most prominent at the later vegetative and early reproductive phase. The trichome phenotype was apparent in approximately
- 30 50% of primary transformants and two out of the three T2 lines.

- G1841:** Overexpression of G1841 markedly reduced the time to flowering. This early flowering phenotype was consistently observed over multiple plantings for each of the three T2 lines, and in a majority of primary transformants. Additionally, 35S::G1841 plants appeared slightly pale
- 35 and had rather flat leaves compared to wild-type controls.



In continuous light conditions, 35S::G1841 plants produced flower buds up to five days earlier than wild-type controls. In repeat sowings the plants appeared to grow slightly faster than controls; although they switched to making flower buds several days early, they had a similar number of primary rosette leaves to wild type.

5

In addition to showing accelerated flowering under 24 hours light, plants from all three T2 populations produced flowers up to 2 weeks earlier than controls under a 12 hour photoperiod.

10 **G979:** Seeds homozygous for a T-DNA insertion within G979 showed delayed ripening, slow germination, and developed into small, poorly fertile plants, indicating that G979 might be involved in seed development processes.

15 Siliques of heterozygous plants were examined for seed abnormalities. Approximately 25% of the seeds contained in young green siliques were pale in coloration. In older, brown siliques, approximately 25% of the seeds were green and appeared slow ripening, whereas the remaining seeds were brown. Thus, it seemed likely that the seeds with altered development were homozygous for the T-DNA insertion, whereas the normal seeds were wild type and heterozygous segregants.

20 Furthermore, it was observed that approximately 25% of the seed from G979 KO heterozygous plants showed impaired (delayed) germination. Upon germination, these seeds produced extremely tiny seedlings that often did not survive transplantation. A few homozygous plants, small and sickly looking, could be grown, and produced siliques that contained seeds that were small and wrinkled compared to wild type.

25

On the basis of these results obtained with G979 knockout mutant lines, G979 can be used to alter or modify seed germination properties and performance.

30 **G1792 (SEQ ID. Nos 5 and 6), G2130 (SEQ ID. Nos 417 and 418), G926 (SEQ ID. Nos. 459 and 460): modified stress response**

**G1792:** 35S::G1792 plants were more tolerant to the fungal pathogens *Fusarium oxysporum* and *Botrytis cinerea*: they showed fewer symptoms after inoculation with a low dose of each pathogen. This result was confirmed using individual T2 lines.

35



35S::G1792 plants also showed more tolerance to growth under nitrogen-limiting conditions. In a root growth assay under conditions of limiting N, 35S::G1792 lines were slightly less stunted. In a germination assay that monitors the effect of C on N signaling through anthocyanin production on high sucrose plus and minus, the 35S::G1792 lines make less anthocyanin on high sucrose plus glutamine, suggesting that the gene could be involved in the plants ability to monitor their carbon and nitrogen status.

G1792 overexpressing plants also showed several mild morphological alterations such as abnormal phyllotaxy, alterations in leaf and flower development, and flowering time.

G2130: G2130 overexpressing lines show more seedling vigor in a heat stress tolerance germination assay compared to wild-type controls. No difference from wild-type was detected in the heat stress response assay performed on older seedlings suggesting the phenotype could be specific for germination in the G2130 overexpressors. Lines G2130-3 and G2130-4 show the heat tolerant phenotype, line G2130-2 show the weakest phenotype. G2130 overexpressing lines are also somewhat more sensitive to chilling, the plants are more chlorotic and stunted when grown at 8°C compared to the wild-type controls. They also show more disease symptoms following inoculation with a low dose of the fungal pathogen *Botrytis cinerea* in two separate experiments.

G926: G926 knockout mutant plants show more tolerance to osmotic stress in a germination assay in three separate experiments. They show more seedling vigor than wild-type controls when germinated on plates containing high salt and high sucrose. They also show insensitivity to ABA in repeated germination assays.

These analyses revealed that in the absence of G926 function, plants are more tolerant to osmotic stress. This osmotic stress tolerance could be related to the plant's apparent insensitivity to the growth hormone ABA because ABA plays an important regulatory role in the initiation and maintenance of seed dormancy. G926 may function as part of a checkpoint for germinating seeds and loss of G926 function promotes germination regardless of the osmotic status of the environment. G926 has utility in modifying plant stress responses.

G280 (SEQ ID. Nos. 461 and 462), G1323 (SEQ ID. Nos 203 and 204): modified biochemistry



**G280:** Overexpression of G280 in *Arabidopsis* resulted in an increase in leaf gamma and delta tocopherol in all three lines tested. Overexpression of G280 produced a reduction in overall plant size and accelerated the rate of leaf senescence in the rosette.

- 5     **G1323:** In two G1323 overexpressing lines, line 5 and 7, seeds had more protein and less oil than controls. Otherwise, overexpression of G1323 in *Arabidopsis* did not result in any biochemical phenotype. These experiments were repeated and a similar biochemical phenotype was observed.

10     **G2557 (SEQ ID Nos. 289 and 290), G2143 (SEQ ID Nos. 285 and 286), G1063 (SEQ ID Nos 167 and 168) (HLH/MYC)**

Overexpression of each of these genes affected plant growth, inflorescence architecture, and resulted in the development of carpelloid tissues in ectopic positions.

- 15     **G2557:** Twenty independent 35S::G2557 *Arabidopsis* primary transformants were obtained. Of these plants, 19/20 exhibited carpelloid tissue in the outer whorl organs of flowers. In some instances ovules developed from these ectopic carpels. The central carpel of 35S::G2557 flowers was also sometimes borne on a long pedicel-like structure, indicating that overexpression of this gene could influence determinacy of the floral meristem. Additionally, 35S::G2557 plants were  
20     often smaller, darker green and possessed narrow leaves and elongated cotyledons compared to wild type.

- G2143:** Twenty independent 35S::G2143 *Arabidopsis* primary transformants were obtained. All 20 plants developed ectopic carpelloid tissue. In some cases entire flowers were replaced by  
25     a disorganized mass of this tissue. Additionally, 35S::G2143 plants were often smaller, darker green and possessed narrow leaves and elongated cotyledons compared to wild type. In some cases the shoot tips of G2413 plants aborted in a 'pin-like' structure.

- G1063:** Seventeen independent 35S::G1063 *Arabidopsis* primary transformants were obtained.  
30     5/17 of these lines exhibited flowers in which outer whorl organs displayed carpelloid features. In some cases flowers were completely replaced by a carpelloid mass of tissue and defined individual organs could not be distinguished. The shoots of these plants also occasionally terminated in a 'pin-like' structure. The majority of 35S::G1063 plants were smaller than wild type and often had altered leaf shape.

35



Based on the above phenotypes, these genes might be applied to manipulate flower structure and development, fertility, seed-pod development, leaf coloration and overall plant architecture. Specifically, the genes might be used to manipulate floral organ identity or instigate the formation of carpel-derived structures including ovules, embryos and seeds.

5

**G2509 (SEQ ID Nos 287 and 288) (AP2)**

Twenty independent 35S::G2509 *Arabidopsis* primary transformants were obtained. All plants exhibited increased secondary shoot development and loss of apical dominance, leading to a shorter bushier stature than wild type. G2509 could be used to modify plant architecture. This could produce plants more resistant to wind and rain and influence yield. Additionally, changing plant architecture could generate novel interesting forms for the ornamental plant market.

10

**G353 (SEQ ID Nos 79 and 80) and G354 (SEQ ID Nos. 81 and 82) (Z(C2H2))**

G353 and G354 constitute a pair of closely related Z(C2H2) genes that influence shoot architecture. Both genes produced comparable effects when overexpressed.

15

G353: A consistent phenotype was noted on inflorescences of 35S::G353 plants. Flowers were oriented downwards and pedicels of flowers and siliques were reduced in length or absent. Floral internodes were also very short. Furthermore, secondary shoots were often observed to grow in a downward direction. These phenotypes were observed in both primary transformants and T2 generation plants. Overexpression of G353 produced additional effects; 35S::G353 were sometimes smaller than wild-type, had abnormal branching patterns and flat leaves.

20

G354: 35S::G354 plants displayed abnormal inflorescences in which flowers were oriented downwards and pedicels were absent or reduced in length. Floral internodes were also short. Additionally, many of the 35S::G354 plants were reduced in size compared to wild type.

25

These genes could be used to modify plant architecture. Specifically, altering the length of flower and fruit stalks could permit more efficient harvesting. In species such as strawberry, changing the length of the fruit stalk could allow fruits to develop above the leaf canopy and reduce the likelihood of fungal infection. The genes might also have applications in producing novel forms of ornamental species in which branches, flowers and fruits develop with unusual orientations.

30

35



**G1494 (SEQ ID Nos. 223 and 224) (HLH/MYC)**

The phenotype of transgenic *Arabidopsis*, over-expressing G1494, indicates that this gene is a core component of the plant light perception/response machinery. 35S::G1494 seedlings displayed very long hypocotyls, bolted early, and exhibited elongation of rosette internodes.

- 5 This latter characteristic resulted in the absence of a defined rosette. The plants also possessed very spindly stems, and narrow pale leaves with elongated petioles. Such features were consistently observed in both primary transformants and T2 generation plants. These phenotypes are comparable to those of mutants defective in the *PHYTOCHROME* genes, which encode proteins involved in the perception of light conditions. In particular, the 35S::G1494 phenotype
- 10 is almost identical to that described for the *phyA;phyB;phyD* triple mutant (Devlin et al., Plant Physiology 119, 909-915). Based upon the 35S::G1494 phenotype, this gene might be applied to manipulate many of the traits which are influenced by the perception and response to light, including seed germination, flowering time, shade response, leaf orientation, architecture and growth habit.

- 15 Additional phenotypes that were observed included G634 (SEQ ID Nos. 3 and 4) (overexpressors had substantially more trichomes on its leaf surfaces), G971 (SEQ ID Nos. 17 and 18) (overexpressors enhanced terpenoid biosynthesis levels) and G1792 (SEQ ID Nos. 5 and 6) (overexpressors showed a broad-based disease resistance).

20

**Example VIII: Identification of Homologous Sequences**

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool

25 (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919).

- 30 Identified *Arabidopsis* homologous sequences are provided in the Tables of the Appendices. The percent sequence identity among these sequences can be as low as 47%, or even 31% or lower sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and
- 35 excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences are compared to sequences representing genes of SEQ IDs Nos. 1-16 using the Washington



University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped alignments with the filter "off," as performed on July 16, 2001 or previously. For each gene of the Sequence Listing, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of  $3.6 \times 10^{-40}$  is  $3.6 \times 10^{-40}$ . In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length.

In addition to computer-based methods for identifying homologs, or indeed in conjunction with them, a fragment of a sequence from the sequence listing, from the Tables of the Appendices, or derived from a homolog sequence identified from a database, is radiolabeled with  $^{32}\text{P}$  by random priming (Sambrook et al., *Molecular Cloning. A Laboratory Manual*, 2<sup>nd</sup> Ed., or 3<sup>rd</sup> Ed., Cold Spring Harbor Laboratory Press, New York) and used to screen a plant cDNA or genomic library. As merely one example, total plant DNA from *Arabidopsis thaliana*, *Nicotiana tabacum*, *Lycopersicon pimpinellifolium*, *Prunus avium*, *Prunus cerasus*, *Cucumis sativus*, or *Oryza sativa* is isolated (Stockinger, E.J., et al., (1996), *J. Heredity*, 87:214-218). Alternatively, cDNA clones of a selected cDNA library are used. Approximately 2 to 10  $\mu\text{g}$  of each DNA sample is restriction digested, transferred to nylon membrane (Micron Separations, Westboro, MA) and hybridized. Alternatively, a library is plated out on growth medium and partially transferred *in situ* to the nylon membrane for hybridization. Exemplary hybridization conditions are: 42°C in 50% formamide, 5X SSC, 20 mM phosphate buffer, 1X Denhardt's, 10% dextran sulfate, and 100  $\mu\text{g}/\text{ml}$  herring sperm DNA. Four low stringency washes at RT in 2X SSC, 0.05% sodium sarcosyl and 0.02% sodium pyrophosphate are performed prior to high stringency washes at 55°C in 0.2X SSC, 0.05% sodium sarcosyl and 0.01% sodium pyrophosphate. High stringency washes are performed until no counts are detected in the washout (Walling, L.L., et al., *Nucl. Acids Res.* 16:10477-10492(1988)). The areas of radioactivity on the membrane correspond to homologous sequences from the library or genomic DNA sample and the associated DNA can be identified, isolated, and cloned into an appropriate vector so that any homologous sequence(s) can be used. Alterations in the stringency of washes, such as employing ultra-high stringency, and ultra-ultra-high stringency, can also be made.

#### Example IX

As noted previously, the introduction of polynucleotides of the invention and full length coding sequences of the invention into the target plant or cell can be accomplished by a variety of techniques known in the art, such as calcium phosphate-DNA precipitation, electroporation,



microinjection, Agrobacterium infection, liposomes, or microprojectile bombardment, for example. Those of ordinary skill in the art can refer to the literature for details and select suitable techniques without undue experimentation. For some plants, using Agrobacterium is a preferred and easy method for transforming plants and cells. This type of transformation has been used for genetic manipulation of more than 120 species of at least 35 different families of plants, including major economic crops such as vegetables, ornamentals, medicinals, fruit, trees and pasture plants (see, for example, Birch, R.G., Annual Rev. Plant Physiology and Plant Molec. Biology 48:297-326 (1997); Gould J.H., Transformation of the Cereals using Agrobacterium, In: R.S. Tuan (Ed.), Methods in Molecular Biology, Humana Press Inc., Totowa, NJ, vol. 62:489-499 (1997)). In fact, this method has become so routine and commonplace that the idea that some species cannot accept the integration of foreign DNA into its genome or that a species lacks the capacity to be transformed has become unacceptable in the art (see de la Riva et al., Electr. J. Biotechnol. Agrobacterium tumefaciens: a natural tool for plant transformation, vol. 1, no. 13, issue of Dec. 15, 1998).

15

A number of vectors can be used to produce transgenic plants. Some of these vectors can replicate in bacterial hosts, plant host cells, and Agrobacterium, as known through many techniques of the art. Expression vectors typically comprise a cassette or region for inserting a coding sequence or transgene that is flanked by a promoter/enhancer and a poly A site. Many variations are possible, including the use of sequences incorporating preferred codons, 5' UTR, 3' UTR, splice donor and acceptor or other intron sequences, internal ribosome entry sites, repressor or suppressor binding sequences, tissue-specific promoters and enhancers, developmentally regulated promoters and enhancers, and inducible promoters and enhancers, for example. Examples of inducible promoters useful in plants include those induced by chemical means, such as the yeast metallothionein promoter, which is activated by concentrations of copper or heavy metal ions. Any appropriate inducible promoter, enhancer, or promoter/enhancer can be selected. One skilled in the art can devise many variations and permutations in selecting and using expression vectors. The vectors may also contain selectable markers for more easily identifying transformed plants. Many types of selectable marker genes are known in the art.

30

If using Agrobacterium, one can select armed or disarmed Ti genes for transforming cells and plants. Either Ti plasmids of Agrobacterium tumefaciens (A. tumefaciens) or root-inducing (Ri) plasmids of Agrobacterium rhizogenes (A. rhizogenes) can be selected. (For reviews of exemplary techniques see, for example, Weissbach & Weissbach, (1988) Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey

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(1988) Plant Molecular Biology, 2d Ed., Blackie, London, Ch. 7-9, and Horsch et al., Science 227:1229 (1985), incorporated herein by reference). The selection of either *A. tumefaciens* or *A. rhizogenes* will depend on the plant being transformed. In general *A. tumefaciens* is the preferred organism for transformation. Most dicotyledons, some gymnosperms, and a few  
5 monocotyledons (e.g. certain members of the Liliales and Arales) are easily susceptible to infection with *A. tumefaciens*. *A. rhizogenes* also has a wide host range, including most dicots and gymnosperms, which includes members of the Leguminosae, Compositae and Chenopodiaceae. Selecting a type of vector and the components of the vector is well within the  
10 ordinary skill of the art.

10 A general and exemplary method for plant transformation with *Agrobacterium* follows. The polynucleotide or the full length coding region (transgene) is inserted into an intermediate or shuttle vector capable of replicating in *E. coli* and suitable for the type of plant used and typically containing a selectable marker. The vector is introduced into an acceptor *A. tumefaciens* strain  
15 through triparental mating (reciprocal recombination between the intermediate vector and the T-DNA region of the acceptor plasmid occurs during triparental mating and the transgene is now part of the T-DNA region that will be transferred). The engineered *A. tumefaciens* strain containing the transgene is cocultivated with a plant explant, from which regenerated plants can be obtained. The explants are cultured in the presence of a selection agent and selecting resistant  
20 cells grow shoots and rooted-shoots. These are regenerated into plants and the regenerated plants screened for the expression of the transgene and selectable marker. The progeny of the transgenic plant is grown and the inheritance of the introduced transgene is determined.

A transgenic plant transformed using *Agrobacterium* typically contains a single copy of the  
25 introduced transgene on one chromosome – it is heterozygous for the transgene. Homozygous plants can also be prepared and can be preferred or more stable in certain plants. One skilled in the art is familiar with breeding and crossing techniques to produce homozygous plants regardless of the type of transformation used. For example, homozygous transgenic plants can be produced through sexually mating an independent segregant that contains a single transgene,  
30 germinating the seed of the plant, and selecting the plants produced for the transgene. In addition, two transformed or transgenic plants can be mated to produce plants having two independently segregating transgenes. Sexually mating progeny produces homozygous plants for both transgenes. Those of skill in the art are also familiar with techniques, such as back-crossing to parental plants, out-crossing with a wild type or non-transgenic plant, and vegetative  
35 propagation, for example, to manipulate plants having one or more transgenes. Any of these



techniques can be employed to produce transgenic plants, seeds, plant cells, or plant tissue or extracts having a polynucleotide or polypeptide of the invention.

- Another common transformation protocol employs plant protoplasts using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these. The selection of a protoplast method depends upon the ability to regenerate that particular plant strain from protoplasts. Many methods for regenerating plants from protoplasts exist and any can be selected for use (see, for example Shillito, R.D. and Saul, M.W., Protoplast Isolation and Transformation, In: Plant molecular biology, A Practical Approach, IRL Press, UK (1988), particularly pp. 161-186; Methods in Enzymology, vol. 118, (Plant Molecular Biology), eds. Weissbach, A. and Weissbach, H., Academic Press, Orlando, Florida (1985); Methods in Enzymology, vol. 153 (Recombinant DNA), eds. Wu, R. and Grossman, L., Academic Press, Orlando, Florida, (1987).
- To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, plants can be regenerated from immature embryos or explants following introduction of vector or expression cassette DNA containing the transgene. The methods used to regenerate transformed cells into whole plants are not critical to this invention and any method suitable for the target plant can be employed. The literature describes numerous techniques for regenerating specific plant types (for example, somatic embryogenesis, Umbeck, P., et al., Genetically transformed cotton (*Gossypium hirsutum* L.) plants, Bio/Technology 5:263 266 (1987)), and other techniques are continually becoming known. One of ordinary skill in the art can refer to the literature for details and select suitable techniques without undue experimentation. In practice, a large number of transformed plants can be routinely regenerated from a transformed plant cell or tissue to increase and maintain a sterile line. Many methods for culturing plant cells and regenerating transformed plants from cells are known in the art and any appropriate method can be selected (see, for example, Plant Tissue and Cell Culture, C. E. Green, D. A. et al., (Eds.), Alan R. Liss, Inc., New York; Experiments in Plant Tissue Culture, Dodds, J. H. et al. (Eds.), 1985, Cambridge University Press; Cell Structure and Somatic Cell Genetics of Plants, Vasil, I. K. (Ed.), 1984, Academic Press; Handbook of Plant Cell Culture, Volume 4, Techniques and Applications, Evans, D.A. et al. (Eds.), 1986, Macmillan Publishing Company).

- In addition, microprojectile bombardment techniques can be used and many have been described in the art. Here, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles (see, for example McCabe et al., Bio/Technology 6:923 (1988)). The metal



particles penetrate through several layers of cells and allow the transformation of cells within tissue explants. These explants or cells of them can then be regenerated into plants.

For example, if soybean is selected, the following method can be used. Somatic embryos, cotyledons, 3-5 mm in length, are dissected from surface of sterilized, immature seeds of the soybean cultivar chosen, and the embryos cultured in light or darkness at 26°C on an appropriate agar medium for 6-10 weeks. Somatic embryos that produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos that multiply, the suspensions are maintained in suspension culture.

10

The soybean embryogenic suspension cultures can be maintained in 35 ml liquid media on a rotary shaker, 150 rpm, at 26°C with fluorescent lighting on a 16:8 hour day/night schedule. Subculturing every two weeks by inoculating approximately 35 mg of tissue into 35 ml of liquid medium maintains the cells.

15

A DuPont Biolistic PDS1000/HE instrument, a BIO RAD PDS-1000/He or other microprojectile device can be used for these transformations. DNA-coated microcarriers, typically tungsten or gold microparticles, are used according to the instruction manual. To 50 µl of a 60 mg/ml 1 µm gold particle suspension is added 5 µl DNA (1 µg/µl), 20 µl spermidine (0.1 M), and 50 µl CaCl<sub>2</sub> (2.5 M). The particle preparation is agitated for three minutes, spun in a microfuge for 10 seconds, and the supernatant is removed. The DNA-coated particles are then washed once in 400 µl 70% ethanol and resuspended in 40 µl of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five µl of the DNA-coated gold particles is loaded on the disk or appropriate carrier for the particle gun.

25

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty petri dish and the residual liquid removed from the tissue with a pipette. For each transformation, approximately 5-10 plates of tissue are normally used. Membrane rupture pressure is set at approximately 1100 psi. The tissue is placed approximately 3.5 inches away from the retaining screen and bombarded three times. Following treatment, the tissue can be divided in half and placed back into liquid and cultured as above.

30

Five to seven days post bombardment, the liquid media is exchanged with fresh media, and eleven to twelve days post bombardment with fresh media containing selection media (if the vector or DNA used also encodes a selectable marker, as it preferably will). The selection media is replaced approximately every week. Seven to eight weeks post bombardment, green,

35



transformed tissue may be observed growing from un-transformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated independently. These suspensions can then be sub-cultured and maintained as clusters of  
5 immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

If maize is selected, immature embryos are excised from cleaned and sterilized ears and placed embryo axis side down (scutellum side up) in a petri plate. These are cultured in 560L medium  
10 for 4 days in the dark. To prepare for bombardment, the embryos are transferred to 560Y medium for 4 hours and arranged within the device target zone.

The DNA is prepared with Tungsten microparticles, for example, using 1 ug DNA in Tris EDTA buffer, 2.5 M CaCl<sub>2</sub>, and 0.1 M spermidine while vortexing. The mixture is sonicated briefly  
15 and incubated under constant vortexing for ten minutes. After a precipitation period, the tubes are centrifuged briefly, and the liquid is removed. The particles are washed with 100% ethanol, centrifuged, and resuspended in 100% ethanol. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated and 10 ul spotted onto the center of each carrier and allowed to dry about 2 minutes before bombardment.

20 All samples receive a single shot at approximately 650 psi. Following bombardment, the embryos are cultured in 560Y medium for 2 days then transferred to 560R selection medium and sub-cultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are sampled by PCR for transgene content and/or activity analysis. Positive lines are  
25 transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation period of 2-4 weeks, well-developed somatic embryos are transferred to 272V medium for germination and then transferred to a lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to potting soil and grown for 1 week in a growth  
30 chamber, and subsequently grown 1-2 weeks in the greenhouse, then grown to maturity.

#### **Example X. Transformation of Cereal Plants with Expression Vector**

A cereal plant, such as corn, wheat, rice, sorghum or barley, can also be transformed with a plasmid vector containing a sequence or polynucleotide of the invention, together with an  
35 operably linked constitutive or inducible promoter, to modify a trait or produce ectopic or altered expression. In these cases, a cloning vector, pMEN020 for example, is modified to replace the



NptII coding region with the BAR gene of *Streptomyces hygroscopicus* to confer resistance to phosphinothricin. The KpnI and BglII sites of the Bar (bialaphos resistance) gene are removed by site-directed mutagenesis with silent codon changes. Preferably, a maize or other plant ubiquitin promoter is inserted in place of the 35S promoter of pMEN020 (see, for example, 5 Christensen et al., *Plant Mol. Biol.* 12:619-632 (1992); and Christensen, et al., *Plant Mol. Biol.* 18:675-689 (1992); Christensen et al., *Transgenic Res.* 5:213-8(1996)). The polypeptide-encoding sequence or cDNA is then inserted downstream of the promoter. Additional expression vector elements can also be inserted, as discussed elsewhere in this document, to optimize expression.

10 Plasmids according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). After microprojectile bombardment 15 the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)).

20 Various homologs, derivative polypeptides, or polypeptide-encoding polynucleotides can be identified and produced from the information in this document. Any technique available can be used and the examples below are merely exemplary.

To identify exemplary variant or derivative polypeptides, polynucleotides, and homologs of the 25 sequences listed here, many techniques, such as using the BLAST program to screen a public (NCBI for example) or commercial (Incyte for example) sequence databases, screening a cDNA or genomic library by hybridization at low or high stringency, and using PCR techniques using degenerate or non-degenerate primers designed to hybridise against the gene you wish to clone, are known in the art. Any GID polynucleotide or cDNA clone can be selected as well as any 30 sequence of the sequence listing. For example, G1073 can be selected. Transgenic plants overexpressing G1073 have the advantageous properties of being large, late flowering, and/or have serrated leaves. The large size and/or late flowering traits would be extremely useful in crops where the vegetative portion of the plant can be commercially harvested (often, vegetative growth stops when plants make the transition to flowering). In this case, it would be 35 advantageous to prevent or delay flowering in order to increase yield or biomass. The plants would also be extremely useful in preparing recombinant therapeutic proteins, such as antibodies



or single chain antibodies. Prevention of flowering would also be useful in plants and crops in order to prevent the spread of transgenic pollen and/or to prevent seed set. G1073 can also be used to manipulate leaf shape.

- 5 In this example, a homolog of G1073 from Glycine max is identified and a construct expressing this Glycine max cDNA is provided. As noted in the Appendices, the NCBI database is screened using the BLAST algorithm and sequences similar to G1073 are identified, including Glycine max cDNA clones or genomic sequences (BF067277, AW349284 and AI736668).
- 10 Using standard techniques, a Glycine max cDNA library is screened using probes derived from the sequence BF067277, AW349284 or AI736668 and a full-length clone is isolated. This full length Glycine max clone can be subcloned into an appropriate expression vector using restriction sites or full-length sequences can be amplified from cDNA or genomic DNA by PCR and subcloned into an appropriate expression vector. Also using standard techniques, a fragment
- 15 incorporating all or part of the Glycine max sequence, or a fragment of another homolog, is produced with substitution or site-specific mutations. This fragment can be used in PCR amplification to replace all or any of the nucleotides to result in amino acid changes or codon changes. Alternatively, oligos incorporating the substitution change(s) can be used in homologous recombination techniques to replace nucleotides in a sequence. Other available
- 20 techniques, known in the art, can also be used. Once the sequence differences between any sequence listed or described here to that of a known sequence is displayed, one of skill in the art can use any available method to make one or more substitution changes in the nucleotides or the polypeptides. These changes will preferably result in changes in the amino acid sequence of the encoded polypeptide, creating a derivative or variant polypeptide.
- 25 The changes or substitutions can also incorporate preferred codons for a particular species or group of plants. Preferred codons for a number of different plants are known in the art. The changes can also delete or add amino acid residues. One skilled in the art is familiar with a variety of techniques for manipulating a polypeptide-encoding sequence to make one or more
- 30 changes, substitutions, deletions, or additions, as desired.

As shown here, the sequences listed have homologs in other plant species. Any of the manipulations, procedures for producing transgenic plants, or analysis of the transgenic plants, can be performed using the homolog sequence in place of the specifically listed sequence. Thus,

35 for example, transgenic plants employing the homolog of G1073 from, for example, *Lycopersicon esculentum*, *Medicago truncatula*, *Oryza sativa*, *Hordeum vulgare*, *Glycine max*,



- Lotus japonicus, Solanum tuberosum, Sorghum propinquum, Pinus taeda, Triticum aestivum, Pisum sativu, Antirrhinum majus, Daucus carota, Nicotiana tabacum, Brassica napus, Zea mays, Volvox carteri f. nagariensis, or Chlamydomonas reinhardtii can be used to create plants having ectopic expression or altered expression of the G1073 homolog. Chimeric sequences, employing
- 5 parts of more than one homolog or parts of a specific sequence, such as G1073, and its homolog(s), can also be created and used. More than one homolog or recombinant polynucleotide can be introduced into a plant to produce a transgenic plant, as known in the art.
- 10 All references, publications, patent documents, web pages, links, sequences of Genbank identifiers, sequences of genomic or EST database identifiers, and other documents cited or mentioned herein are hereby incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to specific embodiments and examples,
- 15 it should be understood that one of ordinary skill can make various modifications without departing from the spirit of the invention. The scope of the invention is not limited to the specific embodiments and examples provided.



What is claimed is:

1. A transgenic plant comprising a recombinant polynucleotide having a nucleotide sequence selected from the group:
  - 5 (a) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from those of SEQ ID NOs.: 2N where N= 1-232, or a complementary nucleotide sequence thereof;
  - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
  - 10 (c) one of SEQ ID NOs.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof;
  - (d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of (c);
  - (e) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
  - 15 (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved domain of any of (a)-(e);
  - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;
  - (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any
  - 20 of (a)-(g);
  - (i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any of (a)-(g);
  - (j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any of (a)-(g);
  - 25 (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
  - (l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232; or
  - 30 (m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
  - (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside
  - 35 of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;



- (o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- 5 (p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 90% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- (q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- 10 (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos.: 2N where N=1-232;
- 15 (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos.: 2N where N=1-232;
- (u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos. 2N where N=1-232;
- (v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos. 2N where N=1-232,
- 20

wherein the plant possesses an altered trait as compared to a wild type or reference plant, or the plant exhibits an altered phenotype as compared to a wild type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild type plant.

25

2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said recombinant nucleotide.
- 30 3. The transgenic plant of claim 1, wherein the plant is selected from the following group: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, *Arabidopsis*, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and other labiates, rosaceous fruits, and vegetable brassicas.
- 35



4. An isolated or recombinant polynucleotide having a nucleotide sequence selected from the following group:
- (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from those of SEQ ID Nos. 2N where N=1-232, or a complementary nucleotide sequence thereof;
  - 5 (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
  - (c) one of SEQ ID NOs. 2N-1 where N=1-232, or a complementary nucleotide sequence thereof;
  - (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
  - (e) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of
  - 10 one or more of: (a), (b), (c), or (d);
  - (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved domain of any of (a)-(e);
  - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;
  - 15 (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
  - (i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any of (a)-(g);
  - (j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any
  - 20 of (a)-(g);
  - (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
  - (l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside
  - 25 of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232; or
  - (m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
  - 30 (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
  - (o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one
  - 35 of SEQ ID Nos.: 2N where N=1-232;



- (p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 90% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232; and
- (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232.
5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to the polynucleotide nucleotide.
6. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.
7. A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide, thereby producing a modified plant, and selecting for a modified trait.
8. The transgenic plant of claim 1, wherein the trait is selected from the group: enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced



tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation;  
enhanced tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to  
fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation;  
decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up  
5 heavy metals; and enhanced growth under poor photoconditions.

9. The transgenic plant of claim 1, wherein the trait is an alteration in the level of one or  
more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols,  
phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins,  
10 prenyllipids, glucosinolates, and terpenoids.

10. The transgenic plant of claim 1, wherein the trait is an alteration in one or more physical  
characteristics selected from the group: number of trichomes; fruit and seed size and number;  
yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of  
15 the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of  
seed coat.

11. The transgenic plant of claim 1, wherein the trait is an alteration in a plant growth  
characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants;  
20 vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time;  
flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical  
dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.

12. The transgenic plant of claim 1, wherein the trait is an alteration in one or more  
25 characteristics selected from the group: protein production; oil production; seed protein  
production; seed oil production; insoluble sugar level; soluble sugar level; and starch  
composition.

13. The method of claim 7, wherein the trait is selected from the group: enhanced tolerance  
30 to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to  
drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced  
tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal  
disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased  
herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy  
35 metals; and enhanced growth under poor photoconditions.



14. The method of claim 7, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenillipids, glucosinolates, and terpenoids.
- 5
15. The method of claim 7, wherein the trait is an alteration in one or more physical characteristics selected from the group: number of trichomes; fruit and seed size and number; yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of seed coat.
- 10
16. The method of claim 7, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.
- 15
17. The method of claim 7, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.
- 20
18. A plant produced by the method of claim 13.
19. A plant produced by the method of claim 14.
- 25
20. A plant produced by the method of claim 15.
21. A plant produced by the method of claim 16.
22. A plant produced by the method of claim 17.
- 30
23. A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that when expressed produces an antisense nucleic acid, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to express the antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait.
- 35



24. The method of claim 23, wherein the trait is selected from the group: enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy metals; and enhanced growth under poor photoconditions.
- 10 25. The method of claim 23, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyl lipids, glucosinolates, and terpenoids.
- 15 26. The method of claim 23, wherein the trait is an alteration in one or more physical characteristics selected from the group consisting of: the number of trichomes, fruit and seed size and number, yield of stems, leaves, or roots, stability of seeds during storage, susceptibility of the seed to shattering, root hair length and quantity, internode distances, or the quality of seed coat.
- 20 27. The method of claim 23, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.
- 25 28. The method of claim 23, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.
- 30 29. A plant produced by the method of claim 24.
30. A plant produced by the method of claim 25.
31. A plant produced by the method of claim 26.
- 35 32. A plant produced by the method of claim 27.



33. A plant produced by the method of claim 28.
34. An isolated or recombinant polypeptide comprising a subsequence of at least about 10  
5 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim  
4, wherein the contiguous amino acids are outside of a conserved domain.
35. An isolated or recombinant polypeptide comprising a subsequence of at least about 20  
10 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim  
4, wherein the contiguous amino acids are outside of a conserved domain.
36. An isolated or recombinant polypeptide comprising a subsequence of at least about 30  
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim  
4, wherein the contiguous amino acids are outside of a conserved domain.  
15
37. An isolated or recombinant polypeptide comprising a subsequence of at least about 10  
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim  
4, wherein the contiguous amino acids are within a conserved domain.
- 20 38. An isolated or recombinant polypeptide comprising a subsequence of at least about 20  
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim  
4, wherein the contiguous amino acids are within a conserved domain.
39. An isolated or recombinant polypeptide comprising a subsequence of at least about 30  
25 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim  
4, wherein the contiguous amino acids are within a conserved domain.
40. An isolated or recombinant polypeptide having at least 31% sequence identity over the  
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N  
30 where N=1-232, or the length of the polypeptide itself.
41. An isolated or recombinant polypeptide having at least 60% sequence identity over the  
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N  
35 where N=1-232, or the length of the polypeptide itself.



42. An isolated or recombinant polypeptide having at least 75% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232, or the length of the polypeptide itself.
- 5 43. An isolated or recombinant polypeptide having at least 95% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232, or the length of the polypeptide itself.
- 10 44. An isolated or recombinant polynucleotide having the sequence one of SEQ ID NOs.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof.
45. The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37.
- 15 46. The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 53, 79, 81, 107, 125, 153, 167, 203, 223, 289, 285, or 287.
47. The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 313, 345, 365, 395, 417, 425, 435, 455, 457, 459, 461, or 463.
- 20 48. A computer readable medium having stored sequence information comprising the polynucleotide sequence of claim 44.
49. The computer readable medium of claim 48, having stored sequence information comprising the sequence of one of SEQ ID Nos.: 1-37.
- 25 50. The computer readable medium of claim 48, having stored sequence information comprising the sequence of one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.
- 30 51. The computer readable medium of claim 48, having stored sequence information comprising the polynucleotide sequence of one of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.
- 35



52. A method of identifying a homolog sequence from a database comprising a plurality of known plant sequences, the method comprising: inputting sequence information selected from one or more of SEQ ID Nos. 1-464; and querying the database to identify a homolog sequence.
53. The method of claim 52, wherein the database being queried comprises a database of known genomic, cDNA, EST, or protein sequences.
54. The method of claim 52, wherein inputting sequence information comprises copying the sequence information from a CD.
55. The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 1-37.
56. The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.
57. The method of claim 52, wherein the sequence data comprises of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.
58. The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 1-37.
59. The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acids region one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.
60. The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.
61. A homolog identified by the method of claim 52.
62. The homolog of claim 61, identified by the method of claim 53.



63. The homolog of claim 61, identified by the method of claim 54.
64. The homolog of claim 61, identified by the method of claim 55.
- 5 65. The homolog of claim 61, identified by the method of claim 55.
66. The homolog of claim 61, identified by the method of claim 56.
- 10 67. The homolog of claim 61, identified by the method of claim 57.
68. The homolog of claim 61, identified by the method of claim 58.
69. The homolog of claim 61, identified by the method of claim 59.
- 15 70. The homolog of claim 61, identified by the method of claim 60.



## SEQUENCE LISTING

<110> Pilgrim, Marsha  
 Creelman, Robert  
 Dubell, Arnold  
 Heard, Jacqueline  
 Jiang, Cai-Zhong  
 Keddie, James  
 Adam, Luc  
 Ratcliffe, Oliver  
 Reuber, T. Lynne  
 Riechmann, Jose Luis  
 Yu, Guo-Liang  
 Pineda, Omaira

<120> Genes for Modifying Plant Traits IV

<130> MBI-0024

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<223> G28

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tt atg tcg atg acg gcg gat tct caa tct gat tat gct ttt ctt gag

107

Met Ser Met Thr Ala Asp Ser Gln Ser Asp Tyr Ala Phe Leu Glu  
 1 5 10 15

tcc ata cga cga cac tta cta gga gaa tcg gag ccg, ata ctc agt gag

155

Ser Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu  
 20 25 30

tcg aca gcg agt tcg gtt act caa tct tgt gta acc ggt cag agc att

203

Ser Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile  
 35 40 45

aaa ccg gtg tac gga cga aac cct agc ttt agc aaa ctg tat cct tgc

251

Lys Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys  
 50 55 60

ttc acc gag agc tgg gga gat ttg ccg ttg aaa gaa aac gat tct gag

299

Phe Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu  
 65 70 75



gat atg tta gtt tac ggt atc ctc aac gac gcc ttt cac ggc ggt tgg  
 347  
 Asp Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp  
 80 85 90 95

gag ccg tct tct tcg tct tcc gac gaa gat cgt agc tct ttc ccg agt  
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 Glu Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser  
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gtt aag atc gag act ccg gag agt ttc gcg gcg gtg gat tct gtt ccg  
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 Val Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro  
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 Val Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala  
 130 135 140

aag gga aag cat tat aga gga gtg aga caa agg ccg tgg ggg aaa ttt  
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 Lys Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe  
 145 150 155

gcg gcg gag att aga gat ccg gcg aag aac gga gct agg gtt tgg tta  
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 Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu  
 160 165 170 175

gga acg ttt gag acg gcg gag gac gcg gcg ttg gct tac gac aga gct  
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 Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala  
 180 185 190

gct ttc agg atg cgt ggt tcc cgc gct ttg ttg aat ttt ccg ttg aga  
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gtt aat tca gga gaa ccc gac ccg gtt cga atc aag tcc aag aga tct  
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 225 230 235

gtg gcc gcc ggt ggt gga atg gat aag gga ttg acg gtg aag tgc gag  
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 240 245 250 255

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 869  
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 260 265



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929

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964

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Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu Ser  
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Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile Lys  
35 40 45

Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys Phe  
50 55 60

Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp  
65 70 75 80

Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu  
85 90 95

Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser Val  
100 105 110

Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro Val  
115 120 125

Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala Lys  
130 135 140

Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala  
145 150 155 160

Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly  
165 170 175

Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala Ala  
180 185 190

Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val  
195 200 205



Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser  
 210 215 220

Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val  
 225 230 235 240

Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu Val  
 245 250 255

Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu  
 260 265

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 1 5 10 15

tca cct att agt tca aga cct cct gct aac aac tta gaa gag ctt atg  
 96  
 Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met  
 20 25 30

aga ttc tca gcc gcc gcg gat gac ggt gga tta gga ggt gga ggt gga  
 144  
 Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly  
 35 40 45

gga gga gga gga gga agt gct tct tct tca tcg gga aat cga tgg ccg  
 192  
 Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro  
 50 55 60

aga gaa gaa act tta gct ctt ctt cgg atc cga tcc gat atg gat tct  
 240  
 Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser  
 65 70 75 80

act ttt cgt gat gct act ctc aaa gct cct ctt tgg gaa cat gtt tcc  
 288  
 Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser  
 85 90 95

agg aag cta ttg gag tta ggt tac aaa cga agt tca aag aaa tgc aaa  
 336  
 Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys  
 100 105 110

gag aaa ttc gaa aac gtt cag aaa tat tac aaa cgt act aaa gaa act  
 384  
 Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr  
 115 120 125



cgc ggt ggt cgt cat gat ggt aaa gct tac aag ttc ttc tct cag ctt  
432

Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu  
130 135 140

gaa gct ctc aac act act cct cct cct cct cct tct cat cct cac gct  
480

Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala  
145 150 155 160

cat caa cca gaa cag aaa caa caa caa caa cca caa caa gag atg gtc  
528

His Gln Pro Glu Gln Lys Gln Gln Gln Gln Pro Gln Gln Glu Met Val  
165 170 175

atg agc tcg gaa caa tca tca tta cca tca tca tca aga tgg cca aag  
576

Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys  
180 185 190

gca gag att cta gcg ctt ata aac ctg aga agt gga atg gaa cca agg  
624

Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg  
195 200 205

tac caa gat aat gta cct aaa gga ctt cta tgg gaa gag atc tca act  
672

Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr  
210 215 220

tca atg aag aga atg gga tac aac aga aac gct aag aga tgt aaa gag  
720

Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu  
225 230 235 240

aaa tgg gaa aac ata aac aaa tac tac aag aaa gtt aaa gaa agc aac  
768

Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn  
245 250 255

aac agc aac tac aac aac aag aat caa tga  
798

Asn Ser Asn Tyr Asn Asn Lys Asn Gln  
260 265

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Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met  
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Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly  
35 40 45

Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro



50                      55                      60  
 Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser  
 65                      70                      75                      80  
 Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser  
                     85                      90                      95  
 Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys  
                     100                      105                      110  
 Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr  
                     115                      120                      125  
 Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu  
                     130                      135                      140  
 Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala  
 145                      150                      155                      160  
 His Gln Pro Glu Gln Lys Gln Gln Gln Gln Pro Gln Gln Glu Met Val  
                     165                      170                      175  
 Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys  
                     180                      185                      190  
 Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg  
                     195                      200                      205  
 Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr  
                     210                      215                      220  
 Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu  
 225                      230                      235                      240  
 Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn  
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 Asn Ser Asn Tyr Asn Asn Lys Asn Gln  
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112

Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser  
1 5 10

caa gat gac aag caa gct cgt ttc cgg gga gtt cga aga agg cct tgg  
160

Gln Asp Asp Lys Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp  
15 20 25

gga aag ttt gca gca gag att cga gac ccg tcg aga aac ggt gcc cgt  
208

Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg  
30 35 40

ctt tgg ctc ggg aca ttt gag acc gct gag gag gca gca agg gct tat  
256

Leu Trp Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr  
45 50 55 60

gac cga gca gcc ttt aac ctt agg ggt cat ctc gct ata ctc aac ttc  
304

Asp Arg Ala Ala Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe  
65 70 75

cct aat gag tat tat cca cgt atg gac gac tac tcg ctt cgc cct cct  
352

Pro Asn Glu Tyr Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro  
80 85 90

tat gct tct tct tct tcg tcg tcg tca tcg ggt tca act tct act aat  
400

Tyr Ala Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn  
95 100 105

gtg agt cga caa aac caa aga gaa gtt ttc gag ttt gag tat ttg gac  
448

Val Ser Arg Gln Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp  
110 115 120

gat aag gtt ctt gaa gaa ctt ctt gat tca gaa gaa agg aag aga taa  
496

Asp Lys Val Leu Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg  
125 130 135

tcacgattag ttttgttttg atattttatg tggcactggt gtggctacct acgtgcatta  
556

tgtgcatgta taggtcgctt gattagtact ttataacatg catgccacga ccataaattg  
616

taagagaaga cgtactttgc gttttcatga aatatgaatg ttagatgggt tgagtacaaa  
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aaaaaaaaa aaaaaaaaaa  
696

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Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser Gln Asp Asp Lys  
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Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala  
20 25 30

Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg Leu Trp Leu Gly  
35 40 45

Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala  
50 55 60

Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe Pro Asn Glu Tyr  
65 70 75 80

Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro Tyr Ala Ser Ser  
85 90 95

Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn Val Ser Arg Gln  
100 105 110

Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp Asp Lys Val Leu  
115 120 125

Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg  
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gag ata aag aag ata gag aat cag acg gcg agg caa gtg acc ttc tcc  
104

Glu Ile Lys Lys Ile Glu Asn Gln Thr Ala Arg Gln Val Thr Phe Ser  
10 15 20

aag aga aga act ggt ctt ata aag aag act cgt gag ctc tct att ctc  
152

Lys Arg Arg Thr Gly Leu Ile Lys Lys Thr Arg Glu Leu Ser Ile Leu  
25 30 35

tgt gac gct cac ato ggt ctc atc gtc ttc tca gcc acc gga aag ctt  
200

Cys Asp Ala His Ile Gly Leu Ile Val Phe Ser Ala Thr Gly Lys Leu  
40 45 50



tcc gag ttc tgc tcc gaa cag aac agg atg cct caa ctc att gac cga  
 248  
 Ser Glu Phe Cys Ser Glu Gln Asn Arg Met Pro Gln Leu Ile Asp Arg  
 55 60 65 70

tac ttg cat acc aac gga ttg cga ctt cct gat cat cat gac gac cag  
 296  
 Tyr Leu His Thr Asn Gly Leu Arg Leu Pro Asp His His Asp Asp Gln  
 75 80 85

gag caa ttg cac cat gag atg gaa cta cta aga aga gag aca tgt aac  
 344  
 Glu Gln Leu His His Glu Met Glu Leu Leu Arg Arg Glu Thr Cys Asn  
 90 95 100

ctt gag ctt cgt ctg cgt cca ttc cat gga cat gac tta gcc tcc att  
 392  
 Leu Glu Leu Arg Leu Arg Pro Phe His Gly His Asp Leu Ala Ser Ile  
 105 110 115

cct cct aat gag ctt gac gga ctc gag aga cag cta gaa cat tct gtc  
 440  
 Pro Pro Asn Glu Leu Asp Gly Leu Glu Arg Gln Leu Glu His Ser Val  
 120 125 130

ctc aaa gtc cgt gag cgt aag agg agg atg cta gaa gaa gat aac aac  
 488  
 Leu Lys Val Arg Glu Arg Lys Arg Arg Met Leu Glu Glu Asp Asn Asn  
 135 140 145 150

aac atg tac cgt tgg ctt cat gag cat cgt gca gcg atg gag ttt caa  
 536  
 Asn Met Tyr Arg Trp Leu His Glu His Arg Ala Ala Met Glu Phe Gln  
 155 160 165

caa gct ggg ata gat acc aaa cca ggg gag tat caa cag ttt ata gag  
 584  
 Gln Ala Gly Ile Asp Thr Lys Pro Gly Glu Tyr Gln Gln Phe Ile Glu  
 170 175 180

cag ctt cag tgc tat aaa cca ggg gag tat cag cag ttt cta gag cag  
 632  
 Gln Leu Gln Cys Tyr Lys Pro Gly Glu Tyr Gln Gln Phe Leu Glu Gln  
 185 190 195

cag caa caa caa cca aac agc gtt ctt cag ctt gct aca ctt cct tct  
 680  
 Gln Gln Gln Gln Pro Asn Ser Val Leu Gln Leu Ala Thr Leu Pro Ser  
 200 205 210

gag att gat cct act tac aat ctc cag ctt gct cag cct aat ctt caa  
 728  
 Glu Ile Asp Pro Thr Tyr Asn Leu Gln Leu Ala Gln Pro Asn Leu Gln  
 215 220 225 230

aac gat cca acg gcc cag aat gat taa tacaattctc aatagatatc  
 775  
 Asn Asp Pro Thr Ala Gln Asn Asp  
 235



tactctttct ttatggagac agattcatga acttttatta cctatatattt gataagccag  
835

tgtcttcttt tgtgtggcta tggaacott gtttaaagca caatgcactt gagttcttgg  
895

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944

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Arg Gln Val Thr Phe Ser Lys Arg Arg Thr Gly Leu Ile Lys Lys Thr  
20 25 30

Arg Glu Leu Ser Ile Leu Cys Asp Ala His Ile Gly Leu Ile Val Phe  
35 40 45

Ser Ala Thr Gly Lys Leu Ser Glu Phe Cys Ser Glu Gln Asn Arg Met  
50 55 60

Pro Gln Leu Ile Asp Arg Tyr Leu His Thr Asn Gly Leu Arg Leu Pro  
65 70 75 80

Asp His His Asp Asp Gln Glu Gln Leu His His Glu Met Glu Leu Leu  
85 90 95

Arg Arg Glu Thr Cys Asn Leu Glu Leu Arg Leu Arg Pro Phe His Gly  
100 105 110

His Asp Leu Ala Ser Ile Pro Pro Asn Glu Leu Asp Gly Leu Glu Arg  
115 120 125

Gln Leu Glu His Ser Val Leu Lys Val Arg Glu Arg Lys Arg Arg Met  
130 135 140

Leu Glu Glu Asp Asn Asn Asn Met Tyr Arg Trp Leu His Glu His Arg  
145 150 155 160

Ala Ala Met Glu Phe Gln Gln Ala Gly Ile Asp Thr Lys Pro Gly Glu  
165 170 175

Tyr Gln Gln Phe Ile Glu Gln Leu Gln Cys Tyr Lys Pro Gly Glu Tyr  
180 185 190

Gln Gln Phe Leu Glu Gln Gln Gln Gln Pro Asn Ser Val Leu Gln



195 200 205

Leu Ala Thr Leu Pro Ser Glu Ile Asp Pro Thr Tyr Asn Leu Gln Leu  
210 215 220

Ala Gln Pro Asn Leu Gln Asn Asp Pro Thr Ala Gln Asn Asp  
225 230 235

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120

aagctgtgta aatctcttgt agtttttctg ccgatataca ttttcattgt gttgagggtg  
180

aacgataatc aagaacgaga gagagagaga gcaagagcaa gagatttcta ctacagaaga  
240

tttattatat tgatcatttt gtgtgatcaa cccataaaaa cagagagaca tagacaagtc  
300

catgtttcga tgtttcgatc tctcttactg tctaaacggc gaaataaaaa gtctgatggg  
360

tgtcacttat tgcattgata ttagtaaatc agcttgagcc caagttaaag ctgaaacttg  
420

ggtttgca atg gct ggt att gat aat aaa gct gct gta atg gga gaa tgg  
470

Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp  
1 5 10

ttc gac tgt agt act act aac cac agg aag aga tcg aaa gcg gaa ctt  
518

Phe Asp Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu  
15 20 25 30

ggt aga gag ttt tct tta aat tac atc aag aat gag gat tct ttg caa  
566

Gly Arg Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln  
35 40 45

acc acc ttt caa gaa agt tca cga gga gct ctt cgt gaa agg att gct  
614

Thr Thr Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala  
50 55 60

gcg aga tcc ggg ttt aat gca ccg tgg tta aac act gag gat att ctt  
662

Ala Arg Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu  
65 70 75



cag tcg aaa tct tta acc atc tct tct cct ggt ctt agt cct gca act  
 710  
 Gln Ser Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr  
 80 85 90

ctg tta gag tet cct gtt ttc ctc tca aac cct ttg cta tct cca aca  
 758  
 Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr  
 95 100 105 110

acc ggg aag ctc tca tca gta cct tct gat aag gct aaa gct gag tta  
 806  
 Thr Gly Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu  
 115 120 125

ttt gac gac att acc aca tcc tta gcc ttc caa acc att tca gga agt  
 854  
 Phe Asp Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser  
 130 135 140

ggc ctt gat cct act aac atc gct tta gaa ccc gat gat tcc caa gac  
 902  
 Gly Leu Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp  
 145 150 155

tat gaa gaa aga cag ctc ggc ggt tta gga gac tcg atg gct tgt tgt  
 950  
 Tyr Glu Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys  
 160 165 170

gca cct gca gat gat gga tac aac tgg aga aaa tat gga caa aag cta  
 998  
 Ala Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu  
 175 180 185 190

gtt aaa gga agt gag tat ccg cgg agc tat tac aag tgc acg cac ccg  
 1046  
 Val Lys Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro  
 195 200 205

aat tgt gag gcc aag aag aag gtt gaa cgg tct cgg gaa ggt cat att  
 1094  
 Asn Cys Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile  
 210 215 220

ata gag atc ata tac aca gga gat cat ata cac agc aaa cct cca cct  
 1142  
 Ile Glu Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro  
 225 230 235

aac cgc cgg tca ggg att gga tca tcc ggt act ggc caa gac atg caa  
 1190  
 Asn Arg Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln  
 240 245 250

ata gat gca acc gaa tac gaa ggt ttt gct gga acc aat gag aac ata  
 1238  
 Ile Asp Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile  
 255 260 265 270



gaa tgg aca tca cct gta tct gca gag ctc gaa tac gga agc cat tca  
 1286  
 Glu Trp Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser  
 275 280 285

gga tca atg cag gtt caa aac ggg act cat cag ttc ggg tat ggt gat  
 1334  
 Gly Ser Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp  
 290 295 300

gca gca gct gat gcc tta tat aga gat gaa aac gaa gat gat cgc acg  
 1382  
 Ala Ala Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr  
 305 310 315

tcc cac atg agt gtt tcc ctg act tac gat gga gag gta gaa gag tcc  
 1430  
 Ser His Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser  
 320 325 330

gaa tca aag aga agg aaa cta gaa gct tat gca aca gaa acg agt gga  
 1478  
 Glu Ser Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly  
 335 340 345 350

tca acc aga gcc agc cgt gag cca aga gtt gtg gtg cag acc aca agt  
 1526  
 Ser Thr Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser  
 355 360 365

gac att gac atc ctc gat gat ggt tat cgc tgg cgc aag tat ggg caa  
 1574  
 Asp Ile Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln  
 370 375 380

aaa gtc gtt aaa gga aac ccg aat cca agg agc tac tat aaa tgc aca  
 1622  
 Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr  
 385 390 395

gct aat gga tgt acc gta acg aag cat gta gag aga gcc tct gat gac  
 1670  
 Ala Asn Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp  
 400 405 410

ttc aag agc gta cta aca act tat ata ggc aag cac acc cac gtt gta  
 1718  
 Phe Lys Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val  
 415 420 425 430

cca gca gca cgc aac agc agc cac gtc ggt gca ggc agt tca ggg act  
 1766  
 Pro Ala Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr  
 435 440 445

ctc caa ggc agt tta gcg act cag acc cac aac cac aat gtg cac tat  
 1814  
 Leu Gln Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr  
 450 455 460



cca atg cca cac agt aga tct gag gga ctg gcc aca gcc aac tca tct  
1862  
Pro Met Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser  
465 470 475

cta ttt gac ttc cag tca cac ctg agg cat cct aca ggt ttc tcc gtt  
1910  
Leu Phe Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val  
480 485 490

tac ata ggc caa tct gag ctt tct gat ctt tca atg cct ggt cta act  
1958  
Tyr Ile Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr  
495 500 505 510

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2006  
Ile Gly Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp  
515 520 525

cca act ggc cta atg ttg cag tta gca gca cag ccg aag gtg gaa cca  
2054  
Pro Thr Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro  
530 535 540

gtg tca cca caa cag gga ctt gat ttg tca gcg agc tca ttg ata tgc  
2102  
Val Ser Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys  
545 550 555

aga gag atg ttg agt aga tta cga cag ata tga aacaaatctc tttgttcact  
2155  
Arg Glu Met Leu Ser Arg Leu Arg Gln Ile  
560 565

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2215

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1 5 10 15

Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu Gly Arg  
20 25 30

Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln Thr Thr  
35 40 45

Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala Ala Arg  
50 55 60

Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu Gln Ser  
65 70 75 80



Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu  
85 90 95

Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr Thr Gly  
100 105 110

Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu Phe Asp  
115 120 125

Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser Gly Leu  
130 135 140

Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp Tyr Glu  
145 150 155 160

Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys Ala Pro  
165 170 175

Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys  
180 185 190

Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys  
195 200 205

Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Ile Glu  
210 215 220

Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro Asn Arg  
225 230 235 240

Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln Ile Asp  
245 250 255

Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile Glu Trp  
260 265 270

Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser Gly Ser  
275 280 285

Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp Ala Ala  
290 295 300

Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr Ser His  
305 310 315 320



Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser Glu Ser  
325 330 335

Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly Ser Thr  
340 345 350

Arg Ala Ser Arg Glu Pro Arg Val Val Gln Thr Thr Ser Asp Ile  
355 360 365

Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val  
370 375 380

Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Asn  
385 390 395 400

Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp Phe Lys  
405 410 415

Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val Pro Ala  
420 425 430

Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr Leu Gln  
435 440 445

Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr Pro Met  
450 455 460

Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser Leu Phe  
465 470 475 480

Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val Tyr Ile  
485 490 495

Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr Ile Gly  
500 505 510

Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp Pro Thr  
515 520 525

Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro Val Ser  
530 535 540

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Met Leu Ser Arg Leu Arg Gln Ile



565

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 102  
 Arg Asn Tyr Ile Ser Gly Val Gly Ala Asp Ser Phe Ala Val Gln Glu  
 10 15 20

gca gct gct tca gga ctg aaa agt atc gaa aat ttc atc ggt tta atg  
 150  
 Ala Ala Ala Ser Gly Leu Lys Ser Ile Glu Asn Phe Ile Gly Leu Met  
 25 30 35

tct cgt gat agc ttt aac tct gat cag cca tct tct tcc gcc tcc  
 198  
 Ser Arg Asp Ser Phe Asn Ser Asp Gln Pro Ser Ser Ser Ser Ala Ser  
 40 45 50 55

gcc tcc gcc tcc gcc gcc gca gat ctt gaa tca gct cgt aac aca acg  
 246  
 Ala Ser Ala Ser Ala Ala Ala Asp Leu Glu Ser Ala Arg Asn Thr Thr  
 60 65 70

gcg gac gcg gct gtt tca aag ttt aaa aga gtc ata tct ctg tta gat  
 294  
 Ala Asp Ala Ala Val Ser Lys Phe Lys Arg Val Ile Ser Leu Leu Asp  
 75 80 85

cga act cga acc gga cac gcc cgg ttt aga cgt gct ccg gtt cat gtt  
 342  
 Arg Thr Arg Thr Gly His Ala Arg Phe Arg Arg Ala Pro Val His Val  
 90 95 100

att tct ccg gtt ctt tta caa gaa gaa cca aaa acg acg ccg ttt cag  
 390  
 Ile Ser Pro Val Leu Leu Gln Glu Glu Pro Lys Thr Thr Pro Phe Gln  
 105 110 115

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 438  
 Ser Pro Leu Pro Pro Pro Pro Gln Met Ile Arg Lys Gly Ser Phe Ser  
 120 125 130 135

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 486  
 Ser Ser Met Lys Thr Ile Asp Phe Ser Ser Leu Ser Ser Val Thr Thr  
 140 145 150

gaa tca gac aac cag aag aag att cat cat cat caa cgt ccc tct gaa  
 534  
 Glu Ser Asp Asn Gln Lys Lys Ile His His His Gln Arg Pro Ser Glu  
 155 160 165



acg gcg ccg ttt gcg tct caa act caa agc ctc tcc acg acg gtc tcg  
582

Thr Ala Pro Phe Ala Ser Gln Thr Gln Ser Leu Ser Thr Thr Val Ser  
170 175 180

tct ttc tca aaa tca aca aag aga aaa tgt aac tct gag aat ctt ctc  
630

Ser Phe Ser Lys Ser Thr Lys Arg Lys Cys Asn Ser Glu Asn Leu Leu  
185 190 195

acc gga aaa tgc gct tcc gct tct tcc tcc ggt cgt tgt cat tgc tcg  
678

Thr Gly Lys Cys Ala Ser Ala Ser Ser Ser Gly Arg Cys His Cys Ser  
200 205 210 215

aag aaa aga aag ata aaa cag agg aga ata att agg gtt ccg gcg ata  
726

Lys Lys Arg Lys Ile Lys Gln Arg Arg Ile Ile Arg Val Pro Ala Ile  
220 225 230

agt gca aaa atg tcc gat gta cca ccg gac gat tat tca tgg agg aaa  
774

Ser Ala Lys Met Ser Asp Val Pro Pro Asp Asp Tyr Ser Trp Arg Lys  
235 240 245

tac gga caa aaa cca att aaa gga tct cca cat cca aga gga tat tat  
822

Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr  
250 255 260

aag tgt agt agc gta aga ggt tgt cca gca cgt aaa cat gtt gag aga  
870

Lys Cys Ser Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg  
265 270 275

gca gct gat gat tcg tcc atg ttg att gtt act tat gaa gga gat cat  
918

Ala Ala Asp Asp Ser Ser Met Leu Ile Val Thr Tyr Glu Gly Asp His  
280 285 290 295

aat cat tct ctc tcc gcc gct gat ctc gcc gga gcc gcc gtt gct gat  
966

Asn His Ser Leu Ser Ala Ala Asp Leu Ala Gly Ala Ala Val Ala Asp  
300 305 310

ctt att ttg gaa tcg tct tga aaagaacaaa tctttattta aggcttttat  
1017

Leu Ile Leu Glu Ser Ser  
315

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1077

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1115

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 Glu Asn Phe Ile Gly Leu Met Ser Arg Asp Ser Phe Asn Ser Asp Gln  
 35 40 45  
 Pro Ser Ser Ser Ser Ala Ser Ala Ser Ala Ser Ala Ala Ala Asp Leu  
 50 55 60  
 Glu Ser Ala Arg Asn Thr Thr Ala Asp Ala Ala Val Ser Lys Phe Lys  
 65 70 75 80  
 Arg Val Ile Ser Leu Leu Asp Arg Thr Arg Thr Gly His Ala Arg Phe  
 85 90 95  
 Arg Arg Ala Pro Val His Val Ile Ser Pro Val Leu Leu Gln Glu Glu  
 100 105 110  
 Pro Lys Thr Thr Pro Phe Gln Ser Pro Leu Pro Pro Pro Gln Met  
 115 120 125  
 Ile Arg Lys Gly Ser Phe Ser Ser Ser Met Lys Thr Ile Asp Phe Ser  
 130 135 140  
 Ser Leu Ser Ser Val Thr Thr Glu Ser Asp Asn Gln Lys Lys Ile His  
 145 150 155 160  
 His His Gln Arg Pro Ser Glu Thr Ala Pro Phe Ala Ser Gln Thr Gln  
 165 170 175  
 Ser Leu Ser Thr Thr Val Ser Ser Phe Ser Lys Ser Thr Lys Arg Lys  
 180 185 190  
 Cys Asn Ser Glu Asn Leu Leu Thr Gly Lys Cys Ala Ser Ala Ser Ser  
 195 200 205  
 Ser Gly Arg Cys His Cys Ser Lys Lys Arg Lys Ile Lys Gln Arg Arg  
 210 215 220  
 Ile Ile Arg Val Pro Ala Ile Ser Ala Lys Met Ser Asp Val Pro Pro  
 225 230 235 240  
 Asp Asp Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser



245 250 255

Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Ser Val Arg Gly Cys Pro  
260 265 270

Ala Arg Lys His Val Glu Arg Ala Ala Asp Asp Ser Ser Met Leu Ile  
275 280 285

Val Thr Tyr Glu Gly Asp His Asn His Ser Leu Ser Ala Ala Asp Leu  
290 295 300

Ala Gly Ala Ala Val Ala Asp Leu Ile Leu Glu Ser Ser  
305 310 315

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118 Met Glu  
1

ggt tcg tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa gaa gat  
166  
Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu Glu Asp  
5 10 15

agt ctc ttg agg cta tgt att gat aag tat gga gaa ggc aaa tgg cat  
214  
Ser Leu Leu Arg Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys Trp His  
20 25 30

caa gtt cct ttg aga gct ggg cta aat cga tgc aga aag agt tgt aga  
262  
Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser Cys Arg  
35 40 45 50

cta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga aga ctt  
310  
Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly Arg Leu  
55 60 65

agc aat gat gaa gtt gat ctt ctt ctt cgc ctt cat aag ctt cta gga  
358  
Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu Leu Gly  
70 75 80

aat agg tgg tcc ttg att gct ggt cga ttg cct ggt cgg acc gct aat  
406  
Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Ala Asn  
85 90 95



gat gtc aaa aat tac tgg aac acc cat ctg agt aaa aaa cat gag tct  
 454  
 Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser  
 100 105 110  
 tcg tgt tgt aag tct aaa atg aaa aag aaa aac att att tcc cct cct  
 502  
 Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro  
 115 120 125 130  
 aca aca ccg gtc caa aaa atc ggt gtt ttt aag cct cga cct cga tcc  
 550  
 Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser  
 135 140 145  
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 598  
 Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro Glu Val  
 150 155 160  
 gat tta att cct tca tgc ctt gga ctc aag aaa aat aat gtt tgt gaa  
 646  
 Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu  
 165 170 175  
 aat agt atc aca tgt aac aaa gat gat gag aaa gat gat ttt gtg aat  
 694  
 Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn  
 180 185 190  
 aat cta atg aat gga gat aat atg tgg ttg gag aat tta ctg ggg gaa  
 742  
 Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu  
 195 200 205 210  
 aac caa gaa gct gat gcg att gtt cct gaa gcg acg aca gct gaa cat  
 790  
 Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His  
 215 220 225  
 ggg gcc act ttg gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat  
 838  
 Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp  
 230 235 240  
 gga gag act gtt gaa ctt gat tag tgtttctcac cgtttggtta agattgtggg  
 892  
 Gly Glu Thr Val Glu Leu Asp  
 245  
 tggcttttct ttcgtatttt agtaatgtat ttttctgtat gaagtaaaga atttcagcat  
 952  
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 1033



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Glu Asp Ser Leu Leu Arg Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys  
20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser  
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
50 55 60

Arg Leu Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu  
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
100 105 110

Glu Ser Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser  
115 120 125

Pro Pro Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro  
130 135 140

Arg Ser Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro  
145 150 155 160

Glu Val Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val  
165 170 175

Cys Glu Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe  
180 185 190

Val Asn Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu  
195 200 205

Gly Glu Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala  
210 215 220

Glu His Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu  
225 230 235 240



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108  
Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser  
1 5 10 15

atc tgt gaa acc ccg gcg ata act ccg gcg aaa aag tcg tcg gta ggt  
156  
Ile Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly  
20 25 30

aac tta tac agg atg gga agc gga tca agc gtt gtg tta gat tca gag  
204  
Asn Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu  
35 40 45

aac ggc gta gaa gct gaa tct agg aag ctt ccg tcg tca aaa tac aaa  
252  
Asn Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys  
50 55 60

ggt gtg gtg cca caa cca aac gga aga tgg gga gct cag att tac gag  
300  
Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu  
65 70 75

aaa cac cag cgc gtg tgg ctc ggg aca ttc aac gaa gaa gac gaa gcc  
348  
Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala  
80 85 90 95

gct cgt gcc tac gac gtc gcg gtt cac agg ttc cgt cgc cgt gac gcc  
396  
Ala Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala  
100 105 110

gtc aca aat ttc aaa gac gtg aag atg gac gaa gac gag gtc gat ttc  
444  
Val Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe  
115 120 125

ttg aat tct cat tcg aaa tct gag atc gtt gat atg ttg agg aaa cat  
492  
Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His  
130 135 140

act tat aac gaa gag tta gag cag agt aaa cgg cgt cgt aat ggt aac  
540  
Thr Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn



145                      150                      155  
 gga aac atg act agg acg ttg tta acg tcg ggg ttg agt aat gat ggt  
 588  
 Gly Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly  
 160                      165                      170                      175  
 gtt tct acg acg ggg ttt aga tcg gcg gag gca ctg ttt gag aaa gcg  
 636  
 Val Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala  
 180                      185                      190  
 gta acg cca agc gac gtt ggg aag cta aac cgt ttg gtt ata ccg aaa  
 684  
 Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys  
 195                      200                      205  
 cat cac gca gag aaa cat ttt ccg tta ccg tca agt aac gtt tcc gtg  
 732  
 His His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val  
 210                      215                      220  
 aaa gga gtg ttg ttg aac ttt gag gac gtt aac ggg aaa gtg tgg agg  
 780  
 Lys Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg  
 225                      230                      235  
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 828  
 Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys  
 240                      245                      250                      255  
 ggt tgg agc agg ttc gtt aag gag aag aat cta cgt gct ggt gac gtg  
 876  
 Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val  
 260                      265                      270  
 gtt agt ttc agt aga tct aac ggt cag gat caa cag ttg tac att ggg  
 924  
 Val Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly  
 275                      280                      285  
 tgg aag tcg aga tcc ggg tca gat tta gat gcg ggt cgg gtt ttg aga  
 972  
 Trp Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg  
 290                      295                      300  
 ttg ttc gga gtt aac att tca ccg gag agt tca aga aac gac gtc gta  
 1020  
 Leu Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val  
 305                      310                      315  
 gga aac aaa aga gtg aac gat act gag atg tta tcg ttg gtg tgt agc  
 1068  
 Gly Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser  
 320                      325                      330                      335  
 aag aag caa cgc atc ttt cac gcc tcg taa caactcttct tctttttttt  
 1118  
 Lys Lys Gln Arg Ile Phe His Ala Ser  
 340



tcttttgttg ttttaataat ttttaaaaac tccattttcg ttttctttat ttgcatcggt  
1178

ttctttcttc ttgtttacca aaggttcatg agttgttttt gttgtattga tgaactgtaa  
1238

atattattta taggataaat ttttaaaaaa aaaaaaaaaa aaa  
1281

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20 25 30

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35 40 45

Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly  
50 55 60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys  
65 70 75 80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala  
85 90 95

Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val  
100 105 110

Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu  
115 120 125

Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr  
130 135 140

Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly  
145 150 155 160

Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val  
165 170 175

Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val  
180 185 190



Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His  
 195 200 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys  
 210 215 220

Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe  
 225 230 235 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly  
 245 250 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val  
 260 265 270

Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp  
 275 280 285

Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu  
 290 295 300

Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly  
 305 310 315 320

Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys  
 325 330 335

Lys Gln Arg Ile Phe His Ala Ser  
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 120

agagaggaag aaggagaaga aaaaaatatt tctttctctc cggctttcaa caaaatctct  
 180

cttttttctt tcatcagtg taaattcgga tccgggtcgg gtgggttttc ggtttttggt  
 240

gttcggatca gagcacagtt ggatgttagc gacggaactg aggatttcag tttgcggctg  
 300



cggcggctgt gacggtgttt gtgtgtcgtc ttctttttatc aatcaggagt ttcacacag  
360

tttgatcaga gattcagcca aattcttgga tactaa atg gct ggt ttt gat gaa  
414

Met Ala Gly Phe Asp Glu  
1 5

aat gtt gct gtg atg gga gaa tgg gtg cct cgt agt cct agt ccc ggg  
462

Asn Val Ala Val Met Gly Glu Trp Val Pro Arg Ser Pro Ser Pro Gly  
10 15 20

aca ctt ttc tcc tct gct att gga gaa gag aag agc tcg aaa cgt gtt  
510

Thr Leu Phe Ser Ser Ala Ile Gly Glu Glu Lys Ser Ser Lys Arg Val  
25 30 35

ctt gaa aga gag tta tct ttg aat cat ggt caa gtt att ggt tta gaa  
558

Leu Glu Arg Glu Leu Ser Leu Asn His Gly Gln Val Ile Gly Leu Glu  
40 45 50

gaa gac act agt agt aat cat aac aag gat tct tca caa agc aat gtt  
606

Glu Asp Thr Ser Ser Asn His Asn Lys Asp Ser Ser Gln Ser Asn Val  
55 60 65 70

ttt cga ggt ggt ctc agt gaa aga att gct gca aga gct gga ttt aat  
654

Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala Ala Arg Ala Gly Phe Asn  
75 80 85

gct cca agg ttg aac act gag aat atc cgc acc aac acc gac ttt tcc  
702

Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg Thr Asn Thr Asp Phe Ser  
90 95 100

att gac tct aac ctt cga tct cct tgc tta acc atc tct tct cct ggc  
750

Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu Thr Ile Ser Ser Pro Gly  
105 110 115

ctt agc cct gca aca ctc ttg gaa tct cct gtt ttc ctt tct aac cca  
798

Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro  
120 125 130

ttg gct caa cct tct cca act acc ggg aaa ttt cca ttt ctt cct ggt  
846

Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys Phe Pro Phe Leu Pro Gly  
135 140 145 150

gtt aat ggt aat gca ttg tct tct gag aaa gcg aaa gac gag ttc ttt  
894

Val Asn Gly Asn Ala Leu Ser Ser Glu Lys Ala Lys Asp Glu Phe Phe  
155 160 165

gat gat att gga gca tca ttc agc ttc cat cct gtt tca aga tca tct  
942

Asp Asp Ile Gly Ala Ser Phe Ser Phe His Pro Val Ser Arg Ser Ser



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170          175          180
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990
Ser Ser Phe Phe Gln Gly Thr Thr Glu Met Met Ser Val Asp Tyr Gly
185          190          195

aac tac aac aat aga tct tct tct cat caa tcc gca gaa gaa gta aaa
1038
Asn Tyr Asn Asn Arg Ser Ser Ser His Gln Ser Ala Glu Glu Val Lys
200          205          210

cct ggc tct gaa aac ata gaa agc tcc aat ctt tat ggg att gaa act
1086
Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn Leu Tyr Gly Ile Glu Thr
215          220          225          230

gac aat caa aac ggg cag aac aag aca tct gat gtc act aca aac acc
1134
Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser Asp Val Thr Thr Asn Thr
235          240          245

agt ctt gaa acc gtg gat cat caa gag gaa gaa gaa gag caa aga cgc
1182
Ser Leu Glu Thr Val Asp His Gln Glu Glu Glu Glu Glu Gln Arg Arg
250          255          260

ggg gat tcg atg gct ggt ggt gcg cct gca gag gat gga tat aac tgg
1230
Gly Asp Ser Met Ala Gly Gly Ala Pro Ala Glu Asp Gly Tyr Asn Trp
265          270          275

agg aaa tac gga caa aag ttg gtc aaa gga agt gag tat ccg cga agc
1278
Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly Ser Glu Tyr Pro Arg Ser
280          285          290

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Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln Val Lys Lys Lys Val Glu
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Ser Ala Ala Val Ser His His Tyr His Asn Gly His His Ser Glu Pro  
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Thr Ala Pro Gly Cys Thr Val Arg Lys His Val Glu Arg Ala Ser His		
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Cys Ser Pro Lys Leu Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg  
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Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser  
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165 170 175

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144

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576

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4011

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Leu Gly Glu Lys Tyr Pro Val Asp Asp Ser Asp Gln Pro Leu Thr Thr  
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Lys Thr Ser Thr Ser Asp Met Leu Lys Ala Tyr Gln Thr Tyr Ile Ser  
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Val Cys Pro Phe Lys Lys Ile Ala Ile Ile Phe Ala Asn His Ser Ile  
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Met Arg Leu Ala Ser Ser Ala Asn Ala Lys Thr Ile His Ile Ile Asp  
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Phe Gly Ile Ser Asp Gly Phe Gln Trp Pro Ser Leu Ile His Arg Leu  
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Ala Trp Arg Arg Gly Ser Ser Cys Lys Leu Arg Ile Thr Gly Ile Glu



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 530                      535                      540  
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 Cys His Trp Leu Leu Gln Gly Trp Lys Gly Arg Ile Val Tyr Gly Ser  
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 Ser Ile Trp Val Pro Phe Phe Phe Tyr Val Gly Arg Ala Thr Arg Val  
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Pro Pro Pro Ser Asp Thr Leu Leu Lys Tyr Val Ser Glu Ile Leu Met  
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Gln Asn Gln Ser Phe Ser Pro Ala Asp Ser Leu Ile Thr Asn Ser Trp  
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Arg Asp Ser Val Lys Glu Glu Met Gly Leu Asp Gln Leu Arg Val Lys  
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Lys Asn His Glu Arg Asp Phe Glu Glu Val Arg Ser Ser Lys Gln Phe  
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Ile Gln Ala Ile Arg Ser Ser Lys Asn Ile Gly Glu Lys Gly Lys Lys  
 930 935 940



Lys Lys Lys Lys Lys Ser Gln Val Val Asp Phe Arg Thr Leu Leu Thr  
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Gln Arg Leu Ala His Cys Phe Ala Asn Ala Leu Glu Ala Arg Leu Gln  
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Glu Pro Gly Leu Val Asn Gln Leu Ser Asp Phe Gln Thr Gly Phe Thr  
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cct tgg gaa ttg aac tgc tcc gat ctc ttc tct aca atc cat ctc gaa  
148

Pro Trp Glu Leu Asn Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu



30	35	40
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Lys Ile Asn Thr Asp Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser 60 65 70 75		
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Ile Lys Thr Asn Ser Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val 80 85 90		
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Pro Ser Pro Gln Ser Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg 95 100 105		
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Ser Asn Ala Thr Asn His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu 110 115 120		
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Gln Val Thr Asp Asp Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu 125 130 135		
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Ser Ala Lys Arg Ser Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu 140 145 150 155		
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Arg Leu Arg Ile Val Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn 175 180 185		
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Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu Pro Val Val Pro Ser  
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Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser Ile Lys Thr Asn Ser  
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Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val Pro Ser Pro Gln Ser  
85 90 95

Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg Ser Asn Ala Thr Asn  
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His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu Gln Val Thr Asp Asp  
115 120 125

Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser  
130 135 140

Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu Lys Asp Glu Ala Asn  
145 150 155 160

Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn Arg Leu Arg Ile Val  
165 170 175

Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn Asn Gln Leu Leu Ser  
180 185 190

Glu Gln Glu Ile Leu Arg Arg Arg Phe Leu Glu Met Arg Gln Ile Leu  
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240

ttgcagaatt ttctctctaaa ggttcagact ttggggtaaa ggtgtcaact ttggcg atg  
299

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347

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395

Gly Glu Arg Glu Glu Asn Glu Glu Gly Ser Trp Gly Arg Asn Gln Glu  
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443

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70 75 80

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587

Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser Gln  
85 90 95

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635

Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr Asn  
100 105 110



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 165 170 175

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 Ala Pro Glu Ser Asn Asn Asn Asn Thr Met Leu Cys Gly Gly Phe Thr  
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 195 200 205

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 Gln Ala Val Ile Ser Cys Phe Asn Gly Phe Ala Leu Asp Val Phe Arg  
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 1739  
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 470 475 480

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 1781  
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 485 490



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1901

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Glu Asp Gly Ser Ser Gln Phe Lys Pro Met Leu Glu Gly Asp Trp Phe  
35 40 45

Ser Ser Asn Gln Pro His Pro Gln Asp Leu Gln Met Leu Gln Asn Gln  
50 55 60

Pro Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn  
65 70 75 80

Leu Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser  
85 90 95

Gln Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr  
100 105 110

Asn Asn Asn Lys Gly Cys Leu Leu Asn Val Pro Ser Ser Ala Asn Pro  
115 120 125

Phe Asp Asn Ala Phe Glu Phe Gly Ser Glu Ser Gly Phe Leu Asn Gln  
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Ile His Ala Pro Ile Ser Met Gly Phe Gly Ser Leu Thr Gln Leu Gly  
145 150 155 160

Asn Arg Asp Leu Ser Ser Val Pro Asp Phe Leu Ser Ala Arg Ser Leu  
165 170 175



Leu Ala Pro Glu Ser Asn Asn Asn Asn Thr Met Leu Cys Gly Gly Phe  
 180 185 190

Thr Ala Pro Leu Glu Leu Glu Gly Phe Gly Ser Pro Ala Asn Gly Gly  
 195 200 205

Phe Val Gly Asn Arg Ala Lys Val Leu Lys Pro Leu Glu Val Leu Ala  
 210 215 220

Ser Ser Gly Ala Gln Pro Thr Leu Phe Gln Lys Arg Ala Ala Met Arg  
 225 230 235 240

Gln Ser Ser Gly Ser Lys Met Gly Asn Ser Glu Ser Ser Gly Met Arg  
 245 250 255

Arg Phe Ser Asp Asp Gly Asp Met Asp Glu Thr Gly Ile Glu Val Ser  
 260 265 270

Gly Leu Asn Tyr Glu Ser Asp Glu Ile Asn Glu Ser Gly Lys Ala Ala  
 275 280 285

Glu Ser Val Gln Ile Gly Gly Gly Gly Lys Gly Lys Lys Lys Gly Met  
 290 295 300

Pro Ala Lys Asn Leu Met Ala Glu Arg Arg Arg Arg Lys Lys Leu Asn  
 305 310 315 320

Asp Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met  
 325 330 335

Asp Arg Ala Ser Ile Leu Gly Asp Ala Ile Asp Tyr Leu Lys Glu Leu  
 340 345 350

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 355 360 365

Gly Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr  
 370 375 380

Pro Gln Thr Leu Ser Cys Arg Val Lys Glu Glu Leu Cys Pro Ser Ser  
 385 390 395 400

Leu Pro Ser Pro Lys Gly Gln Gln Ala Arg Val Glu Val Arg Leu Arg  
 405 410 415



Glu Gly Arg Ala Val Asn Ile His Met Phe Cys Gly Arg Arg Pro Gly  
 420 425 430

Leu Leu Leu Ala Thr Met Lys Ala Leu Asp Asn Leu Gly Leu Asp Val  
 435 440 445

Gln Gln Ala Val Ile Ser Cys Phe Asn Gly Phe Ala Leu Asp Val Phe  
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 240

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 300

tgctattgga tttagattta gggtttttgt atccttgggg atttgaagat caaaaacaga  
 360

gtctttgagt gatacttctg gggaacaaa atg gct gca act gca ata gag cca  
 413

Met Ala Ala Thr Ala Ile Glu Pro  
 1 5

tct tca tct ata agt ttc aca tct tct cac tta tca aac cct tct cct  
 461

Ser Ser Ser Ile Ser Phe Thr Ser Ser His Leu Ser Asn Pro Ser Pro  
 10 15 20

gtt gtt act act tat cac tca gct gct aat ctt gaa gag ctc agc tct  
 509

Val Val Thr Thr Tyr His Ser Ala Ala Asn Leu Glu Glu Leu Ser Ser  
 25 30 35 40

aac ttg gag cag ctt ctc act aat cca gat tgc gat tac act gac gca  
 557

Asn Leu Glu Gln Leu Leu Thr Asn Pro Asp Cys Asp Tyr Thr Asp Ala



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Glu Ile Ile Ile Glu Glu Glu Ala Asn Pro Arg Lys Leu Arg Asn Tyr			
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Val Glu Lys Ser Leu Val Glu Asn Val Leu Pro Ile Leu Leu Val Ala			
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701			
Phe His Cys Asp Leu Thr Gln Leu Leu Asp Gln Cys Ile Glu Arg Val			
	90	95	100
gcg aga tca gac tta gac aga ttc tgt atc gaa aag gag ctt cct tta			
749			
Ala Arg Ser Asp Leu Asp Arg Phe Cys Ile Glu Lys Glu Leu Pro Leu			
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797			
Glu Val Leu Glu Lys Ile Lys Gln Leu Arg Val Lys Ser Val Asn Ile			
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ccc gag gtg gag gat aaa tcg ata gag aga aca ggg aaa gta ctc aag			
845			
Pro Glu Val Glu Asp Lys Ser Ile Glu Arg Thr Gly Lys Val Leu Lys			
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Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu Leu Leu Thr Glu			
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941			
Ser Asp Ile Thr Leu Asp Gln Ala Asn Gly Leu His Tyr Ala Val Ala			
	170	175	180
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989			
Tyr Ser Asp Pro Lys Val Val Thr Gln Val Leu Asp Leu Asp Met Ala			
185	190	195	200
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Asp Val Asn Phe Arg Asn Ser Arg Gly Tyr Thr Val Leu His Ile Ala			
	205	210	215
gct atg cgt aga gag cca aca att atc ata cca ctt att caa aaa gga			
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Ala Met Arg Arg Glu Pro Thr Ile Ile Ile Pro Leu Ile Gln Lys Gly			
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gct aat gct tca gat ttc acg ttt gat gga cgc agt gcg gta aat ata			
1133			
Ala Asn Ala Ser Asp Phe Thr Phe Asp Gly Arg Ser Ala Val Asn Ile			
	235	240	245



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 Lys Glu Pro Ser Lys Tyr Arg Leu Cys Ile Asp Ile Leu Glu Arg Glu  
 265 270 275 280

att aga agg aat cca ttg gtt agt ggg gat aca ccc act tgt tcc cat  
 1277  
 Ile Arg Arg Asn Pro Leu Val Ser Gly Asp Thr Pro Thr Cys Ser His  
 285 290 295

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 1325  
 Ser Met Pro Glu Asp Leu Gln Met Arg Leu Leu Tyr Leu Glu Lys Arg  
 300 305 310

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 1517  
 Asn Glu Thr Pro Tyr Val Gln Thr Lys Arg Met Leu Thr Arg Met Lys  
 365 370 375

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 1565  
 Ala Leu Met Lys Thr Val Glu Thr Gly Arg Arg Tyr Phe Pro Ser Cys  
 380 385 390

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 1613  
 Tyr Glu Val Leu Asp Lys Tyr Met Asp Gln Tyr Met Asp Glu Glu Ile  
 395 400 405

cct gat atg tcg tat ccc gag aaa ggc act gtg aaa gag aga aga cag  
 1661  
 Pro Asp Met Ser Tyr Pro Glu Lys Gly Thr Val Lys Glu Arg Arg Gln  
 410 415 420

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 1709  
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 425 430 435 440



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1757

Ser Lys Asp Lys Val Ala Arg Ser Cys Leu Ser Ser Ser Ser Pro Ala  
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1803

Ser Ser Leu Arg Glu Ala Leu Glu Asn Pro Thr  
460 465

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1863

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1923

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35 40 45

Pro Asp Cys Asp Tyr Thr Asp Ala Glu Ile Ile Ile Glu Glu Glu Ala  
50 55 60

Asn Pro Arg Lys Leu Arg Asn Tyr Val Glu Lys Ser Leu Val Glu Asn  
65 70 75 80

Val Leu Pro Ile Leu Leu Val Ala Phe His Cys Asp Leu Thr Gln Leu  
85 90 95

Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser Asp Leu Asp Arg Phe  
100 105 110

Cys Ile Glu Lys Glu Leu Pro Leu Glu Val Leu Glu Lys Ile Lys Gln  
115 120 125



Leu Arg Val Lys Ser Val Asn Ile Pro Glu Val Glu Asp Lys Ser Ile  
 130 135 140

Glu Arg Thr Gly Lys Val Leu Lys Ala Leu Asp Ser Asp Asp Val Glu  
 145 150 155 160

Leu Val Lys Leu Leu Leu Thr Glu Ser Asp Ile Thr Leu Asp Gln Ala  
 165 170 175

Asn Gly Leu His Tyr Ala Val Ala Tyr Ser Asp Pro Lys Val Val Thr  
 180 185 190

Gln Val Leu Asp Leu Asp Met Ala Asp Val Asn Phe Arg Asn Ser Arg  
 195 200 205

Gly Tyr Thr Val Leu His Ile Ala Ala Met Arg Arg Glu Pro Thr Ile  
 210 215 220

Ile Ile Pro Leu Ile Gln Lys Gly Ala Asn Ala Ser Asp Phe Thr Phe  
 225 230 235 240

Asp Gly Arg Ser Ala Val Asn Ile Cys Arg Arg Leu Thr Arg Pro Lys  
 245 250 255

Asp Tyr His Thr Lys Thr Ser Arg Lys Glu Pro Ser Lys Tyr Arg Leu  
 260 265 270

Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Arg Asn Pro Leu Val Ser  
 275 280 285

Gly Asp Thr Pro Thr Cys Ser His Ser Met Pro Glu Asp Leu Gln Met  
 290 295 300

Arg Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala Gln Leu Phe Phe  
 305 310 315 320

Pro Ala Glu Ala Asn Val Ala Met Asp Val Ala Asn Val Glu Gly Thr  
 325 330 335

Ser Glu Cys Thr Gly Leu Leu Thr Pro Pro Pro Ser Asn Asp Thr Thr  
 340 345 350

Glu Asn Leu Gly Lys Val Asp Leu Asn Glu Thr Pro Tyr Val Gln Thr  
 355 360 365

Lys Arg Met Leu Thr Arg Met Lys Ala Leu Met Lys Thr Val Glu Thr



370 375 380

Gly Arg Arg Tyr Phe Pro Ser Cys Tyr Glu Val Leu Asp Lys Tyr Met  
385 390 395 400

Asp Gln Tyr Met Asp Glu Glu Ile Pro Asp Met Ser Tyr Pro Glu Lys  
405 410 415

Gly Thr Val Lys Glu Arg Arg Gln Lys Arg Met Arg Tyr Asn Glu Leu  
420 425 430

Lys Asn Asp Val Lys Lys Ala Tyr Ser Lys Asp Lys Val Ala Arg Ser  
435 440 445

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107

Gln Glu Phe His Ser Ser Lys Asp Ser Leu Pro Cys Pro Ala Thr Ser  
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tgg gat aac tct gtc ttc acc aac tca aat gtc caa gga tca tca tcc  
155

Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser Ser  
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203

Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln Thr  
35 40 45

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251

Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr Gly  
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299

Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn Arg  
70 75 80



tat ggc cac aac att gtt gtc act cat ctc tca ggt tac aaa gaa aac  
 347  
 Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu Asn  
 85 90 95

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 Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln Asp  
 100 105 110

tca gtg gtt ctt cct att gag gcg gct tct tgg cct tta cac ggc aat  
 443  
 Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly Asn  
 115 120 125

gta acg cca cat ttc aat ggt ttc ttg tct ttt cct tat gca tca caa  
 491  
 Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser Gln  
 130 135 140 145

cac acg gtg cag cat cct caa atc aga ggg ttg gtt ccg tct aga atg  
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 His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg Met  
 150 155 160

cct ttg cct cac aac att cca gag aac gaa cca att ttc gtc aat gca  
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 165 170 175

aaa cag tac caa gcc att ctc cgc cgc aga gag cgc cgt gca aag ctt  
 635  
 Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys Leu  
 180 185 190

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 683  
 Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His Glu  
 195 200 205

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 Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys Phe  
 245 250 255

cgg caa atg gac att tca agg ggt ggg gtt gtg tct agt gtc tcg aca  
 875  
 Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser Thr  
 260 265 270



aca tct tgc tcg gac ata acc ggg aac aac aac gac atg ttc cag caa  
923

Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln Gln  
275 280 285

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971

Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val Ser  
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1011

Val Leu Met

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20 25 30

Ser Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln  
35 40 45

Thr Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr  
50 55 60

Gly Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn  
65 70 75 80

Arg Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu  
85 90 95

Asn Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln  
100 105 110

Asp Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly  
115 120 125

Asn Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser  
130 135 140

Gln His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg  
145 150 155 160

Met Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn  
165 170 175



Ala Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys  
 180 185 190

Leu Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His  
 195 200 205

Glu Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly  
 210 215 220

Arg Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser  
 225 230 235 240

Pro Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys  
 245 250 255

Phe Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser  
 260 265 270

Thr Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln  
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 106  
 Gly Lys Ile Val Ile Gln Arg Ile Asp Asp Ser Thr Ser Arg Gln Val  
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 Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala Lys Glu Leu  
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 Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Ile Ile Phe Ser Ser Thr  
 40 45 50



gga aag ctc tat gac ttt gca agc tcc agc atg aag tcg gtt att gat  
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 394  
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 Ile Ser Leu Arg Gly Ile Arg Met Arg Lys Glu Gln Leu Leu Thr Gln  
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 538  
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ctc gat tta tct agg aaa gta caa cgg att cat caa gaa aat gtg gag  
 586  
 Leu Asp Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu Asn Val Glu  
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ctc tac aag aag gct tat atg gca aac aca aac ggg ttt aca cac cgt  
 634  
 Leu Tyr Lys Lys Ala Tyr Met Ala Asn Thr Asn Gly Phe Thr His Arg  
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gaa gta gct gtt gcg gat gat gaa tca cac act cag att cgg ctg caa  
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 Glu Val Ala Val Ala Asp Asp Glu Ser His Thr Gln Ile Arg Leu Gln  
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 Leu Ser Gln Pro Glu His Ser Asp Tyr Asp Thr Pro Pro Arg Ala Asn  
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gaa taa cagagagatt gaagttggaa gataccatga tggtgaagaa cactccaaag  
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906

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Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Ile Ile Phe  
35 40 45

Ser Ser Thr Gly Lys Leu Tyr Asp Phe Ala Ser Ser Ser Met Lys Ser  
50 55 60

Val Ile Asp Arg Tyr Asn Lys Ser Lys Ile Glu Gln Gln Gln Leu Leu  
65 70 75 80

Asn Pro Ala Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Ala Val Leu  
85 90 95

Arg Gln Glu Leu His Ala Leu Gln Glu Asn His Arg Gln Met Met Gly  
100 105 110

Glu Gln Leu Asn Gly Leu Ser Val Asn Glu Leu Asn Ser Leu Glu Asn  
115 120 125

Gln Ile Glu Ile Ser Leu Arg Gly Ile Arg Met Arg Lys Glu Gln Leu  
130 135 140

Leu Thr Gln Glu Ile Gln Glu Leu Ser Gln Lys Arg Asn Leu Ile His  
145 150 155 160

Gln Glu Asn Leu Asp Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu  
165 170 175



Asn Val Glu Leu Tyr Lys Lys Ala Tyr Met Ala Asn Thr Asn Gly Phe  
180 185 190

Thr His Arg Glu Val Ala Val Ala Asp Asp Glu Ser His Thr Gln Ile  
195 200 205

Arg Leu Gln Leu Ser Gln Pro Glu His Ser Asp Tyr Asp Thr Pro Pro  
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Arg Ala Asn Glu  
225

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1 5 10 15

cac cag caa cca ccg tcg tac tcg cag ctg ccg ccg atg gca tca tcc  
96  
His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser  
20 25 30

aac cct cag tta cgt aat tac tgg att gag cag atg gaa acc gtc tcg  
144  
Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser  
35 40 45

gat ttc aaa aac cgt cag ctt cca ttg gct cga att aag aag atc atg  
192  
Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met  
50 55 60

aag gct gat cca gat gtg cac atg gtc tcc gca gag gct ccg atc atc  
240  
Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile  
65 70 75 80

ttc gca aag gct tgc gaa atg ttc atc gtt gat ctc acg atg cgg tcg  
288  
Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser  
85 90 95

tgg ctc aaa gcc gag gag aac aaa cgc cac acg ctt cag aaa tcg gat  
336  
Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp  
100 105 110

atc tcc aac gca gtg gct agc tct ttc acc tac gat ttc ctt ctt gat  
384  
Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp  
115 120 125



gtt gtc cct aag gac gag tct atc gcc acc gct gat cct ggc ttt gtg  
 432  
 Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val  
 130 135 140  
 gct atg cca cat cct gac ggt gga gga gta ccg caa tat tat tat cca  
 480  
 Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro  
 145 150 155 160  
 ccg gga gtg gtg atg gga act cct atg gtt ggt agt gga atg tac gcg  
 528  
 Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala  
 165 170 175  
 cca tcg cag gcg tgg cca gca gcg gct ggt gac ggg gag gat gat gct  
 576  
 Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala  
 180 185 190  
 gag gat aat gga gga aac ggc ggc gga aat tga  
 609  
 Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn  
 195 200  
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 Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser  
 35 40 45  
 Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met  
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 Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile  
 65 70 75 80  
 Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser  
 85 90 95  
 Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp  
 100 105 110  
 Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp  
 115 120 125



Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val  
 130 135 140

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro  
 145 150 155 160

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala  
 165 170 175

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala  
 180 185 190

Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn  
 195 200

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atttcgtttc ataac atg gat gcc atg agt agc gta gac gag agc tct aca  
 111

Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr  
 1 5 10

act aca gat tcc att ccg gcg aga aag tca tcg tct ccg gcg agt tta  
 159

Thr Thr Asp Ser Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu  
 15 20 25

cta tat aga atg gga agc gga aca agc gtg gta ctt gat tca gag aac  
 207

Leu Tyr Arg Met Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn  
 30 35 40

ggt gtc gaa gtc gaa gtc gaa gcc gaa tca aga aag ctt cct tct tca  
 255

Gly Val Glu Val Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser  
 45 50 55 60

aga ttc aaa ggt gtt gtt cct caa cca aat gga aga tgg gga gct cag  
 303

Arg Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln  
 65 70 75

att tac gag aaa cat caa cgc gtg tgg ctt ggt act ttc aac gag gaa  
 351

Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu  
 80 85 90

gac gaa gca gct cgt gct tac gac gtc gcg gct cac cgt ttc cgt ggc  
 399

Asp Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly



95 100 105  
 cgc gat gcc gtt act aat ttc aaa gac acg acg ttc gaa gaa gag gtt  
 447  
 Arg Asp Ala Val Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val  
 110 115 120  
 gag ttc tta aac gcg cat tcg aaa tca gag atc gta gat atg ttg aga  
 495  
 Glu Phe Leu Asn Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg  
 125 130 135 140  
 aaa cac act tac aaa gaa gag tta gac caa agg aaa cgt aac cgt gac  
 543  
 Lys His Thr Tyr Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp  
 145 150 155  
 ggt aac gga aaa gag acg acg gcg ttt gct ttg gct tcg atg gtg gtt  
 591  
 Gly Asn Gly Lys Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val  
 160 165 170  
 atg acg ggg ttt aaa acg gcg gag tta ctg ttt gag aaa acg gta acg  
 639  
 Met Thr Gly Phe Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr  
 175 180 185  
 cca agt gac gtc ggg aaa cta aac cgt tta gtt ata cca aaa cac caa  
 687  
 Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln  
 190 195 200  
 gcg gag aaa cat ttt ccg tta ccg tta ggt aat aat aac gtc tcc gtt  
 735  
 Ala Glu Lys His Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val  
 205 210 215 220  
 aaa ggt atg ctg ttg aat ttc gaa gac gtt aac ggg aaa gtg tgg agg  
 783  
 Lys Gly Met Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg  
 225 230 235  
 ttc cgt tac tct tat tgg aat agt agt caa agt tat gtg ttg acc aaa  
 831  
 Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys  
 240 245 250  
 ggt tgg agt aga ttc gtt aaa gag aag aga ctt tgt gct ggt gat ttg  
 879  
 Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu  
 255 260 265  
 atc agt ttt aaa aga tcc aac gat caa gat caa aaa ttc ttt atc ggg  
 927  
 Ile Ser Phe Lys Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly  
 270 275 280  
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 975  
 Trp Lys Ser Lys Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg  
 285 290 295 300



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1023

Leu Phe Gly Val Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu  
305 310 315

aca acg gag gtg tta atg tcg tcg tta agg tgt aag aag caa cga gtt  
1071

Thr Thr Glu Val Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val  
320 325 330

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1127

Leu

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1155

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1 5 10 15

Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met  
20 25 30

Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val  
35 40 45

Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly  
50 55 60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys  
65 70 75 80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala  
85 90 95

Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val  
100 105 110

Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn  
115 120 125

Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr  
130 135 140

Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys  
145 150 155 160



Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe  
 165 170 175  
 Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val  
 180 185 190  
 Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His  
 195 200 205  
 Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu  
 210 215 220  
 Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser  
 225 230 235 240  
 Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg  
 245 250 255  
 Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys  
 260 265 270  
 Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys  
 275 280 285  
 Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val  
 290 295 300  
 Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val  
 305 310 315 320  
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 Met Glu Gly Lys Arg Ser Gln Gly Gln Gly Tyr Met Lys Lys Lys Ser  
 1 5 10 15  
 tac ctt gtg gaa gaa gat atg gag act gat acg gat gaa gaa gag gaa  
 96  
 Tyr Leu Val Glu Glu Asp Met Glu Thr Asp Thr Asp Glu Glu Glu Glu  
 20 25 30



gta ggt agg gat aga gtt aga ggg tct aga ggt agc atc aat cgt ggt  
144

Val Gly Arg Asp Arg Val Arg Gly Ser Arg Gly Ser Ile Asn Arg Gly  
35 40 45

ggc tgc ttg cgg ctt tgc caa gta gat aga tgc aca gct gat atg aaa  
192

Gly Ser Leu Arg Leu Cys Gln Val Asp Arg Cys Thr Ala Asp Met Lys  
50 55 60

gag gca aaa ctg tat cac cgg aga cac aaa gtg tgt gaa gtt cat gca  
240

Glu Ala Lys Leu Tyr His Arg Arg His Lys Val Cys Glu Val His Ala  
65 70 75 80

aag gca tct tct gtc ttt ctc tca gga ctt aac caa cgc ttt tgt caa  
288

Lys Ala Ser Ser Val Phe Leu Ser Gly Leu Asn Gln Arg Phe Cys Gln  
85 90 95

caa tgc agt agg ttt cat gac ctc caa gag ttt gat gaa gct aag aga  
336

Gln Cys Ser Arg Phe His Asp Leu Gln Glu Phe Asp Glu Ala Lys Arg  
100 105 110

agt tgc agg agg cgc tta gct gga cac aat gag cga aga agg aag agc  
384

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser  
115 120 125

tct ggt gag agt act tat gga gaa gga tca ggt cgg aga gga atc aat  
432

Ser Gly Glu Ser Thr Tyr Gly Glu Gly Ser Gly Arg Arg Gly Ile Asn  
130 135 140

ggt cag gtg gtg atg cag aat caa gaa aga tca agg gta gag atg aca  
480

Gly Gln Val Val Met Gln Asn Gln Glu Arg Ser Arg Val Glu Met Thr  
145 150 155 160

ctt cct atg cca aac tca tca ttc aag cga cca cag att aga tag  
525

Leu Pro Met Pro Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg  
165 170

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38

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Tyr Leu Val Glu Glu Asp Met Glu Thr Asp Thr Asp Glu Glu Glu Glu  
20 25 30

Val Gly Arg Asp Arg Val Arg Gly Ser Arg Gly Ser Ile Asn Arg Gly  
35 40 45



Gly Ser Leu Arg Leu Cys Gln Val Asp Arg Cys Thr Ala Asp Met Lys  
 50 55 60

Glu Ala Lys Leu Tyr His Arg Arg His Lys Val Cys Glu Val His Ala  
 65 70 75 80

Lys Ala Ser Ser Val Phe Leu Ser Gly Leu Asn Gln Arg Phe Cys Gln  
 85 90 95

Gln Cys Ser Arg Phe His Asp Leu Gln Glu Phe Asp Glu Ala Lys Arg  
 100 105 110

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser  
 115 120 125

Ser Gly Glu Ser Thr Tyr Gly Glu Gly Ser Gly Arg Arg Gly Ile Asn  
 130 135 140

Gly Gln Val Val Met Gln Asn Gln Glu Arg Ser Arg Val Glu Met Thr  
 145 150 155 160

Leu Pro Met Pro Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg  
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Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys  
 1 5 10

aga agg cag cca cct caa gaa gaa gtg cct aac cac gtg gct aca agg  
 99

Arg Arg Gln Pro Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg  
 15 20 25

aag ccg tac aga ggg ata cgg agg agg aag tgg ggc aag tgg gtg gct  
 147

Lys Pro Tyr Arg Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala  
 30 35 40

gag att cgt gag cct aac aaa cgc tca cgg ctt tgg ctt ggc tct tac  
 195

Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr  
 45 50 55 60

aca acc gat atc gcc gcc gct aga gcc tac gac gtg gcc gtc ttc tac  
 243

Thr Thr Asp Ile Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr  
 65 70 75



ctc cgt ggc ccc tcc gca cgt ctc aac ttc cct gat ctt ctc ttg caa  
291

Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln  
80 85 90

gaa gag gac cat ctc tca gcc gcc acc acc gct gac atg ccc gca gct  
339

Glu Glu Asp His Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala  
95 100 105

ctt ata agg gaa aaa gcg gcg gag gtc ggc gcc aga gtc gac gct ctt  
387

Leu Ile Arg Glu Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu  
110 115 120

cta gct tct gcc gct cct tcg atg gct cac tcc act ccg ccg gta ata  
435

Leu Ala Ser Ala Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile  
125 130 135 140

aaa ccc gac ttg aat caa ata ccc gaa tcc gga gat ata tag  
477

Lys Pro Asp Leu Asn Gln Ile Pro Glu Ser Gly Asp Ile  
145 150

tcaatttata tacatgtagt ttgttttggt tgattagaag attacattta catacaagat  
537

acacatagat actggaaaat ataggtatgt atacattcat aaattatctt atgtatcaaa  
597

gaattttata gattctgatt agctttttgt ttttgttttt gataagaact ctgattagtt  
657

gtccggagac aaaaccggct aagagcaatc catgagaagc tagcgagtgt tttttagttc  
717

aagttgtaat ataatgcat attaattctt tagtaatttt gt  
759

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Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg Lys Pro Tyr Arg  
20 25 30

Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu  
35 40 45

Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr Thr Thr Asp Ile  
50 55 60

Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr Leu Arg Gly Pro



76



gaa gct cac ctt tgg gat aag agt acc tgg aac caa aac cag aac aag  
 403  
 Glu Ala His Leu Trp Asp Lys Ser Thr Trp Asn Gln Asn Gln Asn Lys  
 85 90 95  
 aag gga aaa caa gtt tat cta gga gca tat gat gat gaa gag gct gct  
 451  
 Lys Gly Lys Gln Val Tyr Leu Gly Ala Tyr Asp Asp Glu Glu Ala Ala  
 100 105 110 115  
 gct aga gct tac gac ctt gct gcc tta aaa tat tgg ggt cct ggg aca  
 499  
 Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Gly Thr  
 120 125 130  
 ctt ata aat ttt ccg gtg act gat tat acc agg gat tta gaa gaa atg  
 547  
 Leu Ile Asn Phe Pro Val Thr Asp Tyr Thr Arg Asp Leu Glu Glu Met  
 135 140 145  
 caa aat ctc tca agg gaa gaa tac ctt gca tct tta cgt aga tat ccc  
 595  
 Gln Asn Leu Ser Arg Glu Glu Tyr Leu Ala Ser Leu Arg Arg Tyr Pro  
 150 155 160  
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 643  
 Phe Gly Arg Lys Ser Ser Gly Phe Ser Arg Gly Ile Ala Lys Tyr Arg  
 165 170 175  
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 691  
 Gly Leu Gln Ser Arg Trp Asp Ala Ser Ala Ser Arg Met Pro Gly Pro  
 180 185 190 195  
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 739  
 Glu Tyr Phe Ser Asn Ile His Tyr Gly Ala Gly Asp Asp Arg Gly Thr  
 200 205 210  
 gaa ggt gac ttt cta ggt agc ttt tgt ctg gaa aga aag att gat cta  
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 Glu Gly Asp Phe Leu Gly Ser Phe Cys Leu Glu Arg Lys Ile Asp Leu  
 215 220 225  
 aca gga tac ata aag tgg tgg gga gcc aac aag aac cgt caa cca gaa  
 835  
 Thr Gly Tyr Ile Lys Trp Trp Gly Ala Asn Lys Asn Arg Gln Pro Glu  
 230 235 240  
 tct tca tca aaa gca tca gag gat gca aac gtc gaa gat gct ggt act  
 883  
 Ser Ser Ser Lys Ala Ser Glu Asp Ala Asn Val Glu Asp Ala Gly Thr  
 245 250 255  
 gag ctt aaa aca ctg gaa cac aca tcc cat gca aca gaa cca tac aag  
 931  
 Glu Leu Lys Thr Leu Glu His Thr Ser His Ala Thr Glu Pro Tyr Lys  
 260 265 270 275



gcg cca aac ctt ggc gtc ctt tgt gga act cag aga aaa gaa aaa gaa  
 979  
 Ala Pro Asn Leu Gly Val Leu Cys Gly Thr Gln Arg Lys Glu Lys Glu  
 280 285 290  
  
 ata tca tca cca tca agc tct tct gct tta agc atc ttg tct cag tcg  
 1027  
 Ile Ser Ser Pro Ser Ser Ser Ser Ala Leu Ser Ile Leu Ser Gln Ser  
 295 300 305  
  
 cct gcc ttc aag agc cta gag gag aaa gtg ttg aag atc caa gaa agc  
 1075  
 Pro Ala Phe Lys Ser Leu Glu Glu Lys Val Leu Lys Ile Gln Glu Ser  
 310 315 320  
  
 tgc aat aat gaa aac gat gag aat gca aac cgt aac atc atc aat atg  
 1123  
 Cys Asn Asn Glu Asn Asp Glu Asn Ala Asn Arg Asn Ile Ile Asn Met  
 325 330 335  
  
 gag aag aat aac ggc aag gca ata gag aaa cca gtt gtg agt cat gga  
 1171  
 Glu Lys Asn Asn Gly Lys Ala Ile Glu Lys Pro Val Val Ser His Gly  
 340 345 350 355  
  
 gtt gct tta ggc ggt gct gct gct ttg tct ctt cag aaa agc atg tac  
 1219  
 Val Ala Leu Gly Gly Ala Ala Ala Leu Ser Leu Gln Lys Ser Met Tyr  
 360 365 370  
  
 cca ctt acc tct ctc tta acg gct cca ttg ctc acc aac tac aat aca  
 1267  
 Pro Leu Thr Ser Leu Leu Thr Ala Pro Leu Leu Thr Asn Tyr Asn Thr  
 375 380 385  
  
 ttg gat cct ctt gca gac cct att ctc tgg aca cca ttt ctt cct tca  
 1315  
 Leu Asp Pro Leu Ala Asp Pro Ile Leu Trp Thr Pro Phe Leu Pro Ser  
 390 395 400  
  
 gga tcc tct ctt act tca gag gtg aca aag aca gag acc agc tgt tcc  
 1363  
 Gly Ser Ser Leu Thr Ser Glu Val Thr Lys Thr Glu Thr Ser Cys Ser  
 405 410 415  
  
 acg tac agc tac ctc cca caa gag aaa tga gccgttcct ttagacttta  
 1413  
 Thr Tyr Ser Tyr Leu Pro Gln Glu Lys  
 420 425  
  
 tgtatgtcag attctccttt tttagatga attcgtcgac ttgacatctc tttgtctctt  
 1473  
  
 ttatggagaa aaagtggga aaagtgtgac aatggctga agcaggaatg tacaggtttt  
 1533  
  
 gttagtgggt gtgttttttt tttccagtg tggaatatag aatcatgata ttttgtgtaa  
 1593  
  
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 1650



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42.

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Cys Ser Gly Gly Gly Gly Gly Glu Ser Ser Glu Thr Val Ala Ala Ser  
20 25 30

Asp Gln Met Leu Leu Tyr Arg Gly Phe Lys Lys Ala Lys Lys Glu Arg  
35 40 45

Gly Cys Thr Ala Lys Glu Arg Ile Ser Lys Met Pro Pro Cys Thr Ala  
50 55 60

Gly Lys Arg Ser Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr  
65 70 75 80

Gly Arg Tyr Glu Ala His Leu Trp Asp Lys Ser Thr Trp Asn Gln Asn  
85 90 95

Gln Asn Lys Lys Gly Lys Gln Val Tyr Leu Gly Ala Tyr Asp Asp Glu  
100 105 110

Glu Ala Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly  
115 120 125

Pro Gly Thr Leu Ile Asn Phe Pro Val Thr Asp Tyr Thr Arg Asp Leu  
130 135 140

Glu Glu Met Gln Asn Leu Ser Arg Glu Glu Tyr Leu Ala Ser Leu Arg  
145 150 155 160

Arg Tyr Pro Phe Gly Arg Lys Ser Ser Gly Phe Ser Arg Gly Ile Ala  
165 170 175

Lys Tyr Arg Gly Leu Gln Ser Arg Trp Asp Ala Ser Ala Ser Arg Met  
180 185 190

Pro Gly Pro Glu Tyr Phe Ser Asn Ile His Tyr Gly Ala Gly Asp Asp  
195 200 205

Arg Gly Thr Glu Gly Asp Phe Leu Gly Ser Phe Cys Leu Glu Arg Lys  
210 215 220



Ile Asp Leu Thr Gly Tyr Ile Lys Trp Trp Gly Ala Asn Lys Asn Arg  
 225 230 235 240

Gln Pro Glu Ser Ser Ser Lys Ala Ser Glu Asp Ala Asn Val Glu Asp  
 245 250 255

Ala Gly Thr Glu Leu Lys Thr Leu Glu His Thr Ser His Ala Thr Glu  
 260 265 270

Pro Tyr Lys Ala Pro Asn Leu Gly Val Leu Cys Gly Thr Gln Arg Lys  
 275 280 285

Glu Lys Glu Ile Ser Ser Pro Ser Ser Ser Ser Ala Leu Ser Ile Leu  
 290 295 300

Ser Gln Ser Pro Ala Phe Lys Ser Leu Glu Glu Lys Val Leu Lys Ile  
 305 310 315 320

Gln Glu Ser Cys Asn Asn Glu Asn Asp Glu Asn Ala Asn Arg Asn Ile  
 325 330 335

Ile Asn Met Glu Lys Asn Asn Gly Lys Ala Ile Glu Lys Pro Val Val  
 340 345 350

Ser His Gly Val Ala Leu Gly Gly Ala Ala Ala Leu Ser Leu Gln Lys  
 355 360 365

Ser Met Tyr Pro Leu Thr Ser Leu Leu Thr Ala Pro Leu Leu Thr Asn  
 370 375 380

Tyr Asn Thr Leu Asp Pro Leu Ala Asp Pro Ile Leu Trp Thr Pro Phe  
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Leu Pro Ser Gly Ser Ser Leu Thr Ser Glu Val Thr Lys Thr Glu Thr  
 405 410 415

Ser Cys Ser Thr Tyr Ser Tyr Leu Pro Gln Glu Lys  
 420 425

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 Met Thr Thr Glu Lys Glu Asn Val Thr Thr Ala  
 1 5 10



gtg gcc gtg aaa gac ggc gga gaa aag agt aag gaa gtg agt .gac aag  
100

Val Ala Val Lys Asp Gly Gly Glu Lys Ser Lys Glu Val Ser Asp Lys  
15 20 25

ggc gta aag aag aga aag aat gta act aag gcc ctg gcc gtg aat gac  
148

Gly Val Lys Lys Arg Lys Asn Val Thr Lys Ala Leu Ala Val Asn Asp  
30 35 40

ggc gga gaa aag agt aag gaa gtg cgt tac agg ggt gta agg agg aga  
196

Gly Gly Glu Lys Ser Lys Glu Val Arg Tyr Arg Gly Val Arg Arg Arg  
45 50 55

cca tgg ggg aga tat gct gcg gag atc cgt gat ccg gta aag aaa aaa  
244

Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Val Lys Lys Lys  
60 65 70 75

cgg gtc tgg ctc ggg tcc ttc aac acg ggg gag gaa gcc gcc aga gcc  
292

Arg Val Trp Leu Gly Ser Phe Asn Thr Gly Glu Glu Ala Ala Arg Ala  
80 85 90

tac gac tcc gct gcc ata agg ttt cga gga tcg aaa gct act act aac  
340

Tyr Asp Ser Ala Ala Ile Arg Phe Arg Gly Ser Lys Ala Thr Thr Asn  
95 100 105

ttc cct cta atc gga tac tat ggg att tct tcg gcg acg ccg gtg aac  
388

Phe Pro Leu Ile Gly Tyr Tyr Gly Ile Ser Ser Ala Thr Pro Val Asn  
110 115 120

aac aac ctt tcc gag acg gtg agt gat gga aat gcc aac ctc cct ctc  
436

Asn Asn Leu Ser Glu Thr Val Ser Asp Gly Asn Ala Asn Leu Pro Leu  
125 130 135

gtt gga gac gat ggg aat gct ttg gct tct ccg gtg aac aac acc ctt  
484

Val Gly Asp Asp Gly Asn Ala Leu Ala Ser Pro Val Asn Asn Thr Leu  
140 145 150 155

tcc gaa acg gcg cgt gat gga aca ctt cca tcg gat tgt cac gac atg  
532

Ser Glu Thr Ala Arg Asp Gly Thr Leu Pro Ser Asp Cys His Asp Met  
160 165 170

tta tct ccg ggg gtg gct gaa gcg gtt gct gga ttt ttc tta gat ctg  
580

Leu Ser Pro Gly Val Ala Glu Ala Val Ala Gly Phe Phe Leu Asp Leu  
175 180 185

cct gaa gtt att gcg ttg aaa gag gag ctt gat cga gtt tgt cct gac  
628

Pro Glu Val Ile Ala Leu Lys Glu Glu Leu Asp Arg Val Cys Pro Asp  
190 195 200



cag ttt gag tcc att gat atg ggg ttg act att ggt cct caa acc gcc  
 676  
 Gln Phe Glu Ser Ile Asp Met Gly Leu Thr Ile Gly Pro Gln Thr Ala  
 205 210 215  
 gtg gaa gag cct gag act tcc tcc gcc gtg gat tgt aag ctg cga atg  
 724  
 Val Glu Glu Pro Glu Thr Ser Ser Ala Val Asp Cys Lys Leu Arg Met  
 220 225 230 235  
 gaa ccg gat ctt gac ctc aac gca agt ccc taa agattgatct gatgttgttg  
 777  
 Glu Pro Asp Leu Asp Leu Asn Ala Ser Pro  
 240 245  
 tccttgaata agtttgttat cttgtcgctc ttctgattgt ctgtacttct attggttgat  
 837  
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 933  
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 35 40 45  
 Lys Glu Val Arg Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Arg Tyr  
 50 55 60  
 Ala Ala Glu Ile Arg Asp Pro Val Lys Lys Lys Arg Val Trp Leu Gly  
 65 70 75 80  
 Ser Phe Asn Thr Gly Glu Glu Ala Ala Arg Ala Tyr Asp Ser Ala Ala  
 85 90 95  
 Ile Arg Phe Arg Gly Ser Lys Ala Thr Thr Asn Phe Pro Leu Ile Gly  
 100 105 110  
 Tyr Tyr Gly Ile Ser Ser Ala Thr Pro Val Asn Asn Asn Leu Ser Glu  
 115 120 125  
 Thr Val Ser Asp Gly Asn Ala Asn Leu Pro Leu Val Gly Asp Asp Gly



130 135 140

Asn Ala Leu Ala Ser Pro Val Asn Asn Thr Leu Ser Glu Thr Ala Arg  
 145 150 155 160

Asp Gly Thr Leu Pro Ser Asp Cys His Asp Met Leu Ser Pro Gly Val  
 165 170 175

Ala Glu Ala Val Ala Gly Phe Phe Leu Asp Leu Pro Glu Val Ile Ala  
 180 185 190

Leu Lys Glu Glu Leu Asp Arg Val Cys Pro Asp Gln Phe Glu Ser Ile  
 195 200 205

Asp Met Gly Leu Thr Ile Gly Pro Gln Thr Ala Val Glu Glu Pro Glu  
 210 215 220

Thr Ser Ser Ala Val Asp Cys Lys Leu Arg Met Glu Pro Asp Leu Asp  
 225 230 235 240

Leu Asn Ala Ser Pro  
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tctgttagga tata atg cca ccc tct cct cct aaa tct cct ttt att agc  
 110

Met Pro Pro Ser Pro Pro Lys Ser Pro Phe Ile Ser  
 1 5 10

tct tca ctc aaa gga gct cat gaa gat cgc aaa ttt aaa tgc tat agg  
 158

Ser Ser Leu Lys Gly Ala His Glu Asp Arg Lys Phe Lys Cys Tyr Arg  
 15 20 25

ggg gtc cga aag agg tct tgg ggc aaa tgg gtg tct gaa atc aga gtt  
 206

Gly Val Arg Lys Arg Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Val  
 30 35 40

cca aag act gga cga cga ata tgg cta ggt tca tac gat gct cca gag  
 254

Pro Lys Thr Gly Arg Arg Ile Trp Leu Gly Ser Tyr Asp Ala Pro Glu  
 45 50 55 60

aag gca gct aga gcc tat gat gct gct ttg ttc tgt att agg ggt gag  
 302

Lys Ala Ala Arg Ala Tyr Asp Ala Ala Leu Phe Cys Ile Arg Gly Glu



65 70 75  
 aag gga gtt tac aat ttt ccc act gat aaa aag ccg cag ctt cca gaa  
 350  
 Lys Gly Val Tyr Asn Phe Pro Thr Asp Lys Lys Pro Gln Leu Pro Glu  
 80 85 90  
 ggt tct gtc cgg cct ctg tcc aag ctc gac ata cag aca ata gca aca  
 398  
 Gly Ser Val Arg Pro Leu Ser Lys Leu Asp Ile Gln Thr Ile Ala Thr  
 95 100 105  
 aac tat gct tca tca gtt gtg cat gta cct tcc cat gcc acc aca ctc  
 446  
 Asn Tyr Ala Ser Ser Val Val His Val Pro Ser His Ala Thr Thr Leu  
 110 115 120  
 ccg gca aca acc cag gtt ccc tct gaa gtt cct gct tcc tct gat gtt  
 494  
 Pro Ala Thr Thr Gln Val Pro Ser Glu Val Pro Ala Ser Ser Asp Val  
 125 130 135 140  
 tct gct tct act gag att aca gag atg gtc gat gaa tat tat ctc cca  
 542  
 Ser Ala Ser Thr Glu Ile Thr Glu Met Val Asp Glu Tyr Tyr Leu Pro  
 145 150 155  
 acc gat gca act gca gaa tca ata ttc tca gtt gaa gac tta caa ctg  
 590  
 Thr Asp Ala Thr Ala Glu Ser Ile Phe Ser Val Glu Asp Leu Gln Leu  
 160 165 170  
 gac agt ttc ctc atg atg gac att gat tgg ata aac aat cta atc tga  
 638  
 Asp Ser Phe Leu Met Met Asp Ile Asp Trp Ile Asn Asn Leu Ile  
 175 180 185  
 tgtgtaacgt cacttgcaagt gacatttaac atgggttaac tatcagttac ctgtctgctt  
 698  
 cttgtaagggt tataacttgga tccttgctctt tgaacttggt ttatttagca tgcaaa  
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 Gly Ala His Glu Asp Arg Lys Phe Lys Cys Tyr Arg Gly Val Arg Lys  
 20 25 30  
 Arg Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro Lys Thr Gly  
 35 40 45  
 Arg Arg Ile Trp Leu Gly Ser Tyr Asp Ala Pro Glu Lys Ala Ala Arg  
 50 55 60



Ala Tyr Asp Ala Ala Leu Phe Cys Ile Arg Gly Glu Lys Gly Val Tyr  
65 70 75 80

Asn Phe Pro Thr Asp Lys Lys Pro Gln Leu Pro Glu Gly Ser Val Arg  
85 90 95

Pro Leu Ser Lys Leu Asp Ile Gln Thr Ile Ala Thr Asn Tyr Ala Ser  
100 105 110

Ser Val Val His Val Pro Ser His Ala Thr Thr Leu Pro Ala Thr Thr  
115 120 125

Gln Val Pro Ser Glu Val Pro Ala Ser Ser Asp Val Ser Ala Ser Thr  
130 135 140

Glu Ile Thr Glu Met Val Asp Glu Tyr Tyr Leu Pro Thr Asp Ala Thr  
145 150 155 160

Ala Glu Ser Ile Phe Ser Val Glu Asp Leu Gln Leu Asp Ser Phe Leu  
165 170 175

Met Met Asp Ile Asp Trp Ile Asn Asn Leu Ile  
180 185

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54

Met Ala Arg Gly Lys Ile  
1 5

cag ctt aag agg att gag aac ccg gtt cac aga caa gtg act ttt tgc  
102

Gln Leu Lys Arg Ile Glu Asn Pro Val His Arg Gln Val Thr Phe Cys  
10 15 20

aag agg aga act ggt ctt ctc aag aag gct aag gag ctc tct gtg ctc  
150

Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Val Leu  
25 30 35

tgt gat gcc gag atc ggt gtt gtg atc ttc tct cct cag ggc aag ctc  
198

Cys Asp Ala Glu Ile Gly Val Val Ile Phe Ser Pro Gln Gly Lys Leu  
40 45 50

ttt gag ctc gct act aaa gga aca atg gag gga atg att gat aag tac  
246

Phe Glu Leu Ala Thr Lys Gly Thr Met Glu Gly Met Ile Asp Lys Tyr



86



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48

Met Ala Arg Gly Lys Ile Gln Leu Lys Arg Ile Glu Asn Pro Val His  
1 5 10 15

Arg Gln Val Thr Phe Cys Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala  
20 25 30

Lys Glu Leu Ser Val Leu Cys Asp Ala Glu Ile Gly Val Val Ile Phe  
35 40 45

Ser Pro Gln Gly Lys Leu Phe Glu Leu Ala Thr Lys Gly Thr Met Glu  
50 55 60

Gly Met Ile Asp Lys Tyr Met Lys Cys Thr Gly Gly Gly Arg Gly Ser  
65 70 75 80

Ser Ser Ala Thr Phe Thr Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu  
85 90 95

Asp Pro Lys Asp Glu Ile Asn Val Leu Lys Gln Glu Ile Glu Met Leu  
100 105 110

Gln Lys Gly Ile Ser Tyr Met Phe Gly Gly Gly Asp Gly Ala Met Asn  
115 120 125

Leu Glu Glu Leu Leu Leu Leu Glu Lys His Leu Glu Tyr Trp Ile Ser  
130 135 140

Gln Ile Arg Ser Ala Lys Met Asp Val Met Leu Gln Glu Ile Gln Ser  
145 150 155 160

Leu Arg Asn Lys Glu Gly Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu  
165 170 175

Asp Lys Ile Glu Glu Asn Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala  
180 185 190

Val Met Glu Thr Asn Tyr Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile  
195 200 205

Phe Gln Phe  
210



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ttttgatttt ttgtgttgga ttgaagagaa gaatagttaa ttgatgtttt gtgaagaaga  
 120

agaagaagag attttgattt tgggttaata tatagtggg gattaacagg atg gga  
 176

Met Gly  
 1

agg gta aaa ttg aag ata aag aag tta gag aac aca aat gga cgc caa  
 224  
 Arg Val Lys Leu Lys Ile Lys Lys Leu Glu Asn Thr Asn Gly Arg Gln  
           5                                  10                                  15

tct aca ttt gct aaa agg aaa aat ggg atc ttg aaa aag gct aat gag  
 272  
 Ser Thr Phe Ala Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala Asn Glu  
           20                                  25                                  30

cta tct att ctt tgt gac att gat att gtt ctt ctt atg ttc tct cct  
 320  
 Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe Ser Pro  
           35                                  40                                  45                                  50

act ggc aag gct gca ata tgt tgc ggt aca cga aga tgt ttc tct ttc  
 368  
 Thr Gly Lys Ala Ala Ile Cys Cys Gly Thr Arg Arg Cys Phe Ser Phe  
                                   55                                  60                                  65

gaa agc tca gaa ctt gaa gaa aac ttt cca aaa gtt gga tca cga tgt  
 416  
 Glu Ser Ser Glu Leu Glu Glu Asn Phe Pro Lys Val Gly Ser Arg Cys  
                                   70                                  75                                  80

aaa tat acg cga att tat agc ctc aag gac ttg agt act caa gca agg  
 464  
 Lys Tyr Thr Arg Ile Tyr Ser Leu Lys Asp Leu Ser Thr Gln Ala Arg  
                                   85                                  90                                  95

att ctg cag gct cgg att tct gag ata cat gga aga tta agt tat tgg  
 512  
 Ile Leu Gln Ala Arg Ile Ser Glu Ile His Gly Arg Leu Ser Tyr Trp  
           100                                  105                                  110

acg gaa cca gat aag att aac aat gtt gaa cac ttg gga cag ctc gaa  
 560  
 Thr Glu Pro Asp Lys Ile Asn Asn Val Glu His Leu Gly Gln Leu Glu  
           115                                  120                                  125                                  130

att tcg att agg caa tcc ctt gat caa ttg cgt gca cac aag atg caa  
 608  
 Ile Ser Ile Arg Gln Ser Leu Asp Gln Leu Arg Ala His Lys Met Gln  
                                   135                                  140                                  145



gat ggg att cag att cct tta gaa caa cag ctt caa tct atg tca tgg  
 656  
 Asp Gly Ile Gln Ile Pro Leu Glu Gln Gln Leu Gln Ser Met Ser Trp  
 150 155 160

att ctt aat agc aac acc acc aac att gtc acc gag gaa cac aat tca  
 704  
 Ile Leu Asn Ser Asn Thr Thr Asn Ile Val Thr Glu Glu His Asn Ser  
 165 170 175

atc ccg cag agg gaa gtc gag tgc tca gcg agt tct tca ttc ggg agc  
 752  
 Ile Pro Gln Arg Glu Val Glu Cys Ser Ala Ser Ser Ser Phe Gly Ser  
 180 185 190

tat cca ggc tac ttt gga aca ggg aaa tct cct gaa atg aca att ccg  
 800  
 Tyr Pro Gly Tyr Phe Gly Thr Gly Lys Ser Pro Glu Met Thr Ile Pro  
 195 200 205 210

ggt caa gaa aca agc ttt ctt gat gaa cta aac acc gga cag ctg aaa  
 848  
 Gly Gln Glu Thr Ser Phe Leu Asp Glu Leu Asn Thr Gly Gln Leu Lys  
 215 220 225

cag gac aca agc tcg cag cag cag ttc act aat aat aat aat atc aca  
 896  
 Gln Asp Thr Ser Ser Gln Gln Gln Phe Thr Asn Asn Asn Asn Ile Thr  
 230 235 240

gca tac aat ccc aat ctt cac aat gat atg aat cat cac caa acg ttg  
 944  
 Ala Tyr Asn Pro Asn Leu His Asn Asp Met Asn His His Gln Thr Leu  
 245 250 255

cct cct cct cct ctt cct ctt act ctt ccg cat gct cag gtg tat att  
 992  
 Pro Pro Pro Pro Leu Pro Leu Thr Leu Pro His Ala Gln Val Tyr Ile  
 260 265 270

cca atg aat cag aga gag tat cat atg aat gga ttc ttt gaa gca cca  
 1040  
 Pro Met Asn Gln Arg Glu Tyr His Met Asn Gly Phe Phe Glu Ala Pro  
 275 280 285 290

cca cct gat tct tct gct tac aac gac aac acc aac caa acc agg ttt  
 1088  
 Pro Pro Asp Ser Ser Ala Tyr Asn Asp Asn Thr Asn Gln Thr Arg Phe  
 295 300 305

ggt tct agc agc agc tcc ttg cct tgc tca atc tca atg ttc gac gaa  
 1136  
 Gly Ser Ser Ser Ser Ser Leu Pro Cys Ser Ile Ser Met Phe Asp Glu  
 310 315 320

tac ttg ttt tcc cag atg cag cag ccg aac tga gagagatttg atgaatgatg  
 1189  
 Tyr Leu Phe Ser Gln Met Gln Gln Pro Asn  
 325 330



ataaaacatc tcaactgaaga aactcaaacc aatatttttt ttcagaaaca gcaagaaagc  
1249

taaaactctg ccgatttctg aattggttcc aagaagaaaa aaaccagtgg taatccctgg  
1309

tagattgtgc aaccaaacca cacacaatac gtgttcattt attttttcta tatcttcaat  
1369

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1414

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Arg Gln Ser Thr Phe Ala Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala  
20 25 30

Asn Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe  
35 40 45

Ser Pro Thr Gly Lys Ala Ala Ile Cys Cys Gly Thr Arg Arg Cys Phe  
50 55 60

Ser Phe Glu Ser Ser Glu Leu Glu Glu Asn Phe Pro Lys Val Gly Ser  
65 70 75 80

Arg Cys Lys Tyr Thr Arg Ile Tyr Ser Leu Lys Asp Leu Ser Thr Gln  
85 90 95

Ala Arg Ile Leu Gln Ala Arg Ile Ser Glu Ile His Gly Arg Leu Ser  
100 105 110

Tyr Trp Thr Glu Pro Asp Lys Ile Asn Asn Val Glu His Leu Gly Gln  
115 120 125

Leu Glu Ile Ser Ile Arg Gln Ser Leu Asp Gln Leu Arg Ala His Lys  
130 135 140

Met Gln Asp Gly Ile Gln Ile Pro Leu Glu Gln Gln Leu Gln Ser Met  
145 150 155 160

Ser Trp Ile Leu Asn Ser Asn Thr Thr Asn Ile Val Thr Glu Glu His  
165 170 175

Asn Ser Ile Pro Gln Arg Glu Val Glu Cys Ser Ala Ser Ser Ser Phe



180 185 190

Gly Ser Tyr Pro Gly Tyr Phe Gly Thr Gly Lys Ser Pro Glu Met Thr  
195 200 205

Ile Pro Gly Gln Glu Thr Ser Phe Leu Asp Glu Leu Asn Thr Gly Gln  
210 215 220

Leu Lys Gln Asp Thr Ser Ser Gln Gln Gln Phe Thr Asn Asn Asn Asn  
225 230 235 240

Ile Thr Ala Tyr Asn Pro Asn Leu His Asn Asp Met Asn His His Gln  
245 250 255

Thr Leu Pro Pro Pro Pro Leu Pro Leu Thr Leu Pro His Ala Gln Val  
260 265 270

Tyr Ile Pro Met Asn Gln Arg Glu Tyr His Met Asn Gly Phe Phe Glu  
275 280 285

Ala Pro Pro Pro Asp Ser Ser Ala Tyr Asn Asp Asn Thr Asn Gln Thr  
290 295 300

Arg Phe Gly Ser Ser Ser Ser Ser Leu Pro Cys Ser Ile Ser Met Phe  
305 310 315 320

Asp Glu Tyr Leu Phe Ser Gln Met Gln Gln Pro Asn  
325 330

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Met Val Arg Ser Thr Lys  
1 5

ggt cgt cag aaa ata gag atg aaa aaa atg gaa aac gaa agc aac ctt  
103

Gly Arg Gln Lys Ile Glu Met Lys Lys Met Glu Asn Glu Ser Asn Leu  
10 15 20

cag gtt act ttc tca aaa aga aga ttc ggt ctt ttc aaa aaa gct agt  
151

Gln Val Thr Phe Ser Lys Arg Arg Phe Gly Leu Phe Lys Lys Ala Ser  
25 30 35

gaa ctt tgc aca tta agt ggt gca gag att ctg ttg att gtg ttc tct  
199

Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile Leu Leu Ile Val Phe Ser



40 45 50  
 cct ggt ggg aaa gtg ttt tct ttt ggc cat cca agt gtt caa gaa ctc  
 247  
 Pro Gly Gly Lys Val Phe Ser Phe Gly His Pro Ser Val Gln Glu Leu  
 55 60 65 70  
 att cat cgc ttt tcg aat cct aac cat aat tct gcc att gtc cat cat  
 295  
 Ile His Arg Phe Ser Asn Pro Asn His Asn Ser Ala Ile Val His His  
 75 80 85  
 cag aac aac aat ctc caa ctt gtt gaa acc cgt ccg gat aga aat atc  
 343  
 Gln Asn Asn Asn Leu Gln Leu Val Glu Thr Arg Pro Asp Arg Asn Ile  
 90 95 100  
 caa tat ctc aac aat ata ctc act gag gtg ctg gca aac cag gaa aag  
 391  
 Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val Leu Ala Asn Gln Glu Lys  
 105 110 115  
 gag aaa cag aag aga atg gtt ttg gac cta ttg aaa gaa tcc aga gaa  
 439  
 Glu Lys Gln Lys Arg Met Val Leu Asp Leu Leu Lys Glu Ser Arg Glu  
 120 125 130  
 caa gta gga aac tgg tat gaa aaa gat gtg aaa gat ctc gac atg aat  
 487  
 Gln Val Gly Asn Trp Tyr Glu Lys Asp Val Lys Asp Leu Asp Met Asn  
 135 140 145 150  
 gaa acc aac cag ctg ata tct gct ctt caa gat gtg aaa aag aaa ctg  
 535  
 Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln Asp Val Lys Lys Lys Leu  
 155 160 165  
 gta aga gaa atg tct caa tat tct caa gta aat gtt tcg cag aat tac  
 583  
 Val Arg Glu Met Ser Gln Tyr Ser Gln Val Asn Val Ser Gln Asn Tyr  
 170 175 180  
 ttt ggt caa agt tct ggc gtg att ggt ggt ggt aat gtt ggc att gat  
 631  
 Phe Gly Gln Ser Ser Gly Val Ile Gly Gly Gly Asn Val Gly Ile Asp  
 185 190 195  
 ctt ttt gat caa aga aga aat gca ttc aac tat aat cca aac atg gtg  
 679  
 Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn Tyr Asn Pro Asn Met Val  
 200 205 210  
 ttt ccc aat cat aca cca cca atg ttt gga tac aac aat gat gga gtt  
 727  
 Phe Pro Asn His Thr Pro Pro Met Phe Gly Tyr Asn Asn Asp Gly Val  
 215 220 225 230  
 ctc gtt ccg ata tcc aac atg aac tac atg tca agt tac aac ttc aac  
 775  
 Leu Val Pro Ile Ser Asn Met Asn Tyr Met Ser Ser Tyr Asn Phe Asn  
 235 240 245



cag agc tag agtctgaagc tagaagaaca tcctaataca tatttgcgtt  
824

Gln Ser

atattggcta tgggtactgt taggattgtt cttgtattgt gagacttaag tttgtttttt  
884

cttttaattt gtttcagttg gttgggtttt cattttattc gtcgtttgtt ttcctttgtt  
944

tttggatatt tttgtatccc agaataaatt tatttatcct ttaaaaa  
991

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20 25 30

Leu Phe Lys Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile  
35 40 45

Leu Leu Ile Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His  
50 55 60

Pro Ser Val Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn  
65 70 75 80

Ser Ala Ile Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr  
85 90 95

Arg Pro Asp Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val  
100 105 110

Leu Ala Asn Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu  
115 120 125

Leu Lys Glu Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val  
130 135 140

Lys Asp Leu Asp Met Asn Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln  
145 150 155 160

Asp Val Lys Lys Lys Leu Val Arg Glu Met Ser Gln Tyr Ser Gln Val  
165 170 175



Asn Val Ser Gln Asn Tyr Phe Gly Gln Ser Ser Gly Val Ile Gly Gly  
180 185 190

Gly Asn Val Gly Ile Asp Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn  
195 200 205

Tyr Asn Pro Asn Met Val Phe Pro Asn His Thr Pro Pro Met Phe Gly  
210 215 220

Tyr Asn Asn Asp Gly Val Leu Val Pro Ile Ser Asn Met Asn Tyr Met  
225 230 235 240

Ser Ser Tyr Asn Phe Asn Gln Ser  
245

<210> 53 <211> 837 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (54)..(629) <223> G180

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56

Met  
1

aac ttc ctc gtt cct ttt gaa gaa acc aat gtc tta acc ttt ttc tct  
104  
Asn Phe Leu Val Pro Phe Glu Glu Thr Asn Val Leu Thr Phe Phe Ser  
5 10 15

tct tct tct tcc tct tct ctt tct tct cct tct ttc ccc att cac aac  
152  
Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His Asn  
20 25 30

tct tcc tcc act act act act cat gca cct cta ggg ttt tct aat aat  
200  
Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn Asn  
35 40 45

ctt cag ggt gga gga ccc ttg gga tca aag gtg gtt aat gat gat cag  
248  
Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp Gln  
50 55 60 65

gag aat ttt gga ggt gga act aac aat gat gct cat tct aat tct tgg  
296  
Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser Trp  
70 75 80

tgg aga tca aat agt gga agt gga gat atg aag aac aaa gtg aag ata  
344  
Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys Ile  
85 90 95



agg agg aaa cta aga gag cca aga ttc tgt ttc caa acc aaa agc gat  
392

Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser Asp  
100 105 110

gtt gat gtt ctt gac gat ggc tac aaa tgg cgt aaa tat ggt cag aaa  
440

Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln Lys  
115 120 125

gtc gtc aag aac agc ctt cac ccc agg agt tat tac aga tgc aca cac  
488

Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr His  
130 135 140 145

aac aac tgt agg gtg aaa aag aga gtg gag cga cta tcg gaa gat tgt  
536

Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp Cys  
150 155 160

aga atg gtg att act act tac gaa ggt cgt cac aac cac att ccc tct  
584

Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro Ser  
165 170 175

gat gac tcc act tct cct gac cat gat tgt ctc tct tcc ttt taa  
629

Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe  
180 185 190

catctctttc tatatatcta tatatagaca gttatatgtg cacatataga tgtgtgatat  
689

attgcatatt tgatattgca tgtgtttttc aagagtatgt catcagatgt tatgcatata  
749

ttcttgactt gttgcttata gtatacatat gtaataatat atattgacat tggtagttca  
809

tttctgttca aacaaaaaaaa aaaaaaaaa  
837

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54

Met Asn Phe Leu Val Pro Phe Glu Glu Thr Asn Val Leu Thr Phe Phe  
1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His  
20 25 30

Asn Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn  
35 40 45

Asn Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp  
50 55 60



Gln Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser  
65 70 75 80

Trp Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys  
85 90 95

Ile Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser  
100 105 110

Asp Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln  
115 120 125

Lys Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr  
130 135 140

His Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp  
145 150 155 160

Cys Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro  
165 170 175

Ser Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe  
180 185 190

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49

Met Asp Arg Glu Asp Ile Asn Pro Met Leu Ser Arg Leu Asp Val  
1 5 10 15

gaa aac aac aac acc ttc tct tcc ttt gta gac aaa acc cta atg atg  
97

Glu Asn Asn Asn Thr Phe Ser Ser Phe Val Asp Lys Thr Leu Met Met  
20 25 30

atg cct cca tca aca ttt tcc ggt gaa gtg gaa cct tca tct tct tct  
145

Met Pro Pro Ser Thr Phe Ser Gly Glu Val Glu Pro Ser Ser Ser Ser  
35 40 45

tct tgg tat cca gaa agc ttt cat gtg cat gcg ccg cca tta cca cct  
193

Ser Trp Tyr Pro Glu Ser Phe His Val His Ala Pro Pro Leu Pro Pro  
50 55 60

gag aat gat caa ata ggt gag aaa ggg aag gag ctg aaa gag aag aga  
241

Glu Asn Asp Gln Ile Gly Glu Lys Gly Lys Glu Leu Lys Glu Lys Arg  
65 70 75



tcg agg aaa gtt cca agg att gcg ttt cat acg agg agc gat gat gat  
289

Ser Arg Lys Val Pro Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp  
80 85 90 95

gtt ctt gat gat ggt tat cgt tgg cga aaa tat ggg cag aaa tct gtc  
337

Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val  
100 105 110

aag cac aat gct cat ccc agg agc tat tac aga tgt acg tac cac aca  
385

Lys His Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr  
115 120 125

tgc aac gtg aag aaa caa gtg cag aga ttg gca aaa gat cca aac gtc  
433

Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val  
130 135 140

gtc gta acg acc tac gaa ggc gtt cat aac cat cct tgt gag aag ctc  
481

Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu  
145 150 155

atg gag act ctt aat cct ctt ctc agg caa ctc cag ttc ctc tcc agt  
529

Met Glu Thr Leu Asn Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Ser  
160 165 170 175

ttc tct aat ctt tga atatataatg gcttaattaa tgggtgaatt acttaaaggt  
584

Phe Ser Asn Leu

gattaaggtg ttaatcacc cactgaccgt ttgacgaccc acatctccca agtgacaagt  
644

cacaagtgtg tagatcagat tttaaacc aa tgtaacagtt acgacttttt acaaagtgtt  
704

ctgaatttta tcccctgatt tctggttaat gatcggttta cgccgatgat ttgacaaata  
764

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824

ttaaaaaaaa aaaaaaaaaa  
844

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Met Asp Arg Glu Asp Ile Asn Pro Met Leu Ser Arg Leu Asp Val Glu  
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Asn Asn Asn Thr Phe Ser Ser Phe Val Asp Lys Thr Leu Met Met Met  
20 25 30



Pro Pro Ser Thr Phe Ser Gly Glu Val Glu Pro Ser Ser Ser Ser Ser  
                   35                  40                  45

Trp Tyr Pro Glu Ser Phe His Val His Ala Pro Pro Leu Pro Pro Glu  
           50                  55                  60

Asn Asp Gln Ile Gly Glu Lys Gly Lys Glu Leu Lys Glu Lys Arg Ser  
   65                  70                  75                  80

Arg Lys Val Pro Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val  
                   85                  90                  95

Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys  
                   100                  105                  110

His Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys  
           115                  120                  125

Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val  
   130                  135                  140

Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met  
   145                  150                  155                  160

Glu Thr Leu Asn Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Ser Phe  
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Ser Asn Leu

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 120

tttccttttt gatcttccta tatatggaga agcaccaaaa cgttacttac tatacgatac  
 180

tgtacggatc catcaaaactg gattaattat caaaacgtac atttttatct tacctggcaa  
 240

gttacattcc tagggttttg gagaatccaa tcaacaacaa agaaaataat catcggtaca  
 300



ataatcagta tcacgcacag acttag atg ttc cgg ttt cca gtg agt cta ggc  
353

Met Phe Arg Phe Pro Val Ser Leu Gly  
1 5

ggg tca cgt gac gaa gac cgt cac gat cag atc aca ccg ttg gat gac  
401

Gly Ser Arg Asp Glu Asp Arg His Asp Gln Ile Thr Pro Leu Asp Asp  
10 15 20 25

cat cgt gtg gtg gtt gat gag gtt gac ttc ttc tca gag aag aga gat  
449

His Arg Val Val Val Asp Glu Val Asp Phe Phe Ser Glu Lys Arg Asp  
30 35 40

agg gtt tca cgt gag aac atc aac gac gac gac gac gaa ggc aat aag  
497

Arg Val Ser Arg Glu Asn Ile Asn Asp Asp Asp Asp Glu Gly Asn Lys  
45 50 55

gtt ctc atc aaa atg gag ggt tca cga gtt gaa gaa aac gat cgt tcc  
545

Val Leu Ile Lys Met Glu Gly Ser Arg Val Glu Glu Asn Asp Arg Ser  
60 65 70

aga gat gtc aat atc ggt ctg aat ctt ctg acc gcg aat acg gga agc  
593

Arg Asp Val Asn Ile Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser  
75 80 85

gat gag tca acg gtg gat gat gga cta tca atg gat atg gaa gat aaa  
641

Asp Glu Ser Thr Val Asp Asp Gly Leu Ser Met Asp Met Glu Asp Lys  
90 95 100 105

cgt gca aag att gag aac gca caa cta caa gaa gag ctc aag aag atg  
689

Arg Ala Lys Ile Glu Asn Ala Gln Leu Gln Glu Glu Leu Lys Lys Met  
110 115 120

aaa ata gag aat caa agg cta aga gat atg ttg agc caa gcg acg acc  
737

Lys Ile Glu Asn Gln Arg Leu Arg Asp Met Leu Ser Gln Ala Thr Thr  
125 130 135

aac ttc aat gcc tta caa atg caa ctt gtt gcc gtc atg agg caa caa  
785

Asn Phe Asn Ala Leu Gln Met Gln Leu Val Ala Val Met Arg Gln Gln  
140 145 150

gaa caa cgt aac tct tca caa gat cat ctc ctg gag agc aaa gca gaa  
833

Glu Gln Arg Asn Ser Ser Gln Asp His Leu Leu Glu Ser Lys Ala Glu  
155 160 165

gga agg aaa cgg cag gaa ctg caa atc atg gtg cca agg cag ttc atg  
881

Gly Arg Lys Arg Gln Glu Leu Gln Ile Met Val Pro Arg Gln Phe Met  
170 175 180 185



gac ctt ggg ccg tcg tct gga gca gca gag cat gga gcc gaa gtg tca  
 929  
 Asp Leu Gly Pro Ser Ser Gly Ala Ala Glu His Gly Ala Glu Val Ser  
 190 195 200

tct gaa gag agg aca acg gtt cgt tca ggt tct cct cct tcg ctt cta  
 977  
 Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro Ser Leu Leu  
 205 210 215

gaa agt tcc aat ccc cga gag aac gga aag agg ttg ctt gga aga gaa  
 1025  
 Glu Ser Ser Asn Pro Arg Glu Asn Gly Lys Arg Leu Leu Gly Arg Glu  
 220 225 230

gaa agc tca gag gaa tca gag tct aac gcc tgg gga aac cct aac aaa  
 1073  
 Glu Ser Ser Glu Glu Ser Glu Ser Asn Ala Trp Gly Asn Pro Asn Lys  
 235 240 245

gtc ccc aaa cat aat cca tcc tct agc aat agc aat gga aac aga aac  
 1121  
 Val Pro Lys His Asn Pro Ser Ser Ser Asn Ser Asn Gly Asn Arg Asn  
 250 255 260 265

gga aat gtt att gat cag tcg gcc gca gaa gcc acc atg cgg aaa gcc  
 1169  
 Gly Asn Val Ile Asp Gln Ser Ala Ala Glu Ala Thr Met Arg Lys Ala  
 270 275 280

cgt gtc tca gtt cgt gcc cga tct gaa gct gcc atg ata agc gat gga  
 1217  
 Arg Val Ser Val Arg Ala Arg Ser Glu Ala Ala Met Ile Ser Asp Gly  
 285 290 295

tgt caa tgg aga aag tac gga caa aaa atg gct aaa gga aac ccg tgt  
 1265  
 Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met Ala Lys Gly Asn Pro Cys  
 300 305 310

ccg cgg gct tat tat cgt tgc aca atg gcc ggt gga tgt cca gtt cgc  
 1313  
 Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala Gly Gly Cys Pro Val Arg  
 315 320 325

aag caa gtg cag cgt tgc gca gaa gac aga tct att ctc ata acc acc  
 1361  
 Lys Gln Val Gln Arg Cys Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr  
 330 335 340 345

tac gaa gga aac cac aac cat cca ctc cca cca gcc gct acg gcc atg  
 1409  
 Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro Ala Ala Thr Ala Met  
 350 355 360

gcc tca aca acc acc gca gct gca agc atg ctc ctc tcg ggc tca atg  
 1457  
 Ala Ser Thr Thr Thr Ala Ala Ala Ser Met Leu Leu Ser Gly Ser Met  
 365 370 375



tcg agt caa gac ggt tta atg aac cca aca aac ctc cta gct cga gct  
1505

Ser Ser Gln Asp Gly Leu Met Asn Pro Thr Asn Leu Leu Ala Arg Ala  
380 385 390

atc ttg cct tgc tcc tca agc atg gct aca atc tca gcc tcc gca cca  
1553

Ile Leu Pro Cys Ser Ser Ser Met Ala Thr Ile Ser Ala Ser Ala Pro  
395 400 405

ttc cca acc atc aca ttg gac ctc acc aat tca ccc aac ggt aac aac  
1601

Phe Pro Thr Ile Thr Leu Asp Leu Thr Asn Ser Pro Asn Gly Asn Asn  
410 415 420 425

cct aat atg acc act aat aac ccg ttg atg cag ttc gct caa cgg ccc  
1649

Pro Asn Met Thr Thr Asn Asn Pro Leu Met Gln Phe Ala Gln Arg Pro  
430 435 440

ggt ttc aac ccg gca gtt ttg cct caa gtg gtt ggt caa gct atg tac  
1697

Gly Phe Asn Pro Ala Val Leu Pro Gln Val Val Gly Gln Ala Met Tyr  
445 450 455

aat aac caa caa cag tcc aag ttt tct ggt tta cag tta ccg gct cag  
1745

Asn Asn Gln Gln Gln Ser Lys Phe Ser Gly Leu Gln Leu Pro Ala Gln  
460 465 470

cca ctg cag atc gcg gcc act tcc tcg gtg gcc gag agc gtt agt gct  
1793

Pro Leu Gln Ile Ala Ala Thr Ser Ser Val Ala Glu Ser Val Ser Ala  
475 480 485

gcc agt gca gca att gcg tcc gat cca aac ttt gcg gcg gct cta gcg  
1841

Ala Ser Ala Ala Ile Ala Ser Asp Pro Asn Phe Ala Ala Ala Leu Ala  
490 495 500 505

gca gcg atc acg tcc att atg aac ggt tcc agt cat caa aat aat aac  
1889

Ala Ala Ile Thr Ser Ile Met Asn Gly Ser Ser His Gln Asn Asn Asn  
510 515 520

acc aat aat aat aat gtg gct acg agc aac aat gac agt agg caa taa  
1937

Thr Asn Asn Asn Asn Val Ala Thr Ser Asn Asn Asp Ser Arg Gln  
525 530 535

gagttttcat tttgatggtc gatttttttt tttgggg  
1974

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58

Met Phe Arg Phe Pro Val Ser Leu Gly Gly Ser Arg Asp Glu Asp Arg  
1 5 10 15



His Asp Gln Ile Thr Pro Leu Asp Asp His Arg Val Val Val Asp Glu  
 20 25 30

Val Asp Phe Phe Ser Glu Lys Arg Asp Arg Val Ser Arg Glu Asn Ile  
 35 40 45

Asn Asp Asp Asp Asp Glu Gly Asn Lys Val Leu Ile Lys Met Glu Gly  
 50 55 60

Ser Arg Val Glu Glu Asn Asp Arg Ser Arg Asp Val Asn Ile Gly Leu  
 65 70 75 80

Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Thr Val Asp Asp  
 85 90 95

Gly Leu Ser Met Asp Met Glu Asp Lys Arg Ala Lys Ile Glu Asn Ala  
 100 105 110

Gln Leu Gln Glu Glu Leu Lys Lys Met Lys Ile Glu Asn Gln Arg Leu  
 115 120 125

Arg Asp Met Leu Ser Gln Ala Thr Thr Asn Phe Asn Ala Leu Gln Met  
 130 135 140

Gln Leu Val Ala Val Met Arg Gln Gln Glu Gln Arg Asn Ser Ser Gln  
 145 150 155 160

Asp His Leu Leu Glu Ser Lys Ala Glu Gly Arg Lys Arg Gln Glu Leu  
 165 170 175

Gln Ile Met Val Pro Arg Gln Phe Met Asp Leu Gly Pro Ser Ser Gly  
 180 185 190

Ala Ala Glu His Gly Ala Glu Val Ser Ser Glu Glu Arg Thr Thr Val  
 195 200 205

Arg Ser Gly Ser Pro Pro Ser Leu Leu Glu Ser Ser Asn Pro Arg Glu  
 210 215 220

Asn Gly Lys Arg Leu Leu Gly Arg Glu Glu Ser Ser Glu Glu Ser Glu  
 225 230 235 240

Ser Asn Ala Trp Gly Asn Pro Asn Lys Val Pro Lys His Asn Pro Ser  
 245 250 255

Ser Ser Asn Ser Asn Gly Asn Arg Asn Gly Asn Val Ile Asp Gln Ser



260	265	270
Ala Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg		
275	280	285
Ser Glu Ala Ala Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly		
290	295	300
Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys		
305	310	315
Thr Met Ala Gly Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala		
325	330	335
Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His		
340	345	350
Pro Leu Pro Pro Ala Ala Thr Ala Met Ala Ser Thr Thr Thr Ala Ala		
355	360	365
Ala Ser Met Leu Leu Ser Gly Ser Met Ser Ser Gln Asp Gly Leu Met		
370	375	380
Asn Pro Thr Asn Leu Leu Ala Arg Ala Ile Leu Pro Cys Ser Ser Ser		
385	390	395
Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp		
405	410	415
Leu Thr Asn Ser Pro Asn Gly Asn Asn Pro Asn Met Thr Thr Asn Asn		
420	425	430
Pro Leu Met Gln Phe Ala Gln Arg Pro Gly Phe Asn Pro Ala Val Leu		
435	440	445
Pro Gln Val Val Gly Gln Ala Met Tyr Asn Asn Gln Gln Gln Ser Lys		
450	455	460
Phe Ser Gly Leu Gln Leu Pro Ala Gln Pro Leu Gln Ile Ala Ala Thr		
465	470	475
Ser Ser Val Ala Glu Ser Val Ser Ala Ala Ser Ala Ala Ile Ala Ser		
485	490	495
Asp Pro Asn Phe Ala Ala Ala Leu Ala Ala Ala Ile Thr Ser Ile Met		
500	505	510



Asn Gly Ser Ser His Gln Asn Asn Asn Thr Asn Asn Asn Asn Val Ala  
 515 520 525

Thr Ser Asn Asn Asp Ser Arg Gln  
 530 535

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 112

Met Glu Lys Asn His Ser Ser Gly Glu Trp Glu Lys  
 1 5 10

atg aag aac gag atc aac gag cta atg ata gaa gga aga gac tat gca  
 160

Met Lys Asn Glu Ile Asn Glu Leu Met Ile Glu Gly Arg Asp Tyr Ala  
 15 20 25

cac cag ttt gga tca gct tca tct caa gaa aca cgt gaa cat tta gcc  
 208

His Gln Phe Gly Ser Ala Ser Ser Gln Glu Thr Arg Glu His Leu Ala  
 30 35 40

aaa aag att ctt caa tct tac cac aag tct ctc acc atc atg aac tac  
 256

Lys Lys Ile Leu Gln Ser Tyr His Lys Ser Leu Thr Ile Met Asn Tyr  
 45 50 55 60

tcc ggc gaa ctt gac caa gtt tct cag ggt gga gga agc ccc aag agc  
 304

Ser Gly Glu Leu Asp Gln Val Ser Gln Gly Gly Gly Ser Pro Lys Ser  
 65 70 75

gat gat tcc gat caa gaa cca ctt gtc atc aag agt tcg aag aag tca  
 352

Asp Asp Ser Asp Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser  
 80 85 90

atg cca agg tgg agt tca aaa gtc aga att gcc cct gga gct ggt gtt  
 400

Met Pro Arg Trp Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val  
 95 100 105

gat aga acg ctg gac gat gga ttc agt tgg aga aag tac ggc cag aag  
 448

Asp Arg Thr Leu Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys  
 110 115 120

gat att ctc gga gcc aaa ttt cca aga gga tac tat aga tgc acg tat  
 496

Asp Ile Leu Gly Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr  
 125 130 135 140



aga aag tct caa gga tgt gaa gcc act aaa caa gtc caa aga tct gat  
544

Arg Lys Ser Gln Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp  
145 150 155

gaa aat cag atg ctc ctt gag atc agt tac cga gga ata cat tct tgc  
592

Glu Asn Gln Met Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys  
160 165 170

tct caa gct gca aat gtc ggt aca aca atg ccg ata caa aac ctc gaa  
640

Ser Gln Ala Ala Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu  
175 180 185

ccg aac cag acc caa gaa cac gga aat ctt gac atg gta aag gaa agt  
688

Pro Asn Gln Thr Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser  
190 195 200

gta gac aac tac aat cac caa gca cat ttg cat cac aac ctt cac tat  
736

Val Asp Asn Tyr Asn His Gln Ala His Leu His His Asn Leu His Tyr  
205 210 215 220

cca ttg tca tct acc cca aat cta gag aat aac aat gcc tat atg ctt  
784

Pro Leu Ser Ser Thr Pro Asn Leu Glu Asn Asn Asn Ala Tyr Met Leu  
225 230 235

caa atg cga gat caa aac atc gaa tat ttt gga tct acg agc ttc tct  
832

Gln Met Arg Asp Gln Asn Ile Glu Tyr Phe Gly Ser Thr Ser Phe Ser  
240 245 250

agt gat cta gga act agt atc aac tac aat ttt cca gca tct ggc tcg  
880

Ser Asp Leu Gly Thr Ser Ile Asn Tyr Asn Phe Pro Ala Ser Gly Ser  
255 260 265

gct tct cac tca gca tca aac tct ccg tcc acc gtc cct ttg gaa tcc  
928

Ala Ser His Ser Ala Ser Asn Ser Pro Ser Thr Val Pro Leu Glu Ser  
270 275 280

ccg ttt gaa agc tat gat cca aat cat cca tat gga gga ttt ggt ggg  
976

Pro Phe Glu Ser Tyr Asp Pro Asn His Pro Tyr Gly Gly Phe Gly Gly  
285 290 295 300

ttc tat tct tag ttatctactt aaggaggga cggaactttt tacatgacct  
1028

Phe Tyr Ser

cttgattaaa gagagagttt tcataatagc taatcaattt cctattcaaa tatccgagtt  
1088

ttttttctaa tcatgtttat caattgtctt attacagaag gcttattttc aggtctatgt  
1148



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1205

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60

Met Glu Lys Asn His Ser Ser Gly Glu Trp Glu Lys Met Lys Asn Glu  
1 5 10 15

Ile Asn Glu Leu Met Ile Glu Gly Arg Asp Tyr Ala His Gln Phe Gly  
20 25 30

Ser Ala Ser Ser Gln Glu Thr Arg Glu His Leu Ala Lys Lys Ile Leu  
35 40 45

Gln Ser Tyr His Lys Ser Leu Thr Ile Met Asn Tyr Ser Gly Glu Leu  
50 55 60

Asp Gln Val Ser Gln Gly Gly Gly Ser Pro Lys Ser Asp Asp Ser Asp  
65 70 75 80

Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser Met Pro Arg Trp  
85 90 95

Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val Asp Arg Thr Leu  
100 105 110

Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys Asp Ile Leu Gly  
115 120 125

Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr Arg Lys Ser Gln  
130 135 140

Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp Glu Asn Gln Met  
145 150 155 160

Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys Ser Gln Ala Ala  
165 170 175

Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu Pro Asn Gln Thr  
180 185 190

Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser Val Asp Asn Tyr  
195 200 205

Asn His Gln Ala His Leu His His Asn Leu His Tyr Pro Leu Ser Ser



Thr	Pro	Asn	Leu	Glu	Asn	Asn	Asn	Ala	Tyr	Met	Leu	Gln	Met	Arg	Asp
225					230					235					240
Gln	Asn	Ile	Glu	Tyr	Phe	Gly	Ser	Thr	Ser	Phe	Ser	Ser	Asp	Leu	Gly
				245					250						255
Thr	Ser	Ile	Asn	Tyr	Asn	Phe	Pro	Ala	Ser	Gly	Ser	Ala	Ser	His	Ser
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		275					280					285			
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5 10 15

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Phe Asp Leu Pro Ser Lys Asn Leu Ser Pro Gln Gly Ala Phe Glu Leu  
55 60 65

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 70 75 80

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85 90 95



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 165 170 175

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 245 250 255

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 260 265 270

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968

Asn Val Asn Pro Ser Tyr His Gln Gln Gln His Gly Phe His Gln Gln  
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1016

Glu Ser Glu Phe Glu Leu Leu Lys Glu Met Phe Pro Ser Val Phe Phe  
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1071

Lys Gln Glu Pro  
325

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1131

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1191

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1241

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Glu Leu Gly Phe Glu Leu Ser Pro Ser Ser Ser Asp Phe Phe Asn Pro  
65 70 75 80

Ser Leu Asp Gln Glu Asn Gly Leu Tyr Asn Ala Tyr Asn Tyr Asn Ser  
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Ser Gln Lys Ser His Glu Val Val Gly Asp Gly Cys Ala Thr Ile Lys  
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His Pro Gly Glu Asp Ser Gly Lys Ile Arg Lys Lys Arg Glu Val Arg



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 165                      170                      175  
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 Asp Tyr Asn Pro Ser Ser Ser Pro Ile Phe Ser Asp Leu Ile Ile Asn  
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 Ser Val Asn Val Asn Pro Ser Tyr His Gln Gln Gln His Gly Phe His  
 290                      295                      300  
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 Trp Ser Ala Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys  
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 Phe Ser Pro Glu Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe  
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 Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro Phe Ser Pro Glu



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 85                      90                      95  
 Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser Gly Gly Val Ala  
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 Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp Arg Pro Lys Lys  
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 Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln Leu Phe Lys Pro  
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 180                      185                      190  
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 245                      250                      255  
 Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr Met Ala Glu Met  
 260                      265                      270  
 Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu Tyr Glu Ser Gly  
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Cys Cys Glu Lys Val Gly Ile Lys Arg Gly Arg Trp Thr Ala Glu Glu  
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gac cag att ctc tcc aac tac att caa tcc aat ggt gaa ggt tct tgg  
 151

Asp Gln Ile Leu Ser Asn Tyr Ile Gln Ser Asn Gly Glu Gly Ser Trp  
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 199

Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys  
 40 45 50

aga ttg aga tgg ata aac tat cta aga tca gac ctc aag cgt gga aac  
 247

Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp Leu Lys Arg Gly Asn  
 55 60 65

ata act cca gaa gaa gaa gaa ctc gtt gtt aaa ttg cat tcc act ttg  
 295

Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys Leu His Ser Thr Leu  
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gga aac agg tgg tca cta atc gcg ggt cat cta cca ggg aga aca gac  
 343

Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu Pro Gly Arg Thr Asp  
 90 95 100

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 391

Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys Leu His  
 105 110 115

aac ttc att agg aag cca tcc atc tct caa gac gtc tcc gcc gta atc  
 439

Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp Val Ser Ala Val Ile  
 120 125 130

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 487

Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro Gln Ala Lys Arg Arg  
 135 140 145

ctt ggg aga acg agt agg tcc gct atg aaa cca aaa atc cgc aga aca  
 535

Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro Lys Ile Arg Arg Thr  
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gat gta gct ggg gct gat aaa gaa gca tta atg gtg gag tca agt gga  
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 185 190 195

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 679  
 Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr Tyr Gly Asp Asp Cys  
 200 205 210

aac aaa aat ctc atg agc att aat ggc gat aat gga gtt tta acg ttt  
 727  
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 265 270 275

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 280 285 290

aac tac gac cac caa gtt aac gac gcg tcg acg gat gag ttt atc gat  
 967  
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 295 300 305

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 1015  
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 310 315 320 325

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 1063  
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 330 335 340

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 1111  
 Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn Phe Gly Glu Pro Leu  
 345 350 355



gat cat gac gac gaa agc gct ttg gtc gct tgg ctt ctg tca tga  
1156

Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp Leu Leu Ser  
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35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp  
50 55 60

Leu Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys  
65 70 75 80

Leu His Ser Thr Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu  
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu  
100 105 110

Ser Arg Lys Leu His Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp  
115 120 125

Val Ser Ala Val Ile Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro  
130 135 140

Gln Ala Lys Arg Arg Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro  
145 150 155 160

Lys Ile Arg Arg Thr Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro  
165 170 175

Pro Glu Pro Asn Ala Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met  
180 185 190

Val Glu Ser Ser Gly Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr



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 Val Glu Ser Phe Leu Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr  
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 Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg  
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 50 55 60  
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 302  
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 65 70 75  
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 Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val  
 80 85 90 95  
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 398  
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 100 105 110  
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 115 120 125  
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 494  
 Val Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro  
 130 135 140  
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 Gly Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile  
 145 150 155  
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 686  
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 195 200 205  
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 Asn Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg



210 215 220  
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 225 230 235  
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 830  
 Arg Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly  
 240 245 250 255  
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 878  
 Glu Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser  
 260 265 270  
 tac atg acg gag atg caa cgg aac aat ggt ggc gga ttc gtc gga gga  
 926  
 Tyr Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly  
 275 280 285  
 ttc att gat aat ggc atg att ccg atg agt caa att gga gtt ggg aga  
 974  
 Phe Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg  
 290 295 300  
 atc gag tag acaaagtgag attattagga aactgtttta attggagaag  
 1023  
 Ile Glu  
 305  
 aagaaaaatg ctctgttttt ttctcctttg gattaggcct aagaattttg ggttttaagg  
 1083  
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 20 25 30  
 Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp  
 35 40 45  
 Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu  
 50 55 60



Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp  
 65 70 75 80

Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys  
 85 90 95

Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His  
 100 105 110

Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val  
 115 120 125

Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly  
 130 135 140

Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu  
 145 150 155 160

Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Val Val  
 165 170 175

Leu Pro Leu Pro Ile Glu Thr Ser Ser Phe Ser Asp Asp Pro Pro Thr  
 180 185 190

Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn  
 195 200 205

Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His  
 210 215 220

Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg  
 225 230 235 240

Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu  
 245 250 255

Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr  
 260 265 270

Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe  
 275 280 285

Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile  
 290 295 300

Glu



305

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 96  
 Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr Val Arg Thr His  
 20 25 30  
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 144  
 Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg  
 35 40 45  
 tgt ggg aaa agc,tgt agg ttg aga tgg atg aac tac tta agc cct aat  
 192  
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn  
 50 55 60  
 gtt aac aga ggc aat ttt act gac caa gaa gaa gat ctc atc atc aga  
 240  
 Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg  
 65 70 75 80  
 ctc cac aag ctc ctc ggc aac aga tgg tgg ttg ata gcg aaa aga gtt  
 288  
 Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val  
 85 90 95  
 ccg gga aga aca gac aac caa gta aag aat tac tgg aac aca cat ctc  
 336  
 Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu  
 100 105 110  
 agc aag aaa ctt ggt ctc gga gat cat tca act gcc gtc aaa gcc gca  
 384  
 Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala  
 115 120 125  
 tgc ggt gta gag tct cca ccg tct atg gcc ctt ata acc aca acg tcc  
 432  
 Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser  
 130 135 140  
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 480  
 Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe  
 145 150 155 160  
 gac act tta gtt gac gaa tcc aaa ctc aaa cca aaa tcc aaa cta gtc  
 528  
 Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val  
 165 170 175



cac gca aca cca act gac gta gaa gtt gca gct acg gtt cca aat ctg  
576

His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu  
180 185 190

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624

Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu  
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210 215

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35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn  
50 55 60

Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg  
65 70 75 80

Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val  
85 90 95

Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu  
100 105 110

Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala  
115 120 125

Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser  
130 135 140

Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe  
145 150 155 160

Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val



165 170 175

His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu  
180 185 190

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195 200 205

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101  
Ser Ala Ser Val Ser Gly Gly Glu Gly Ala Gly Gly Pro Ala Pro Phe  
10 15 20  
ttg gtg aaa acc tac gag atg gtc gac gat tca tca acg gac cag atc  
149  
Leu Val Lys Thr Tyr Glu Met Val Asp Asp Ser Ser Thr Asp Gln Ile  
25 30 35 40  
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197  
Val Ser Trp Ser Ala Asn Asn Asn Ser Phe Ile Val Trp Asn His Ala  
45 50 55  
gaa ttt tca cgc ctc ctt ctt cca acc tac ttc aaa cac aat aac ttc  
245  
Glu Phe Ser Arg Leu Leu Leu Pro Thr Tyr Phe Lys His Asn Asn Phe  
60 65 70  
tot tcc ttc att cgt cag ctc aat acc tat ggg ttt agg aag att gat  
293  
Ser Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Asp  
75 80 85  
cca gag agg tgg gag ttt ttg aat gat gat ttt att aag gat cag aag  
341  
Pro Glu Arg Trp Glu Phe Leu Asn Asp Asp Phe Ile Lys Asp Gln Lys  
90 95 100  
cat ctt ctc aag aat ata cat aga agg aaa cct ata cac agc cac agt  
389  
His Leu Leu Lys Asn Ile His Arg Arg Lys Pro Ile His Ser His Ser  
105 110 115 120  
cat cca cct gct tcg tcg act gat caa gaa aga gca gtg ttg caa gag  
437



His Pro Pro Ala Ser Ser Thr Asp Gln Glu Arg Ala Val Leu Gln Glu  
 125 130 135  
 caa atg gac aag ctt tca cgt gag aaa gct gca att gaa gct aag ctt  
 485  
 Gln Met Asp Lys Leu Ser Arg Glu Lys Ala Ala Ile Glu Ala Lys Leu  
 140 145 150  
 tta aag ttc aaa caa cag aag gtt gta gca aag cat cag ttt gaa gaa  
 533  
 Leu Lys Phe Lys Gln Gln Lys Val Val Ala Lys His Gln Phe Glu Glu  
 155 160 165  
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 581  
 Met Thr Glu His Val Asp Asp Met Glu Asn Arg Gln Lys Lys Leu Leu  
 170 175 180  
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 629  
 Asn Phe Leu Glu Thr Ala Ile Arg Asn Pro Thr Phe Val Lys Asn Phe  
 185 190 195 200  
 ggt aag aaa gtc gag cag ttg gat att tca gct tac aac aaa aag cga  
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 Gly Lys Lys Val Glu Gln Leu Asp Ile Ser Ala Tyr Asn Lys Lys Arg  
 205 210 215  
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 725  
 Arg Leu Pro Glu Val Glu Gln Ser Lys Pro Pro Ser Glu Asp Ser His  
 220 225 230  
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 773  
 Leu Asp Asn Ser Ser Gly Ser Ser Arg Arg Glu Ser Gly Asn Ile Phe  
 235 240 245  
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 821  
 His Gln Asn Phe Ser Asn Lys Leu Arg Leu Glu Leu Ser Pro Ala Asp  
 250 255 260  
 tca gat atg aac atg gtt tca cac agt ata caa agt tcc aat gaa gaa  
 869  
 Ser Asp Met Asn Met Val Ser His Ser Ile Gln Ser Ser Asn Glu Glu  
 265 270 275 280  
 ggt gcg agt ccc aaa ggg ata ctg tca gga ggt gat cca aat act aca  
 917  
 Gly Ala Ser Pro Lys Gly Ile Leu Ser Gly Gly Asp Pro Asn Thr Thr  
 285 290 295  
 cta aca aaa aga gaa ggc cta cca ttt gca cct gaa gct cta gag ctt  
 965  
 Leu Thr Lys Arg Glu Gly Leu Pro Phe Ala Pro Glu Ala Leu Glu Leu  
 300 305 310  
 gcg gat acc ggg aca tgc ccg agg aga tta ctg tta aat gat aat aca  
 1013  
 Ala Asp Thr Gly Thr Cys Pro Arg Arg Leu Leu Leu Asn Asp Asn Thr



315 320 325  
 agg gtg gag acc ttg cag cag agg cta act tct tca gag gag act gat  
 1061  
 Arg Val Glu Thr Leu Gln Gln Arg Leu Thr Ser Ser Glu Glu Thr Asp  
 330 335 340  
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 1109  
 Gly Ser Phe Ser Cys His Leu Asn Leu Thr Leu Ala Ser Ala Pro Leu  
 345 350 355 360  
 ccg gac aaa aca gct tca cag ata gct aag acg act ctt aaa agt cag  
 1157  
 Pro Asp Lys Thr Ala Ser Gln Ile Ala Lys Thr Thr Leu Lys Ser Gln  
 365 370 375  
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 1205  
 Glu Leu Asn Phe Asn Ser Ile Glu Thr Ser Ala Ser Glu Lys Asn Arg  
 380 385 390  
 ggt aga caa gag att gca gtt gga ggt agc caa gca aat gca gct cct  
 1253  
 Gly Arg Gln Glu Ile Ala Val Gly Gly Ser Gln Ala Asn Ala Ala Pro  
 395 400 405  
 cca gca aga gtg aat gat gta ttc tgg gaa cag ttc cta aca gaa agg  
 1301  
 Pro Ala Arg Val Asn Asp Val Phe Trp Glu Gln Phe Leu Thr Glu Arg  
 410 415 420  
 cca ggg tct tca gat aat gag gag gca agt tcg act tat aga ggt aac  
 1349  
 Pro Gly Ser Ser Asp Asn Glu Glu Ala Ser Ser Thr Tyr Arg Gly Asn  
 425 430 435 440  
 cca tac gaa gag caa gag gag aaa aga aac ggg agt atg atg tta cgt  
 1397  
 Pro Tyr Glu Glu Gln Glu Glu Lys Arg Asn Gly Ser Met Met Leu Arg  
 445 450 455  
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 1450  
 Asn Thr Lys Asn Ile Glu Gln Leu Thr Leu  
 460 465  
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 1510  
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126



Arg Leu Glu Leu Ser Pro Ala Asp Ser Asp Met Asn Met Val Ser His  
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Ser Ile Gln Ser Ser Asn Glu Glu Gly Ala Ser Pro Lys Gly Ile Leu  
 275 280 285

Ser Gly Gly Asp Pro Asn Thr Thr Leu Thr Lys Arg Glu Gly Leu Pro  
 290 295 300

Phe Ala Pro Glu Ala Leu Glu Leu Ala Asp Thr Gly Thr Cys Pro Arg  
 305 310 315 320

Arg Leu Leu Leu Asn Asp Asn Thr Arg Val Glu Thr Leu Gln Gln Arg  
 325 330 335

Leu Thr Ser Ser Glu Glu Thr Asp Gly Ser Phe Ser Cys His Leu Asn  
 340 345 350

Leu Thr Leu Ala Ser Ala Pro Leu Pro Asp Lys Thr Ala Ser Gln Ile  
 355 360 365

Ala Lys Thr Thr Leu Lys Ser Gln Glu Leu Asn Phe Asn Ser Ile Glu  
 370 375 380

Thr Ser Ala Ser Glu Lys Asn Arg Gly Arg Gln Glu Ile Ala Val Gly  
 385 390 395 400

Gly Ser Gln Ala Asn Ala Ala Pro Pro Ala Arg Val Asn Asp Val Phe  
 405 410 415

Trp Glu Gln Phe Leu Thr Glu Arg Pro Gly Ser Ser Asp Asn Glu Glu  
 420 425 430

Ala Ser Ser Thr Tyr Arg Gly Asn Pro Tyr Glu Glu Gln Glu Glu Lys  
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Thr Leu  
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113

Met Asp Thr Thr Ile Asp Gly  
1 5

ttc gcc gat tct tat gaa atc agc agc act agt ttc gtc gct acc gat  
161  
Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp  
10 15 20

aac acc gac tcc tct att gtt tat ctg gcc gcc gaa caa gta ctc acc  
209  
Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr  
25 30 35

gga cct gat gta tct gct ctg caa ttg ctc tcc aac agc ttc gaa tcc  
257  
Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser  
40 45 50 55

gtc ttt gac tcg ccg gat gat ttc tac agc gac gct aag ctt gtt ctc  
305  
Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu  
60 65 70

tcc gac ggc cgg gaa gtt tct ttc cac cgg tgc gtt ttg tca gcg aga  
353  
Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg  
75 80 85

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401  
Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Lys Lys Glu Lys Asp  
90 95 100

tcc aac aac acc gcc gcc gtg aag ctc gag ctt aag gag att gcc aag  
449  
Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys  
105 110 115

gat tac gaa gtc ggt ttc gat tcg gtt gtg act gtt ttg gct tat gtt  
497  
Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val  
120 125 130 135

tac agc agc aga gtg aga ccg ccg cct aaa gga gtt tct gaa tgc gca  
545  
Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala  
140 145 150

gac gag aat tgc tgc cac gtg gct tgc cgg ccg gcg gtg gat ttc atg  
593  
Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met  
155 160 165

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641



Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile  
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 185 190 195  
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 737  
 Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala  
 200 205 210 215  
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 785  
 Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn  
 220 225 230  
 gta gat atg gtt agt ctt gaa aag tca ttg ccg gaa gag ctt gtt aaa  
 833  
 Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys  
 235 240 245  
 gag ata att gat aga cgt aaa gag ctt ggt ttg gag gta cct aaa gta  
 881  
 Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val  
 250 255 260  
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 Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile  
 265 270 275  
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 977  
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 280 285 290 295  
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 1025  
 Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala  
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 1121  
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 330 335 340  
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 1169  
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 345 350 355  
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 1217  
 Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala



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360          365          370          375
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          380          385          390

cga cta tgt gta gaa ata cta gag caa gaa gac aaa cga gaa caa att
1313
Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile
          395          400          405

cct aga gat gtt cct ccc tct ttt gca gtg gcg gcc gat gaa ttg aag
1361
Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys
          410          415          420

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Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu
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ttt cca acg gaa gca caa gct gca atg gag atc gcc gaa atg aag gga
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Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly
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aca tgt gag ttc ata gtg act agc ctc gag cct gac cgt ctc act ggt
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Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly
          460          465          470

acg aag aga aca tca ccg ggt gta aag ata gca cct ttc aga atc cta
1553
Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu
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gaa gag cat caa agt aga cta aaa gcg ctt tct aaa acc gtg gaa ctc
1601
Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu
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ggg aaa cga ttc ttc ccg cgc tgt tcg gca gtg ctc gac cag att atg
1649
Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met
          505          510          515

aac tgt gag gac ttg act caa ctg gct tgc gga gaa gac gac act gct
1697
Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala
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gag aaa cga cta caa aag aag caa agg tac atg gaa ata caa gag aca
1745
Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr
          540          545          550

cta aag aag gcc ttt agt gag gac aat ttg gaa tta gga aat tcg tcc
1793
Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly Asn Ser Ser
          555          560          565

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570 575 580

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1894

Ser Asn Arg Lys Leu Ser His Arg Arg Arg  
585 590

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1954

tggcgtcata tagtttcgct ctctgttttg catcctgtgt attattgctg caggtgtgct  
2014

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2074

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2104

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Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu  
35 40 45

Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr  
50 55 60

Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His  
65 70 75 80

Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala  
85 90 95

Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu  
100 105 110

Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val  
115 120 125

Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro  
130 135 140



Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys  
 145 150 155 160

Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile  
 165 170 175

Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp  
 180 185 190

Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu  
 195 200 205

Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys  
 210 215 220

Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser  
 225 230 235 240

Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu  
 245 250 255

Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys  
 260 265 270

Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu  
 275 280 285

Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala  
 290 295 300

Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala  
 305 310 315 320

Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala  
 325 330 335

Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly  
 340 345 350

Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile  
 355 360 365

Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln  
 370 375 380



Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln  
 385 390 395 400

Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala  
 405 410 415

Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg  
 420 425 430

Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met  
 435 440 445

Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu  
 450 455 460

Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys  
 465 470 475 480

Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala  
 485 490 495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser  
 500 505 510

Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala  
 515 520 525

Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg  
 530 535 540

Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn  
 545 550 555 560

Leu Glu Leu Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser  
 565 570 575

Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg  
 580 585 590

Arg

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<400> 75



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tcaaatcaat tctcgcgatt aagcaaaacc ctagatttat tctactcttc gaagtcgatt  
120

tca atg gaa ggt tcc tcg tca gcc atc gcg agg aag aca tgg gag cta  
168

Met Glu Gly Ser Ser Ser Ala Ile Ala Arg Lys Thr Trp Glu Leu  
1 5 10 15

gag aac aac att ctc cca gtg gaa cca acc gat tca gcc tcc gac agt  
216

Glu Asn Asn Ile Leu Pro Val Glu Pro Thr Asp Ser Ala Ser Asp Ser  
20 25 30

ata ttc cac tac gac gac gct tca caa gcc aaa atc cag cag gag aag  
264

Ile Phe His Tyr Asp Asp Ala Ser Gln Ala Lys Ile Gln Gln Glu Lys  
35 40 45

cta tgg gcc tcc gat cct aac tac ttc aag cgc gtt cac atc tca gcc  
312

Pro Trp Ala Ser Asp Pro Asn Tyr Phe Lys Arg Val His Ile Ser Ala  
50 55 60

ctt gct ctt ctc aag atg gtg gtt cac gct cgc tcc ggt ggc aca atc  
360

Leu Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile  
65 70 75

gag atc atg ggt ctt atg cag ggt aaa acc gag ggt gat aca atc atc  
408

Glu Ile Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile  
80 85 90 95

gtt atg gat gct ttt gct ttg cct gtt gaa ggt act gag act agg gtt  
456

Val Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val  
100 105 110

aat gct cag tct gat gcc tat gag tat atg gtt gaa tac tct cag acc  
504

Asn Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr  
115 120 125

agc aag ctg gct ggg agg ttg gag aac gtt gtt gga tgg tat cac tct  
552

Ser Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser  
130 135 140

cac cct ggg tat gga tgt tgg ctc tcg ggt att gat gtt tcg aca cag  
600

His Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln  
145 150 155

atg ctt aac caa cag tat cag gag cca ttc tta gct gtt gtt att gat  
648

Met Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp  
160 165 170 175



cca aca agg act gtt tgc gct ggt aag gtt gag att ggg gca ttc aga  
 696  
 Pro Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg  
 180 185 190

aca tat cca gag gga cat aag atc tgc gat gat cat gtt tct gag tat  
 744  
 Thr Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr  
 195 200 205

cag act atc cct ctt aac aag att gag gac ttt ggt gta cat tgc aaa  
 792  
 Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys  
 210 215 220

cag tac tac tca ttg gac atc act tat ttc aag tca tct ctc gat agt  
 840  
 Gln Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser  
 225 230 235

cac ctt ctg gat ctc ctt tgg aac aag tac tgg gtg aac act ctt tct  
 888  
 His Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser  
 240 245 250 255

tct tcc cca ctg ttg ggc aat gga gac tat gtt gcc ggg caa ata tca  
 936  
 Ser Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser  
 260 265 270

gac ttg gct gag aag ctc gag caa gcg gag agt cag ctc gct aac tcc  
 984  
 Asp Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser  
 275 280 285

cgg tat gga gga att gcg cca gcc ggt cac caa agg agg aaa gag gat  
 1032  
 Arg Tyr Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp  
 290 295 300

gag cct caa ctc gcg aag ata act cgg gat agt gca aag ata act gtc  
 1080  
 Glu Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val  
 305 310 315

gag cag gtc cat gga cta atg tca cag gtt atc aaa gac atc ttg ttc  
 1128  
 Glu Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe  
 320 325 330 335

aat tcc gct cgt cag tcc aag aag tct gct gac gac tca tca gat cca  
 1176  
 Asn Ser Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro  
 340 345 350

gag ccc atg att aca tgc tga agttggtcta ttcttttggt ttttggtgc  
 1227  
 Glu Pro Met Ile Thr Ser  
 355



ggaaattgac tatcggtttg acccggttta tgaggcaatg cccattgttc cctatatctc  
1287

tagtgtagta tctgcttcag acaaagatct ttgggttatt aaatgacatt aacataaaaa  
1347

aaa  
1350

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20 25 30

Phe His Tyr Asp Asp Ala Ser Gln Ala Lys Ile Gln Gln Glu Lys Pro  
35 40 45

Trp Ala Ser Asp Pro Asn Tyr Phe Lys Arg Val His Ile Ser Ala Leu  
50 55 60

Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu  
65 70 75 80

Ile Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val  
85 90 95

Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn  
100 105 110

Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser  
115 120 125

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His  
130 135 140

Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met  
145 150 155 160

Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro  
165 170 175

Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr  
180 185 190



Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln  
195 200 205

Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln  
210 215 220

Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His  
225 230 235 240

Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser  
245 250 255

Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp  
260 265 270

Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg  
275 280 285

Tyr Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu  
290 295 300

Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu  
305 310 315 320

Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn  
325 330 335

Ser Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu  
340 345 350

Pro Met Ile Thr Ser  
355

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48  
Met Asp Val Tyr Gly Leu Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp  
1 5 10 15

ctt ctt gat ttc tcc aac gaa gac atc ttc tcc gct tct tct tcc ggt  
96  
Leu Leu Asp Phe Ser Asn Glu Asp Ile Phe Ser Ala Ser Ser Ser Gly  
20 25 30

ggt tcc acc gcc gct act tcc tct tct tct ttc cct cct cct caa aac  
144  
Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn



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35          40          45
cct agt ttc cac cac cac cat ctc cct tcc tcc gcc gat cat cac tcc
192
Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser
50          55          60

ttc ctc cac gac att tgc gtt ccc agt gat gac gca gct cat ctt gaa
240
Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu
65          70          75          80

tgg ctt tcg caa ttc gtg gac gat tct ttc gct gat ttt ccg gcg aat
288
Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn
85          90          95

cca tta gga gga act atg act tct gtc aaa act gaa act tcc ttt ccg
336
Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro
100          105          110

ggg aaa cca aga agc aaa cga tca aga gct cct gct cct ttc gcc gga
384
Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly
115          120          125

aca tgg tct ccg atg cca ctg gaa tcc gag cat cag cag ctt cac tcc
432
Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser
130          135          140

gcc gcc aaa ttc aag cca aag aaa gaa caa tcc ggc gga gga gga
480
Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly
145          150          155          160

gga gga gga aga cat cag tca tcg tca tcg gag act acg gaa gga gga
528
Gly Gly Gly Arg His Gln Ser Ser Ser Ser Glu Thr Thr Glu Gly Gly
165          170          175

gga atg agg aga tgt act cac tgt gca tcg gag aaa acg cca cag tgg
576
Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp
180          185          190

agg aca gga cca ctt gga cct aaa aca cta tgt aac gct tgt gga gtc
624
Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val
195          200          205

cgg ttt aaa tcc ggt aga ctt gta ccg gaa tat aga ccg gct tcg agt
672
Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser
210          215          220

cct act ttt gtt ttg act cag cat tca aac tct cac cgg aaa gtg atg
720
Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met
225          230          235          240

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gag ctt cga cgg cag aaa gaa gtt atg aga caa cca caa caa gtt caa  
768

Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln  
245 250 255

ctt cat cac cac cac cac ccg ttt tag

795

Leu His His His His His Pro Phe  
260

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20 25 30

Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn  
35 40 45

Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser  
50 55 60

Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu  
65 70 75 80

Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn  
85 90 95

Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro  
100 105 110

Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly  
115 120 125

Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser  
130 135 140

Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly  
145 150 155 160

Gly Gly Gly Arg His Gln Ser Ser Ser Ser Glu Thr Thr Glu Gly Gly  
165 170 175

Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp  
180 185 190



Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val  
 195 200 205

Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser  
 210 215 220

Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met  
 225 230 235 240

Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln  
 245 250 255

Leu His His His His His Pro Phe  
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 60

atcatcatca tcagaagaaa a atg gtt gcg ata tcg gag atc aag tcg acg  
 111

Met Val Ala Ile Ser Glu Ile Lys Ser Thr  
 1 5 10

gtg gat gtc acg gcg gcg aat tgt ttg atg ctt tta tct aga gtt gga  
 159

Val Asp Val Thr Ala Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly  
 15 20 25

caa gaa aac gtt gac ggt ggc gat caa aaa cgc gtt ttc aca tgt aaa  
 207

Gln Glu Asn Val Asp Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys  
 30 35 40

acg tgt ttg aag cag ttt cat tcg ttc caa gcc tta gga ggt cac cgt  
 255

Thr Cys Leu Lys Gln Phe His Ser Phe Gln Ala Leu Gly Gly His Arg  
 45 50 55

gcg agt cac aag aag cct aac aac gac gct ttg tcg tct gga ttg atg  
 303

Ala Ser His Lys Lys Pro Asn Asn Asp Ala Leu Ser Ser Gly Leu Met  
 60 65 70

aag aag gtg aaa acg tcg tcg cat cct tgt ccc ata tgt gga gtg gag  
 351

Lys Lys Val Lys Thr Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu  
 75 80 85 90

ttt ccg atg gga caa gct ttg gga gga cac atg agg aga cac agg aac  
 399



Phe Pro Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn  
95 100 105

gag agt ggg gct gct ggt ggc gcg ttg gtt aca cgc gct ttg ttg ccg  
447

Glu Ser Gly Ala Ala Gly Gly Ala Leu Val Thr Arg Ala Leu Leu Pro  
110 115 120

gag ccc acg gtg act acg ttg aag aaa tct agc agt ggg aag aga gtg  
495

Glu Pro Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val  
125 130 135

gct tgt ttg gat ctg agt cta ggg atg gtg gac aat ttg aat ctc aag  
543

Ala Cys Leu Asp Leu Ser Leu Gly Met Val Asp Asn Leu Asn Leu Lys  
140 145 150

ttg gag ctt gga aga aca gtt tat tga ttttatttat tttccttaaa  
590

Leu Glu Leu Gly Arg Thr Val Tyr  
155 160

ttttctgaat atatttggtt ctctcattct ttgaattttt cttaatatc tagattatac  
650

atacatccgc agatttagga aactttcata gagtgtaatc ttttctttct gtaaaaatat  
710

attttacttg tagcaaa  
727

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80

Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala  
1 5 10 15

Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly  
20 25 30

Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe  
35 40 45

His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro  
50 55 60

Asn Asn Asp Ala Leu Ser Ser Gly Leu Met Lys Lys Val Lys Thr Ser  
65 70 75 80

Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala  
85 90 95

Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Gly Ala Ala Gly



389  
Arg Arg His Arg Asn Glu Lys Val Ser Gly Ser Leu Val Thr Arg Ser



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110              115              120
ttt cta ccg gag acg acg acg gtg acg gct ttg aag aaa ttt agt agt
437
Phe Leu Pro Glu Thr Thr Thr Val Thr Ala Leu Lys Lys Phe Ser Ser
125              130              135

ggg aag aga gtg gct tgt ttg gat ttg gac tta gat tcg atg gag agt
485
Gly Lys Arg Val Ala Cys Leu Asp Leu Asp Leu Asp Ser Met Glu Ser
140              145              150

ttg gtc aat tgg aag ttg gag ttg gga aga acg att tct tgg agt taa
533
Leu Val Asn Trp Lys Leu Glu Leu Gly Arg Thr Ile Ser Trp Ser
155              160              165

gtttttgggt tgtatacagt ttcacatgat tttgtaatct ttgttgatcc aattatcgta
593

ccgatcgatg tgaatattat tttgatacaa taaaa
628

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82

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1              5              10              15

Ala Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly
20              25              30

Cys Gly Gly Asp Glu Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu
35              40              45

Phe Ser Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys
50              55              60

Leu Ile Asn Ser Asp Asn Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys
65              70              75              80

Lys Thr Lys Thr Ser His Pro Cys Pro Ile Cys Gly Val Lys Phe Pro
85              90              95

Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Lys
100              105              110

Val Ser Gly Ser Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
115              120              125

Val Thr Ala Leu Lys Lys Phe Ser Ser Gly Lys Arg Val Ala Cys Leu
130              135              140

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Asp Leu Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu  
 145 150 155 160

Leu Gly Arg Thr Ile Ser Trp Ser  
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 1 5 10 15  
 ggc aga gca ctt ggt ggt cac atg aag tct cac ttg gtc tca tct cag  
 96  
 Gly Arg Ala Leu Gly Gly His Met Lys Ser His Leu Val Ser Ser Gln  
 20 25 30  
 tct tca gct cgg aag aaa cta ggt gac tcg gtc tat tct tct tct tcc  
 144  
 Ser Ser Ala Arg Lys Lys Leu Gly Asp Ser Val Tyr Ser Ser Ser Ser  
 35 40 45  
 tct tcc tcc gat ggt aaa gcg ctc gcc tac ggg tta cga gag aac ccg  
 192  
 Ser Ser Ser Asp Gly Lys Ala Leu Ala Tyr Gly Leu Arg Glu Asn Pro  
 50 55 60  
 agg aag agt ttc cgg gtc ttt aat ccg gat cct gag tca tcc aca att  
 240  
 Arg Lys Ser Phe Arg Val Phe Asn Pro Asp Pro Glu Ser Ser Thr Ile  
 65 70 75 80  
 tac aac agt gag aca gag acc gaa cct gaa tcc gga gac ccg gtt aag  
 288  
 Tyr Asn Ser Glu Thr Glu Thr Glu Pro Glu Ser Gly Asp Pro Val Lys  
 85 90 95  
 aaa cgg gtc aga gga gat gtt tca aag aag aag aag aag gca aag  
 336  
 Lys Arg Val Arg Gly Asp Val Ser Lys Lys Lys Lys Lys Lys Ala Lys  
 100 105 110  
 agt aag aga gtg ttt gag aac tcg aag aag caa aag aca att cac gag  
 384  
 Ser Lys Arg Val Phe Glu Asn Ser Lys Lys Gln Lys Thr Ile His Glu  
 115 120 125  
 tca cca gaa cca gcg agt tct gtc tct gat ggt tct cct gaa caa gat  
 432  
 Ser Pro Glu Pro Ala Ser Ser Val Ser Asp Gly Ser Pro Glu Gln Asp  
 130 135 140  
 tta gct atg tgc ttg atg atg ctg tca aga gat tca agg gag ctc gag  
 480



Leu Ala Met Cys Leu Met Met Leu Ser Arg Asp Ser Arg Glu Leu Glu  
145 150 155 160

att aaa ctg aaa aaa ccg gag gaa gag agg aag ccg gaa aaa aga cat  
528

Ile Lys Leu Lys Lys Pro Glu Glu Glu Arg Lys Pro Glu Lys Arg His  
165 170 175

ttc cct gag ctc cgt cgc tgt atg ata gat ctg aat ctt cct ccg ccg  
576

Phe Pro Glu Leu Arg Arg Cys Met Ile Asp Leu Asn Leu Pro Pro Pro  
180 185 190

caa gaa gct gaa gct gtc acc gtc gtt tca gcc ata taa  
615

Gln Glu Ala Glu Ala Val Thr Val Val Ser Ala Ile  
195 200

<210> 84 <211> 204 <212> PRT <213> Arabidopsis thaliana <400>  
84

Met Gln Asn Lys His Lys Cys Lys Leu Cys Ser Lys Ser Phe Cys Asn  
1 5 10 15

Gly Arg Ala Leu Gly Gly His Met Lys Ser His Leu Val Ser Ser Gln  
20 25 30

Ser Ser Ala Arg Lys Lys Leu Gly Asp Ser Val Tyr Ser Ser Ser Ser  
35 40 45

Ser Ser Ser Asp Gly Lys Ala Leu Ala Tyr Gly Leu Arg Glu Asn Pro  
50 55 60

Arg Lys Ser Phe Arg Val Phe Asn Pro Asp Pro Glu Ser Ser Thr Ile  
65 70 75 80

Tyr Asn Ser Glu Thr Glu Thr Glu Pro Glu Ser Gly Asp Pro Val Lys  
85 90 95

Lys Arg Val Arg Gly Asp Val Ser Lys Lys Lys Lys Lys Lys Ala Lys  
100 105 110

Ser Lys Arg Val Phe Glu Asn Ser Lys Lys Gln Lys Thr Ile His Glu  
115 120 125

Ser Pro Glu Pro Ala Ser Ser Val Ser Asp Gly Ser Pro Glu Gln Asp  
130 135 140

Leu Ala Met Cys Leu Met Met Leu Ser Arg Asp Ser Arg Glu Leu Glu  
145 150 155 160



Ile Lys Leu Lys Lys Pro Glu Glu Glu Arg Lys Pro Glu Lys Arg His  
 165 170 175

Phe Pro Glu Leu Arg Arg Cys Met Ile Asp Leu Asn Leu Pro Pro Pro  
 180 185 190

Gln Glu Ala Glu Ala Val Thr Val Val Ser Ala Ile  
 195 200

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ggt atg gac tac cag cca aac aca tcc cta cgt cta agc cta cca agt  
 108  
 Met Asp Tyr Gln Pro Asn Thr Ser Leu Arg Leu Ser Leu Pro Ser  
 1 5 10 15

tac aag aac cac caa cta aac cta gaa ctt gtt ctc gag cct tct tcc  
 156  
 Tyr Lys Asn His Gln Leu Asn Leu Glu Leu Val Leu Glu Pro Ser Ser  
 20 25 30

atg tct tct tct tca tct tct tcc acg aac tca tca tca tgt ttg gag  
 204  
 Met Ser Ser Ser Ser Ser Ser Ser Thr Asn Ser Ser Ser Cys Leu Glu  
 35 40 45

cag cct agg gta ttc tca tgt aac tat tgt caa aga aag ttt tac agc  
 252  
 Gln Pro Arg Val Phe Ser Cys Asn Tyr Cys Gln Arg Lys Phe Tyr Ser  
 50 55 60

tct caa gct ctt ggt ggt cat caa aac gct cat aag ctt gag aga acc  
 300  
 Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Leu Glu Arg Thr  
 65 70 75

tta gcc aag aag agt cga gaa ctc ttt aga tcc tca aac act gtt gat  
 348  
 Leu Ala Lys Lys Ser Arg Glu Leu Phe Arg Ser Ser Asn Thr Val Asp  
 80 85 90 95

tct gat cag cct tac ccg ttc tcc ggt cgc ttt gag ctt tac ggc cgt  
 396  
 Ser Asp Gln Pro Tyr Pro Phe Ser Gly Arg Phe Glu Leu Tyr Gly Arg  
 100 105 110

ggc tac caa gga ttt ctc gaa agt ggc ggc tcg agg gac ttc tcc gcc  
 444  
 Gly Tyr Gln Gly Phe Leu Glu Ser Gly Gly Ser Arg Asp Phe Ser Ala  
 115 120 125



cgc cgt gtg ccg gag agt ggt ctt gat cag gat cag gag aag agt cac  
492

Arg Arg Val Pro Glu Ser Gly Leu Asp Gln Asp Gln Glu Lys Ser His  
130 135 140

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35 40 45

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Tyr Gln Gly Phe Leu Glu Ser Gly Gly Ser Arg Asp Phe Ser Ala Arg  
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102

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198

Ser Pro Asn Thr Lys Ser Gly Ser Glu Asn Gln Glu Gly Gly Ser Gly  
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246

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294

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342

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390

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438

Met Lys Asn His His Glu Arg His Glu Asn Ser His Leu Arg Ala Glu  
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486

Asn Glu Lys Leu Arg Asn Asp Asn Leu Arg Tyr Arg Glu Ala Leu Ala  
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185 190 195

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Trp Ile Pro Val Pro Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu  
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1830

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2118

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2166

Leu Gly Ser Val Ala Thr Val Asn Asn Leu Ile Ala Cys Thr Val Glu  
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 457

Ala Lys Pro Thr Ser Met Lys Lys Ile Asp Val Ala Thr Lys Pro Val  
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Lys Leu Tyr Arg Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala  
 115 120 125

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 553

Glu Ile Arg Leu Pro Lys Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe  
 130 135 140



gaa acg gct caa gaa gct gca tta gct tac gat caa gca gct cat aag

601

Glu Thr Ala Gln Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala His Lys  
145 150 155

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649

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697

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745

Ser Ile Cys Asn Ser Ser Asp Leu Pro Leu Pro Gln Ile Glu Lys Gln  
195 200 205

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793

Asn Lys Thr Glu Glu Val Leu Ser Gly Phe Ser Lys Pro Glu Lys Glu  
210 215 220

ccg gaa ttt ggg gag ata tac gga tgc gga tac tcg ggc tca tct cct

841

Pro Glu Phe Gly Glu Ile Tyr Gly Cys Gly Tyr Ser Gly Ser Ser Pro  
225 230 235

gag tcg gat ata acg ttg ttg gat ttc tca agc gac tgt gtg aaa gaa

889

Glu Ser Asp Ile Thr Leu Leu Asp Phe Ser Ser Asp Cys Val Lys Glu  
240 245 250

gat gag agt ttc ttg atg ggt ttg cac aag tat cct tct ttg gag att

937

Asp Glu Ser Phe Leu Met Gly Leu His Lys Tyr Pro Ser Leu Glu Ile  
255 260 265 270

gat tgg gac gct ata gag aaa ctc ttc tga atccatttta tctttttgat

987

Asp Trp Asp Ala Ile Glu Lys Leu Phe  
275

tcatttgtct ctaaattgta gaattttatt ttcagagctt tgtaagggaa gttcttgaat

1047

gagagttgca gaggactagt ggaacctaac tctgttttct tttgtaagta ttgtttataa

1107

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1167

aaaaaaaaaa

1177

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 20 25 30  
 Ser Ser Asn Pro Lys Pro Leu Thr Pro Asn Phe Ile Pro Asn Asn Asp  
 35 40 45  
 Gln Val Leu Pro Val Ser Asn Gln Thr Gly Pro Ile Gly Leu Asn Gln  
 50 55 60  
 Leu Thr Pro Thr Gln Ile Leu Gln Ile Gln Thr Glu Leu His Leu Arg  
 65 70 75 80  
 Gln Asn Gln Ser Arg Arg Arg Ala Gly Ser His Leu Leu Thr Ala Lys  
 85 90 95  
 Pro Thr Ser Met Lys Lys Ile Asp Val Ala Thr Lys Pro Val Lys Leu  
 100 105 110  
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 115 120 125  
 Arg Leu Pro Lys Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe Glu Thr  
 130 135 140  
 Ala Gln Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala His Lys Ile Arg  
 145 150 155 160  
 Gly Asp Asn Ala Arg Leu Asn Phe Pro Asp Ile Val Arg Gln Gly His  
 165 170 175  
 Tyr Lys Gln Ile Leu Ser Pro Ser Ile Asn Ala Lys Ile Glu Ser Ile  
 180 185 190  
 Cys Asn Ser Ser Asp Leu Pro Leu Pro Gln Ile Glu Lys Gln Asn Lys  
 195 200 205  
 Thr Glu Glu Val Leu Ser Gly Phe Ser Lys Pro Glu Lys Glu Pro Glu  
 210 215 220  
 Phe Gly Glu Ile Tyr Gly Cys Gly Tyr Ser Gly Ser Ser Pro Glu Ser  
 225 230 235 240  
 Asp Ile Thr Leu Leu Asp Phe Ser Ser Asp Cys Val Lys Glu Asp Glu



245 250 255

Ser Phe Leu Met Gly Leu His Lys Tyr Pro Ser Leu Glu Ile Asp Trp  
 260 265 270

Asp Ala Ile Glu Lys Leu Phe  
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 103

Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala Glu Ser Glu Leu Glu  
 10 15 20

ttg gga tta ggg ctc agc ctc ggt ggt ggc gcg tgg aaa gag cgt ggg  
 151

Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala Trp Lys Glu Arg Gly  
 25 30 35

agg att ctt act gct aag gat ttt cct tcc gtt ggg tct aaa cgc tct  
 199

Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ser  
 40 45 50

gct gaa tct tcc tct cac caa gga gct tct cct cct cgt tca agt caa  
 247

Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro Pro Arg Ser Ser Gln  
 55 60 65

gtg gta gga tgg cca cca att ggg tta cac agg atg aac agt ttg gtt  
 295

Val Val Gly Trp Pro Pro Ile Gly Leu His Arg Met Asn Ser Leu Val  
 70 75 80 85

aat aac caa gct atg aag gca gca aga gcg gaa gaa gga gac ggg gag  
 343

Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu Glu Gly Asp Gly Glu  
 90 95 100

aag aaa gtt gtg aag aat gat gag ctc aaa gat gtg tca atg aag gtg  
 391

Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp Val Ser Met Lys Val  
 105 110 115

aat ccg aaa gtt cag ggc tta ggg ttt gtt aag gtg aat atg gat gga  
 439

Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys Val Asn Met Asp Gly  
 120 125 130



gtt ggt ata ggc aga aaa gtg gat atg aga gct cat tcg tct tac gaa  
 487  
 Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala His Ser Ser Tyr Glu  
 135 140 145  
 aac ttg gct cag acg ctt gag gaa atg ttc ttt gga atg aca ggt act  
 535  
 Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe Gly Met Thr Gly Thr  
 150 155 160 165  
 act tgt cga gaa aag gtt aaa cct tta agg ctt tta gat gga tca tca  
 583  
 Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser  
 170 175 180  
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 631  
 Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val  
 185 190 195  
 gga gat gtt cca tgg aga atg ttt atc aac tcg gtg aaa agg ctt cgg  
 679  
 Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg  
 200 205 210  
 atc atg gga acc tca gaa gct agt gga cta gct cca aga cgt caa gag  
 727  
 Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala Pro Arg Arg Gln Glu  
 215 220 225  
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 780  
 Gln Lys Asp Arg Gln Arg Asn Asn Pro Val  
 230 235  
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 Trp Lys Glu Arg Gly Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val  
 35 40 45



Gly Ser Lys Arg Ser Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro  
50 55 60

Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Leu His Arg  
65 70 75 80

Met Asn Ser Leu Val Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu  
85 90 95

Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp  
100 105 110

Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys  
115 120 125

Val Asn Met Asp Gly Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala  
130 135 140

His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe  
145 150 155 160

Gly Met Thr Gly Thr Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu  
165 170 175

Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly  
180 185 190

Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser  
195 200 205

Val Lys Arg Leu Arg Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala  
210 215 220

Pro Arg Arg Gln Glu Gln Lys Asp Arg Gln Arg Asn Asn Pro Val  
225 230 235

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1 5 10 15  
ctt tta cct tgt gat act ttt gct aag aat aga aga ttt gaa cag aga  
96



Leu Leu Pro Cys Asp Thr Phe Ala Lys Asn Arg Arg Phe Glu Gln Arg  
 20 25 30  
 ctc tct aat aat gat gat gtg ttg att tct gac atg gct ggt aac tcc  
 144  
 Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser  
 35 40 45  
 aat gga ttc agt gct gtt tct att act aaa gtt gtt cct gaa gag gaa  
 192  
 Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu  
 50 55 60  
 gat gag gag aac ata tct tct tct tca aag ttc tct agt cag gaa ttg  
 240  
 Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu  
 65 70 75 80  
 aat agg ata gat ttc aaa ctt agg agc ttt ttg gat tta gga aat gat  
 288  
 Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp  
 85 90 95  
 gat gat gat aca tcc tct aga ggt ttt gct ctg cca tct aaa aag tct  
 336  
 Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser  
 100 105 110  
 cga gct tca aac ttg tgc tct cag aat ccc ttg tgt caa gtt tat ggg  
 384  
 Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly  
 115 120 125  
 tgt agt aag gat ctg agc tct tcg aaa gat tac cac aaa agg cat aga  
 432  
 Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg  
 130 135 140  
 gtt tgc gag gct cat tcg aaa act tct gtg gtc ata gtt aat ggt ctt  
 480  
 Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu  
 145 150 155 160  
 gaa cag agg ttt tgt caa cag tgc agc agg ttt cat ttc ctc tca gag  
 528  
 Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu  
 165 170 175  
 ttt gat gat ggc aaa aga agt tgc aga agg cga tta gcc ggt cac aat  
 576  
 Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn  
 180 185 190  
 gaa cga aga agg aaa cct gca ttc tat ttc cta ccg ggt aag cgc cat  
 624  
 Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His  
 195 200 205  
 aag ctt ctt cgc acc tct caa gat gta gta ggc aac aag ttt ctg gag  
 672  
 Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu



210	215	220
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Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr 225 230 235 240		
aga gta ata gat gaa gac gac cac cgt aca agt aga ctc gtg agt ttc 768		
Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe 245 250 255		
aaa gat gaa cct act tgt tcc atg ttt cct act aat gag caa aac agc 816		
Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser 260 265 270		
agc aga act tat gaa tct aaa cca gca att tat tcc acg gaa gta tcc 864		
Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser 275 280 285		
tcc att tgg gac tta cat gag acg gcg gca tca cgc tct act cgt gct 912		
Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala 290 295 300		
ctc tct ctt ctg tca gct cag tcc caa caa cac ttg tct aag ttt cca 960		
Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro 305 310 315 320		
aac aca acg ttc tca atc acc caa ccc aac caa aat ctc aat cac tca 1008		
Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser 325 330 335		
tca tca act gac tat cat cag atg gaa caa ccg ttg tgg atc gat cct 1056		
Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro 340 345 350		
ggc aag acc aat tct gct ggt tct agt tct tgt aaa gga aaa gga aca 1104		
Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr 355 360 365		
tcc acg gtt gat cta ctg caa ctg tca tca cat ctt caa aga atc gag 1152		
Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu 370 375 380		
caa cag agg aat tac act ggt gat gtg aag cag gaa tat aat gag ctt 1200		
Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu 385 390 395 400		
tat ttc cct ggc tcc taa 1218		
Tyr Phe Pro Gly Ser 405		



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Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser  
 35 40 45

Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu  
 50 55 60

Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu  
 65 70 75 80

Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp  
 85 90 95

Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser  
 100 105 110

Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly  
 115 120 125

Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg  
 130 135 140

Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu  
 145 150 155 160

Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu  
 165 170 175

Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn  
 180 185 190

Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His  
 195 200 205

Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu  
 210 215 220



Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr  
 225 230 235 240

Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe  
 245 250 255

Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser  
 260 265 270

Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser  
 275 280 285

Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala  
 290 295 300

Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro  
 305 310 315 320

Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser  
 325 330 335

Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro  
 340 345 350

Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr  
 355 360 365

Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu  
 370 375 380

Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu  
 385 390 395 400

Tyr Phe Pro Gly Ser  
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 cgt tca cat aac acg atg cca atg ctt gat caa ttt cga tct aat cat  
 96  
 Arg Ser His Asn Thr Met Pro Met Leu Asp Gln Phe Arg Ser Asn His  
 20 25 30



cct gaa aca agc aag atc gag ggg gtc tct tcg ttg gac aca gct ctg  
 144  
 Pro Glu Thr Ser Lys Ile Glu Gly Val Ser Ser Leu Asp Thr Ala Leu  
           35                          40                          45

aag gtg ttt tgg aat aat caa agg gag cag cta gga aac ttt gca ggc  
 192  
 Lys Val Phe Trp Asn Asn Gln Arg Glu Gln Leu Gly Asn Phe Ala Gly  
           50                          55                          60

caa act cat ttg ccg cta tct agg gtc aga aag att ttg aaa tct gat  
 240  
 Gln Thr His Leu Pro Leu Ser Arg Val Arg Lys Ile Leu Lys Ser Asp  
           65                          70                          75                          80

cct gaa gtc aag aag ata agc tgt gat gtt cct gct ttg ttt tcg aaa  
 288  
 Pro Glu Val Lys Lys Ile Ser Cys Asp Val Pro Ala Leu Phe Ser Lys  
                           85                          90                          95

gcc tgt gaa tac ttc att cta gag gta aca tta cga gct tgg atg cat  
 336  
 Ala Cys Glu Tyr Phe Ile Leu Glu Val Thr Leu Arg Ala Trp Met His  
                           100                          105                          110

act caa tca tgc act cgt gag acc atc cgg cgt tgt gat atc ttc cag  
 384  
 Thr Gln Ser Cys Thr Arg Glu Thr Ile Arg Arg Cys Asp Ile Phe Gln  
                           115                          120                          125

gcc gta aag aac tca gga act tat gat ttc ctg att gat cgt gtc cct  
 432  
 Ala Val Lys Asn Ser Gly Thr Tyr Asp Phe Leu Ile Asp Arg Val Pro  
           130                          135                          140

ttt gga ccg cac tgt gtc acc cat cag ggt gtg caa cct cct gct gaa  
 480  
 Phe Gly Pro His Cys Val Thr His Gln Gly Val Gln Pro Pro Ala Glu  
           145                          150                          155                          160

atg att ttg ccg gat atg aat gtt cca atc gat atg gac cag att gag  
 528  
 Met Ile Leu Pro Asp Met Asn Val Pro Ile Asp Met Asp Gln Ile Glu  
                           165                          170                          175

gag gag aat atg atg gaa gag cgc tct gtc ggg ttt gac ctc aac tgt  
 576  
 Glu Glu Asn Met Met Glu Glu Arg Ser Val Gly Phe Asp Leu Asn Cys  
                           180                          185                          190

gat ctc cag tga  
 588  
 Asp Leu Gln  
           195

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                     20                      25                      30  
 Pro Glu Thr Ser Lys Ile Glu Gly Val Ser Ser Leu Asp Thr Ala Leu  
                     35                      40                      45  
 Lys Val Phe Trp Asn Asn Gln Arg Glu Gln Leu Gly Asn Phe Ala Gly  
                     50                      55                      60  
 Gln Thr His Leu Pro Leu Ser Arg Val Arg Lys Ile Leu Lys Ser Asp  
                     65                      70                      75                      80  
 Pro Glu Val Lys Lys Ile Ser Cys Asp Val Pro Ala Leu Phe Ser Lys  
                     85                      90                      95  
 Ala Cys Glu Tyr Phe Ile Leu Glu Val Thr Leu Arg Ala Trp Met His  
                     100                      105                      110  
 Thr Gln Ser Cys Thr Arg Glu Thr Ile Arg Arg Cys Asp Ile Phe Gln  
                     115                      120                      125  
 Ala Val Lys Asn Ser Gly Thr Tyr Asp Phe Leu Ile Asp Arg Val Pro  
                     130                      135                      140  
 Phe Gly Pro His Cys Val Thr His Gln Gly Val Gln Pro Pro Ala Glu  
                     145                      150                      155                      160  
 Met Ile Leu Pro Asp Met Asn Val Pro Ile Asp Met Asp Gln Ile Glu  
                     165                      170                      175  
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                     180                      185                      190  
 Asp Leu Gln  
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Met  
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gcg ctc gag gct ctt aca tca cca aga tta gct tct ccg att cct cct  
 105  
 Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro  
           5                                  10                                  15

ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag  
 153  
 Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys  
           20                                  25                                  30

ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc  
 201  
 Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu  
           35                                  40                                  45

act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac  
 249  
 Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp  
           50                                  55                                  60                                  65

aac cgt cag cct cct cct cct ccg gcg gtg gag aag ttg agc tac aag  
 297  
 Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr Lys  
                                   70                                  75                                  80

tgt agc gtc tgc gac aag acg ttc tct tct tac caa gct ctc ggt ggt  
 345  
 Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly  
                                   85                                  90                                  95

cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga  
 393  
 His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly  
           100                                  105                                  110

gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act  
 441  
 Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val Thr  
           115                                  120                                  125

act gga agt ggg aaa tca cac gtt tgc acc atc tgt aac aag tct ttt  
 489  
 Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe  
           130                                  135                                  140                                  145

cct tcc ggt caa gct ctc ggc gga cac aag cgg tgc cac tac gaa gga  
 537  
 Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly  
                                   150                                  155                                  160

aac aac aac atc aac act agt agc gtg tcc aac tcc gaa ggt gcg ggg  
 585  
 Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala Gly  
                                   165                                  170                                  175

tcc act agc cac gtt agc agt agc cac cgt ggg ttt gac ctc aac atc  
 633  
 Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile  
           180                                  185                                  190



cct ccg atc cct gaa ttc tcg atg gtc aac gga gac gac gaa gtc atg  
 681  
 Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met  
 195 200 205

agc cct atg ccg gcg aag aag cct cgg ttt gac ttt ccg gtc aaa ctt  
 729  
 Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu  
 210 215 220 225

caa ctt taa ggaaatttac ttagacgata agatttcgtt tgtatactgt  
 778  
 Gln Leu

tgagagttgt gtaggaattt gttgactgta cataccaaat tggactttga ctgattccaa  
 838

ttcttcttgt tctttcattt taaaaattat taaaccgatt ctttaccaca aa  
 890

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Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn  
 35 40 45

Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg  
 50 55 60

Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr  
 65 70 75 80

Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly  
 85 90 95

Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly  
 100 105 110

Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val  
 115 120 125

Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser  
 130 135 140



Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu  
145 150 155 160

Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala  
165 170 175

Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn  
180 185 190

Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val  
195 200 205

Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys  
210 215 220

Leu Gln Leu  
225

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120

cagcttgcgt actaagacaa caaatctttc cctctctctc tcgcctgata gatcttcaaa  
180

gagtaagaaa a atg cag gaa caa gcg act agc tct tta gct gca agc tct  
230

Met Gln Glu Gln Ala Thr Ser Ser Leu Ala Ala Ser Ser  
1 5 10

tta cca tca agc agc gag agg tca tca agc tct gct cca cat ttg gag  
278

Leu Pro Ser Ser Ser Glu Arg Ser Ser Ser Ser Ala Pro His Leu Glu  
15 20 25

atc aaa gaa gga att gaa agc gat gag gag ata cgg cga gtg ccg gag  
326

Ile Lys Glu Gly Ile Glu Ser Asp Glu Glu Ile Arg Arg Val Pro Glu  
30 35 40 45

ttt gga gga gaa gct gtc gga aaa gaa act tcc ggt aga gaa tct gga  
374

Phe Gly Gly Glu Ala Val Gly Lys Glu Thr Ser Gly Arg Glu Ser Gly  
50 55 60

tcg gcg acc ggt cag gag cgg aca cag gcg act gtc gga gaa agt caa  
422

Ser Ala Thr Gly Gln Glu Arg Thr Gln Ala Thr Val Gly Glu Ser Gln  
65 70 75



agg aag cga ggg agg aca ccg gcg gag aaa gag aac aag cgg ctg aag  
470

Arg Lys Arg Gly Arg Thr Pro Ala Glu Lys Glu Asn Lys Arg Leu Lys  
80 85 90

agg ttg ttg agg aac aga gtt tca gct cag caa gca aga gag agg aaa  
518

Arg Leu Leu Arg Asn Arg Val Ser Ala Gln Gln Ala Arg Glu Arg Lys  
95 100 105

aag gct tac ttg agc gag ttg gaa aac aga gtg aaa gac ttg gag aac  
566

Lys Ala Tyr Leu Ser Glu Leu Glu Asn Arg Val Lys Asp Leu Glu Asn  
110 115 120 125

aaa aac tct gaa ctt gaa gag cga ctc tct act ctt cag aac gag aac  
614

Lys Asn Ser Glu Leu Glu Glu Arg Leu Ser Thr Leu Gln Asn Glu Asn  
130 135 140

cag atg ctt aga cat att ctg aag aac aca aca gga aac aag aga gga  
662

Gln Met Leu Arg His Ile Leu Lys Asn Thr Thr Gly Asn Lys Arg Gly  
145 150 155

ggt ggt ggt ggt tct aat gct gat gca agc ctt tga tctccttctt  
708

Gly Gly Gly Gly Ser Asn Ala Asp Ala Ser Leu  
160 165

cttcttgtgt tatatttttg tggataaaat ttacagagaa ttgtatcaat aattatcatg  
768

ttaaattat atgggatgtg agagctaata ttgcaattgt agaccaagtt ctcttaaaaa  
828

aaaaaaaaaa aaaa  
842

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102

Met Gln Glu Gln Ala Thr Ser Ser Leu Ala Ala Ser Ser Leu Pro Ser  
1 5 10 15

Ser Ser Glu Arg Ser Ser Ser Ser Ala Pro His Leu Glu Ile Lys Glu  
20 25 30

Gly Ile Glu Ser Asp Glu Glu Ile Arg Arg Val Pro Glu Phe Gly Gly  
35 40 45

Glu Ala Val Gly Lys Glu Thr Ser Gly Arg Glu Ser Gly Ser Ala Thr  
50 55 60

Gly Gln Glu Arg Thr Gln Ala Thr Val Gly Glu Ser Gln Arg Lys Arg



Gly Arg Thr Pro Ala Glu Lys Glu Asn Lys Arg Leu Lys Arg Leu Leu  
85 90 95

Arg Asn Arg Val Ser Ala Gln Gln Ala Arg Glu Arg Lys Lys Ala Tyr  
100 105 110

Leu Ser Glu Leu Glu Asn Arg Val Lys Asp Leu Glu Asn Lys Asn Ser  
115 120 125

Glu Leu Glu Glu Arg Leu Ser Thr Leu Gln Asn Glu Asn Gln Met Leu  
130 135 140

Arg His Ile Leu Lys Asn Thr Thr Gly Asn Lys Arg Gly Gly Gly Gly  
145 150 155 160

Gly Ser Asn Ala Asp Ala Ser Leu  
165

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120  
cacttctggtt ctcttttcca atg ttg tca tca gct aag cat cag aga aac cat  
173  
Met Leu Ser Ser Ala Lys His Gln Arg Asn His  
1 5 10  
aga ctc tct gct aca aac aag aac cag act ctc acc aaa gtt tct tcc  
221  
Arg Leu Ser Ala Thr Asn Lys Asn Gln Thr Leu Thr Lys Val Ser Ser  
15 20 25  
att tca tcc tca tca cca tcg tct tct tct tca tca tca tca acc tca  
269  
Ile Ser Ser Ser Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser  
30 35 40  
tca tca tct cct tta cct tct caa gac tct caa gcc cag aag aga tct  
317  
Ser Ser Ser Pro Leu Pro Ser Gln Asp Ser Gln Ala Gln Lys Arg Ser  
45 50 55  
ctt gtc acc atg gaa gaa gtt tgg aat gac atc aac ctt gct tcc atc  
365  
Leu Val Thr Met Glu Glu Val Trp Asn Asp Ile Asn Leu Ala Ser Ile  
60 65 70 75



cac cac cta aac cga cac agc cct cat cca caa cac aac cac gag cca  
 413  
 His His Leu Asn Arg His Ser Pro His Pro Gln His Asn His Glu Pro  
 80 85 90  
 agg ttc agg ggc caa aac cac cac aac caa aac cct aac tca atc ttc  
 461  
 Arg Phe Arg Gly Gln Asn His His Asn Gln Asn Pro Asn Ser Ile Phe  
 95 100 105  
 caa gat ttt ctc aaa gga tct ttg aac cag gaa cca gca ccc aca agc  
 509  
 Gln Asp Phe Leu Lys Gly Ser Leu Asn Gln Glu Pro Ala Pro Thr Ser  
 110 115 120  
 cag acc acg ggt tct gcg cct aat ggc gat tcc acc acg gtc act gtt  
 557  
 Gln Thr Thr Gly Ser Ala Pro Asn Gly Asp Ser Thr Thr Val Thr Val  
 125 130 135  
 ctt tac agc tct cct ttt cca cct cct gca act gtt ctg agc ttg aat  
 605  
 Leu Tyr Ser Ser Pro Phe Pro Pro Pro Ala Thr Val Leu Ser Leu Asn  
 140 145 150 155  
 tcc ggc gct ggc ttc gag ttt ctc gat aac caa gat cct ctt gtt acc  
 653  
 Ser Gly Ala Gly Phe Glu Phe Leu Asp Asn Gln Asp Pro Leu Val Thr  
 160 165 170  
 tca aac tct aat ctt cat acc cac cat cac ctc tca aac gct cat gcc  
 701  
 Ser Asn Ser Asn Leu His Thr His His His His Leu Ser Asn Ala His Ala  
 175 180 185  
 ttc aac acc tct ttc gag gct ctg gtt cca tcc agt tct ttt ggt aag  
 749  
 Phe Asn Thr Ser Phe Glu Ala Leu Val Pro Ser Ser Ser Phe Gly Lys  
 190 195 200  
 aaa aga ggc caa gat tcc aat gaa ggt tca ggg aat aga aga cat aag  
 797  
 Lys Arg Gly Gln Asp Ser Asn Glu Gly Ser Gly Asn Arg Arg His Lys  
 205 210 215  
 cgt atg atc aag aac aga gaa tct gca gct cgt tcc cgc gct agg aaa  
 845  
 Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys  
 220 225 230 235  
 cag gct tat aca aac gag tta gaa ctt gaa gtt gct cac ttg cag gca  
 893  
 Gln Ala Tyr Thr Asn Glu Leu Glu Leu Glu Val Ala His Leu Gln Ala  
 240 245 250  
 gaa aat gca aga ctc aag aga caa caa gat caa aaa atg gct gca gca  
 941  
 Glu Asn Ala Arg Leu Lys Arg Gln Gln Asp Gln Lys Met Ala Ala Ala  
 255 260 265



att cag caa ccc aaa aag aac aca ctt caa cgg tct tcc aca gct cca  
989

Ile Gln Gln Pro Lys Lys Asn Thr Leu Gln Arg Ser Ser Thr Ala Pro  
270 275 280

ttt tga gaaatctaca agtccttggt tctcttttgg ggattgagat tgtctcatga  
1045  
Phe

agaagtgaag aaatggcaaa agtttggtacc cttttttatt agctataagt ataactaagc  
1105

ctaaaattgt agaactaaga tattgtaggg gaaaaaagaa gatgtaaaac aaaagacccg  
1165

gaaagagaaa aggatctttc aatttcctaa ggcacaggaa cacctgtcct gggtcctctc  
1225

ttaatgttct gtcgttttcc tatgcaaacc cttttttcac ttctgtacta acttatactt  
1285

gtattcttg  
1294

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Met Leu Ser Ser Ala Lys His Gln Arg Asn His Arg Leu Ser Ala Thr  
1 5 10 15

Asn Lys Asn Gln Thr Leu Thr Lys Val Ser Ser Ile Ser Ser Ser Ser  
20 25 30

Pro Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Pro Leu  
35 40 45

Pro Ser Gln Asp Ser Gln Ala Gln Lys Arg Ser Leu Val Thr Met Glu  
50 55 60

Glu Val Trp Asn Asp Ile Asn Leu Ala Ser Ile His His Leu Asn Arg  
65 70 75 80

His Ser Pro His Pro Gln His Asn His Glu Pro Arg Phe Arg Gly Gln  
85 90 95

Asn His His Asn Gln Asn Pro Asn Ser Ile Phe Gln Asp Phe Leu Lys  
100 105 110

Gly Ser Leu Asn Gln Glu Pro Ala Pro Thr Ser Gln Thr Thr Gly Ser  
115 120 125



Ala Pro Asn Gly Asp Ser Thr Thr Val Thr Val Leu Tyr Ser Ser Pro  
130 135 140

Phe Pro Pro Pro Ala Thr Val Leu Ser Leu Asn Ser Gly Ala Gly Phe  
145 150 155 160

Glu Phe Leu Asp Asn Gln Asp Pro Leu Val Thr Ser Asn Ser Asn Leu  
165 170 175

His Thr His His His Leu Ser Asn Ala His Ala Phe Asn Thr Ser Phe  
180 185 190

Glu Ala Leu Val Pro Ser Ser Ser Phe Gly Lys Lys Arg Gly Gln Asp  
195 200 205

Ser Asn Glu Gly Ser Gly Asn Arg Arg His Lys Arg Met Ile Lys Asn  
210 215 220

Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn  
225 230 235 240

Glu Leu Glu Leu Glu Val Ala His Leu Gln Ala Glu Asn Ala Arg Leu  
245 250 255

Lys Arg Gln Gln Asp Gln Lys Met Ala Ala Ala Ile Gln Gln Pro Lys  
260 265 270

Lys Asn Thr Leu Gln Arg Ser Ser Thr Ala Pro Phe  
275 280

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54

Met Leu Ser Ser  
1

gca aag cat aat aag atc aac aac cat agt gcc ttt tca att tcc tct  
102

Ala Lys His Asn Lys Ile Asn Asn His Ser Ala Phe Ser Ile Ser Ser  
5 10 15 20

tca tca tca tca tta tca aca tca tcc tcc cta ggc cat aac aaa tct  
150

Ser Ser Ser Ser Leu Ser Thr Ser Ser Ser Leu Gly His Asn Lys Ser  
25 30 35

caa gtc acc atg gaa gaa gta tgg aaa gaa atc aac ctt ggt tca ctt  
198



Gln Val Thr Met Glu Glu Val Trp Lys Glu Ile Asn Leu Gly Ser Leu  
 40 45 50  
 cac tac cat cgg caa cta aac att ggt cat gaa cca atg tta aag aac  
 246  
 His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro Met Leu Lys Asn  
 55 60 65  
 caa aac cct aat aac tcc atc ttt caa gat ttc ctc aac atg cct ctg  
 294  
 Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu Asn Met Pro Leu  
 70 75 80  
 aat caa cca cca cca cca cca cca cct tcc tct tcc acc att gtc  
 342  
 Asn Gln Pro Pro Pro Pro Pro Pro Pro Ser Ser Ser Thr Ile Val  
 85 90 95 100  
 act gct ctc tat ggc tct ctg cct ctt ccg cct cct gcc act gtc ctc  
 390  
 Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro Ala Thr Val Leu  
 105 110 115  
 agc tta aac tcc ggt gtt gga ttc gag ttt ctt gat acc aca gaa aat  
 438  
 Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp Thr Thr Glu Asn  
 120 125 130  
 ctt ctt gct tct aac cct cgc tcc ttt gag gaa tct gca aag ttt ggt  
 486  
 Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser Ala Lys Phe Gly  
 135 140 145  
 tgt ctt ggt aag aaa aga ggc caa gat tct gat gat act aga gga gac  
 534  
 Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp Thr Arg Gly Asp  
 150 155 160  
 aga agg tat aag cgt atg atc aag aac aga gaa tct gct gct cgt tca  
 582  
 Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg Ser  
 165 170 175 180  
 agg gct agg aag cag gca tat aca aac gaa ctt gag ctt gaa att gct  
 630  
 Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu Leu Glu Ile Ala  
 185 190 195  
 cac ttg cag aca gag aat gca aga ctc aag ata caa caa gag cag ctg  
 678  
 His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln Gln Glu Gln Leu  
 200 205 210  
 aaa ata gcc gaa gca act caa aac caa gta aag aaa aca cta caa cgg  
 726  
 Lys Ile Ala Glu Ala Thr Gln Asn Gln Val Lys Lys Thr Leu Gln Arg  
 215 220 225  
 tct tcc aca gct cca ttt tga gaaaaatcta ctatttcttt ttgggggagt  
 777  
 Ser Ser Thr Ala Pro Phe



230

ttcaagtgtt tcttatgaag atgagaaaaa cagaaaaagt ttgtacattt tagctaagtt  
837

aaatttgtgg tggtaagtaa tgtaaaagaa aagtgtgtgt agaagaaaag tgtctagaaa  
897

aagaaagcaa ctaactttct tcttcttctc tggtttccta tcaactcttt tgacttttgt  
957

acttttttc ttctctactt aacctctatt attgtaatgc caagtcaagt ccttatctag  
1017

ctagtacatg agtttctggt ttcaactgggt aagccat  
1054

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106

Met Leu Ser Ser Ala Lys His Asn Lys Ile Asn Asn His Ser Ala Phe  
1 5 10 15

Ser Ile Ser Ser Ser Ser Ser Ser Leu Ser Thr Ser Ser Ser Leu Gly  
20 25 30

His Asn Lys Ser Gln Val Thr Met Glu Glu Val Trp Lys Glu Ile Asn  
35 40 45

Leu Gly Ser Leu His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro  
50 55 60

Met Leu Lys Asn Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu  
65 70 75 80

Asn Met Pro Leu Asn Gln Pro Pro Pro Pro Pro Pro Pro Ser Ser  
85 90 95

Ser Thr Ile Val Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro  
100 105 110

Ala Thr Val Leu Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp  
115 120 125

Thr Thr Glu Asn Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser  
130 135 140

Ala Lys Phe Gly Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp  
145 150 155 160



Thr Arg Gly Asp Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser  
165 170 175

Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu  
180 185 190

Leu Glu Ile Ala His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln  
195 200 205

Gln Glu Gln Leu Lys Ile Ala Glu Ala Thr Gln Asn Gln Val Lys Lys  
210 215 220

Thr Leu Gln Arg Ser Ser Thr Ala Pro Phe  
225 230

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aatgttttag cttaaactgc tttttttttg ttgttggtgt a atg ata tca cag aga  
116

Met Ile Ser Gln Arg  
1 5

gaa gaa aga gaa gag aag aag cag aga gtg atg gga gat aag aaa ttg  
164

Glu Glu Arg Glu Glu Lys Lys Gln Arg Val Met Gly Asp Lys Lys Leu  
10 15 20

att tca tct tct tct tct tcc tcg gtt tac gat act cgt atc aat cat  
212

Ile Ser Ser Ser Ser Ser Ser Val Tyr Asp Thr Arg Ile Asn His  
25 30 35

cat ctt cat cat cct ccg tct tct tcc gac gaa atc tct cag ttt ctc  
260

His Leu His His Pro Pro Ser Ser Ser Asp Glu Ile Ser Gln Phe Leu  
40 45 50

cgg cat att ttc gac cgt tct tct cct tta cct tct tac tac tcc ccg  
308

Arg His Ile Phe Asp Arg Ser Ser Pro Leu Pro Ser Tyr Tyr Ser Pro  
55 60 65

gcg acg act aca acg acg gcg tct ttg att ggt gtg cac ggg agc ggt  
356

Ala Thr Thr Thr Thr Thr Ala Ser Leu Ile Gly Val His Gly Ser Gly  
70 75 80 85

gac cca cat gca gat aac tcg aga agt ctc gtt tct cat cat cca ccg  
404

Asp Pro His Ala Asp Asn Ser Arg Ser Leu Val Ser His His Pro Pro  
90 95 100



tca gat tct gtg ctt atg tcg aaa cgt gtc gga gat ttc tct gag gtt  
 452  
 Ser Asp Ser Val Leu Met Ser Lys Arg Val Gly Asp Phe Ser Glu Val  
 105 110 115  
 tta atc ggc gga gga tca ggc tca gcc gcc gcg tgt ttt ggt ttc tcc  
 500  
 Leu Ile Gly Gly Gly Ser Gly Ser Ala Ala Ala Cys Phe Gly Phe Ser  
 120 125 130  
 ggt ggt ggt aat aat aac aac gtt caa gga aat agc tct ggg act cga  
 548  
 Gly Gly Gly Asn Asn Asn Asn Val Gln Gly Asn Ser Ser Gly Thr Arg  
 135 140 145  
 gta tcg tct tct tcc gtt gga gct agt ggc aac gag aca gat gag tat  
 596  
 Val Ser Ser Ser Ser Val Gly Ala Ser Gly Asn Glu Thr Asp Glu Tyr  
 150 155 160 165  
 gac tgt gaa agc gag gaa gga gga gaa gct gta gtt gat gaa gct ccc  
 644  
 Asp Cys Glu Ser Glu Glu Gly Gly Glu Ala Val Val Asp Glu Ala Pro  
 170 175 180  
 tct tcc aag tca ggt cct tct tct cgt agt tca tct aaa aga tgc aga  
 692  
 Ser Ser Lys Ser Gly Pro Ser Ser Arg Ser Ser Ser Lys Arg Cys Arg  
 185 190 195  
 gct gct gaa gtt cat aat ctc tct gag aag agg agg aga agt aga att  
 740  
 Ala Ala Glu Val His Asn Leu Ser Glu Lys Arg Arg Arg Ser Arg Ile  
 200 205 210  
 aat gaa aaa atg aaa gct tta caa agt ctc atc cct aat tca aat aag  
 788  
 Asn Glu Lys Met Lys Ala Leu Gln Ser Leu Ile Pro Asn Ser Asn Lys  
 215 220 225  
 acg gat aag gct tca atg ctt gat gaa gcc att gag tat ctg aaa cag  
 836  
 Thr Asp Lys Ala Ser Met Leu Asp Glu Ala Ile Glu Tyr Leu Lys Gln  
 230 235 240 245  
 ctt cag ctc caa gtt cag atg ttg act atg aga aat gga ata aac ttg  
 884  
 Leu Gln Leu Gln Val Gln Met Leu Thr Met Arg Asn Gly Ile Asn Leu  
 250 255 260  
 cat cct ttg tgt tta cct gga act aca tta cac cca ttg caa ctc tct  
 932  
 His Pro Leu Cys Leu Pro Gly Thr Thr Leu His Pro Leu Gln Leu Ser  
 265 270 275  
 cag att cga ccc cct gaa gca acc aat gat cct ctg ctt aat cat acc  
 980  
 Gln Ile Arg Pro Pro Glu Ala Thr Asn Asp Pro Leu Leu Asn His Thr  
 280 285 290



aat cag ttt gct tcg act tct aat gca ccg gaa atg atc aat act gtg  
1028

Asn Gln Phe Ala Ser Thr Ser Asn Ala Pro Glu Met Ile Asn Thr Val  
295 300 305

gct tct tca tac gct ttg gaa cct tct att cgc agt cac ttt gga cct  
1076

Ala Ser Ser Tyr Ala Leu Glu Pro Ser Ile Arg Ser His Phe Gly Pro  
310 315 320 325

ttc cct ctc ctt act tca ccc gtg gag atg agt cgg gaa ggt ggg tta  
1124

Phe Pro Leu Leu Thr Ser Pro Val Glu Met Ser Arg Glu Gly Gly Leu  
330 335 340

act cat cca agg ttg aac att ggt cat tcc aac gca aac ata acc ggg  
1172

Thr His Pro Arg Leu Asn Ile Gly His Ser Asn Ala Asn Ile Thr Gly  
345 350 355

gaa caa gct ctg ttt gat gga caa cct gac cta aaa gat cga att act  
1220

Glu Gln Ala Leu Phe Asp Gly Gln Pro Asp Leu Lys Asp Arg Ile Thr  
360 365 370

tga acagtgtccc aacttcggga tctctatgtg ttcttgtttc ttagaacgca  
1273

agccataaag ctgtctgac  
1292

<210> 108 <211> 373 <212> PRT <213> Arabidopsis thaliana <400>  
108

Met Ile Ser Gln Arg Glu Glu Arg Glu Glu Lys Lys Gln Arg Val Met  
1 5 10 15

Gly Asp Lys Lys Leu Ile Ser Ser Ser Ser Ser Ser Val Tyr Asp  
20 25 30

Thr Arg Ile Asn His His Leu His His Pro Pro Ser Ser Ser Asp Glu  
35 40 45

Ile Ser Gln Phe Leu Arg His Ile Phe Asp Arg Ser Ser Pro Leu Pro  
50 55 60

Ser Tyr Tyr Ser Pro Ala Thr Thr Thr Thr Thr Ala Ser Leu Ile Gly  
65 70 75 80

Val His Gly Ser Gly Asp Pro His Ala Asp Asn Ser Arg Ser Leu Val  
85 90 95

Ser His His Pro Pro Ser Asp Ser Val Leu Met Ser Lys Arg Val Gly  
100 105 110



Asp Phe Ser Glu Val Leu Ile Gly Gly Gly Ser Gly Ser Ala Ala Ala  
 115 120 125

Cys Phe Gly Phe Ser Gly Gly Gly Asn Asn Asn Asn Val Gln Gly Asn  
 130 135 140

Ser Ser Gly Thr Arg Val Ser Ser Ser Ser Val Gly Ala Ser Gly Asn  
 145 150 155 160

Glu Thr Asp Glu Tyr Asp Cys Glu Ser Glu Glu Gly Gly Glu Ala Val  
 165 170 175

Val Asp Glu Ala Pro Ser Ser Lys Ser Gly Pro Ser Ser Arg Ser Ser  
 180 185 190

Ser Lys Arg Cys Arg Ala Ala Glu Val His Asn Leu Ser Glu Lys Arg  
 195 200 205

Arg Arg Ser Arg Ile Asn Glu Lys Met Lys Ala Leu Gln Ser Leu Ile  
 210 215 220

Pro Asn Ser Asn Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Ala Ile  
 225 230 235 240

Glu Tyr Leu Lys Gln Leu Gln Leu Gln Val Gln Met Leu Thr Met Arg  
 245 250 255

Asn Gly Ile Asn Leu His Pro Leu Cys Leu Pro Gly Thr Thr Leu His  
 260 265 270

Pro Leu Gln Leu Ser Gln Ile Arg Pro Pro Glu Ala Thr Asn Asp Pro  
 275 280 285

Leu Leu Asn His Thr Asn Gln Phe Ala Ser Thr Ser Asn Ala Pro Glu  
 290 295 300

Met Ile Asn Thr Val Ala Ser Ser Tyr Ala Leu Glu Pro Ser Ile Arg  
 305 310 315 320

Ser His Phe Gly Pro Phe Pro Leu Leu Thr Ser Pro Val Glu Met Ser  
 325 330 335

Arg Glu Gly Gly Leu Thr His Pro Arg Leu Asn Ile Gly His Ser Asn  
 340 345 350



Ala Asn Ile Thr Gly Glu Gln Ala Leu Phe Asp Gly Gln Pro Asp Leu  
 355 360 365

Lys Asp Arg Ile Thr  
 370

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 57

Met Asp Leu Ser  
 1

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 105  
 Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln Met Val Ser Pro  
 5 10 15 20

gag ttt ctt cag ata ctt ggc tca gat ggg aga gaa gag ctc aaa aga  
 153  
 Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu Glu Leu Lys Arg  
 25 30 35

gtt gag agt tac ttg gga aac aac aat gat gag ctg cag agt ttc aga  
 201  
 Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu Gln Ser Phe Arg  
 40 45 50

cat ttt ccc gaa ttc gga ccg gat tat gat act act gat ggc tgc att  
 249  
 His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr Asp Gly Cys Ile  
 55 60 65

tct agg aca agt agc ttc cat atg gag cca gtg aag aat aat gga cac  
 297  
 Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys Asn Asn Gly His  
 70 75 80

agc aga gcc att acc ttg cag aac aag aga aaa cca gag ggt aag aca  
 345  
 Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro Glu Gly Lys Thr  
 85 90 95 100

gaa aag aga gag aag aag aag atc aaa gca gag gat gaa aca gag cca  
 393  
 Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp Glu Thr Glu Pro  
 105 110 115

agc atg aaa ggg aaa tca aac atg agt aac aca gag aca tct tca gaa  
 441  
 Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu Thr Ser Ser Glu  
 120 125 130

att cag aaa cca gat tac att cat gtt agg gct aga cga ggt gaa gcc  
 489  
 Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala



135                      140                      145  
 acc gac aga cat agc tta gca gag agg gca aga aga gaa aag ata agc  
 537  
 Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser  
 150                      155                      160  
 aag aag atg aaa tgt cta caa gat att gtt cct gga tgc aac aaa gtt  
 585  
 Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val  
 165                      170                      175                      180  
 act gga aaa gct ggt atg ctt gat gag atc atc aac tat gtc caa tct  
 633  
 Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser  
 185                      190                      195  
 ctg caa caa caa gtc gag ttc ttg tcg atg aaa ctc tct gtc ata aat  
 681  
 Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn  
 200                      205                      210  
 cca gaa ctt gag tgt cat atc gat gat tta tcc gca aaa cag ttt cag  
 729  
 Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln  
 215                      220                      225  
 gct tac ttc aca ggt cct cca gaa ggt gac tcg aag cag tca atc atg  
 777  
 Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met  
 230                      235                      240  
 gcg gat ttt cgg tct ttt cca tta cat cag caa gga tct tta gat tac  
 825  
 Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr  
 245                      250                      255                      260  
 tca gtc ata aac tca gac cac acc aca tct ctc ggc gct aaa gat cat  
 873  
 Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly Ala Lys Asp His  
 265                      270                      275  
 aca tca tca agc tgg gaa act cac tca cag tgt ctt tac aac agc ttg  
 921  
 Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu Tyr Asn Ser Leu  
 280                      285                      290  
 aga acc gat tct gtt tcc aat ttc ttc agc ctc aag taa aaaaattagg  
 970  
 Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys  
 295                      300  
 gatagcctca ttaaaaaaat cgcggttttt tgttggtgtc ttatccattt atctatctta  
 1030  
 tctgaaattt gaaccagaaa gacagaggaa accaatccaa agatctttct caatctatta  
 1090  
 tcttcataca aatatagtga tttacatata ttccagggga tatgtatatg tgtagaagaa  
 1150



agagaaaaaa ctcttggtggt catagcaatt cctttttttg tacattgtag aatcaaactc  
1210

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1270

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1292

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20 25 30

Glu Leu Lys Arg Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu  
35 40 45

Gln Ser Phe Arg His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr  
50 55 60

Asp Gly Cys Ile Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys  
65 70 75 80

Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro  
85 90 95

Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp  
100 105 110

Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu  
115 120 125

Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg  
130 135 140

Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg  
145 150 155 160

Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly  
165 170 175

Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn  
180 185 190



Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu  
195 200 205

Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala  
210 215 220

Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys  
225 230 235 240

Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly  
245 250 255

Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly  
260 265 270

Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu  
275 280 285

Tyr Asn Ser Leu Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys  
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120

ctctctctct tcaactctctc tttctttcaa a atg gaa aaa ctc atg gtt ccg  
172

Met Glu Lys Leu Met Val Pro  
1 5

aca tgg aga ccc gac ccg gtt tac cgt cca ccg gaa aca cca ctc gaa  
220

Thr Trp Arg Pro Asp Pro Val Tyr Arg Pro Pro Glu Thr Pro Leu Glu  
10 15 20

ccg atg gag ttt tta gct cgt tca tgg agc gtc tct gct ctc gaa gtc  
268

Pro Met Glu Phe Leu Ala Arg Ser Trp Ser Val Ser Ala Leu Glu Val  
25 30 35

tcc aag gct cta aca cca ccc aac cct cag att ctc ctc tcc aaa acc  
316

Ser Lys Ala Leu Thr Pro Pro Asn Pro Gln Ile Leu Leu Ser Lys Thr  
40 45 50 55

gaa gaa gaa gaa gaa gaa gaa ccc atc tcc tct gtc gta gac ggc gac  
364

Glu Glu Glu Glu Glu Glu Glu Pro Ile Ser Ser Val Val Asp Gly Asp



	60	65	70
ggc gac acg gaa gac acc gga ctt gtc acc gga aac cca ttc tcc ttc			
412			
Gly Asp Thr Glu Asp Thr Gly Leu Val Thr Gly Asn Pro Phe Ser Phe			
	75	80	85
gct tgt tca gaa act tct caa atg gtc atg gat cgt atc ttg tct cac			
460			
Ala Cys Ser Glu Thr Ser Gln Met Val Met Asp Arg Ile Leu Ser His			
	90	95	100
tct caa gaa gta tca cca aga aca tct ggt cgg cta tct cac agt agt			
508			
Ser Gln Glu Val Ser Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser			
	105	110	115
ggt cca ctt aat ggt tct ttg acc gac agt cct cct gtg tct cct ccc			
556			
Gly Pro Leu Asn Gly Ser Leu Thr Asp Ser Pro Pro Val Ser Pro Pro			
	120	125	130 135
gaa tcc gac gac att aag caa ttt tgc aga gcg aac aaa aat tca ttg			
604			
Glu Ser Asp Asp Ile Lys Gln Phe Cys Arg Ala Asn Lys Asn Ser Leu			
	140	145	150
aac agt gta aat tct cag ttc cgt tca acg gcg gca act ccg gga cct			
652			
Asn Ser Val Asn Ser Gln Phe Arg Ser Thr Ala Ala Thr Pro Gly Pro			
	155	160	165
ata acc gct aca gct aca cag tcc aag acg gtg gga cgg tgg ctt aag			
700			
Ile Thr Ala Thr Ala Thr Gln Ser Lys Thr Val Gly Arg Trp Leu Lys			
	170	175	180
gac cgg aga gag aaa aag aaa gag gag act cgg gct cat aac gct cag			
748			
Asp Arg Arg Glu Lys Lys Lys Glu Glu Thr Arg Ala His Asn Ala Gln			
	185	190	195
att cac gct gct gtc tct gtc gcc gcc gtt gct gca gct gtt gct gct			
796			
Ile His Ala Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala			
	200	205	210 215
att gca gca gcc acc gct gcg tct tct agc tgt ggt aag gat gag cag			
844			
Ile Ala Ala Ala Thr Ala Ala Ser Ser Ser Cys Gly Lys Asp Glu Gln			
	220	225	230
atg gct aaa act gac atg gcc gtt gct tct gct gcg acc ctt gtg gct			
892			
Met Ala Lys Thr Asp Met Ala Val Ala Ser Ala Ala Thr Leu Val Ala			
	235	240	245
gct cag tgt gtg gaa gct gct gaa gtt atg gga gct gag aga gag tat			
940			
Ala Gln Cys Val Glu Ala Ala Glu Val Met Gly Ala Glu Arg Glu Tyr			
	250	255	260



ttg gct tct gtt gtt agc tcc gcc gtc aat gtt cgt tct gcc gga gat  
 988  
 Leu Ala Ser Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp  
 265 270 275  
 att atg act ctc acc gcc gga gca gct aca gct tta aga gga gtg caa  
 1036  
 Ile Met Thr Leu Thr Ala Gly Ala Ala Thr Ala Leu Arg Gly Val Gln  
 280 285 290 295  
 aca ttg aag gca agg gca atg aag gaa gtg tgg aac ata gca tca gtg  
 1084  
 Thr Leu Lys Ala Arg Ala Met Lys Glu Val Trp Asn Ile Ala Ser Val  
 300 305 310  
 ata cca atg gat aaa gga ctc act tct aca gga gga agc agc aat aat  
 1132  
 Ile Pro Met Asp Lys Gly Leu Thr Ser Thr Gly Gly Ser Ser Asn Asn  
 315 320 325  
 gtt aat ggt agc aat gga agc tca agc agt agt cac agt ggt gaa ctt  
 1180  
 Val Asn Gly Ser Asn Gly Ser Ser Ser Ser Ser His Ser Gly Glu Leu  
 330 335 340  
 gta caa cag gag aat ttc ttg gga act tgt agt aga gaa tgg ctc gct  
 1228  
 Val Gln Gln Glu Asn Phe Leu Gly Thr Cys Ser Arg Glu Trp Leu Ala  
 345 350 355  
 aga ggt tgt gaa ctc ctc aaa cgc act cgc aaa ggt gat ctc cac tgg  
 1276  
 Arg Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His Trp  
 360 365 370 375  
 aag ata gta tct gtt tac atc aac aaa atg aat cag gtt atg ttg aag  
 1324  
 Lys Ile Val Ser Val Tyr Ile Asn Lys Met Asn Gln Val Met Leu Lys  
 380 385 390  
 atg aag agc agg cat gtt gga gga acc ttc acc aag aag aaa aag aac  
 1372  
 Met Lys Ser Arg His Val Gly Gly Thr Phe Thr Lys Lys Lys Lys Asn  
 395 400 405  
 att gtg ctt gat gtg atc aag aat gtc ccg gcc tgg cct gga cga cat  
 1420  
 Ile Val Leu Asp Val Ile Lys Asn Val Pro Ala Trp Pro Gly Arg His  
 410 415 420  
 ttg cta gag gga gga gat gat cta aga tac ttc ggt ttg aag acg gtt  
 1468  
 Leu Leu Glu Gly Gly Asp Asp Leu Arg Tyr Phe Gly Leu Lys Thr Val  
 425 430 435  
 atg cga ggt gat gtt gaa ttc gag gtc aag agc caa agg gaa tat gaa  
 1516  
 Met Arg Gly Asp Val Glu Phe Glu Val Lys Ser Gln Arg Glu Tyr Glu  
 440 445 450 455



atg tgg aca caa ggt gtc tca agg ctt ctt gtt ctt gct gct gag agg  
 1564  
 Met Trp Thr Gln Gly Val Ser Arg Leu Leu Val Leu Ala Ala Glu Arg  
                     460                    465                    470

aag ttt agg atg tga ataaacgttc aatggctgct tggtttaagt gtgagttttt  
 1619  
 Lys Phe Arg Met  
                     475

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 1679

gttgggtata ggataaaatg gacctaccag tcaagggtgag gaagcatttg ggtaaacaaa  
 1739

acttagtggg ggtgatctgt aatatctatg ttcttagttt ttttttgggt gttggtggtc  
 1799

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 1857

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Pro Pro Glu Thr Pro Leu Glu Pro Met Glu Phe Leu Ala Arg Ser Trp  
                     20                    25                    30

Ser Val Ser Ala Leu Glu Val Ser Lys Ala Leu Thr Pro Pro Asn Pro  
                     35                    40                    45

Gln Ile Leu Leu Ser Lys Thr Glu Glu Glu Glu Glu Glu Glu Pro Ile  
   50                    55                    60

Ser Ser Val Val Asp Gly Asp Gly Asp Thr Glu Asp Thr Gly Leu Val  
   65                    70                    75                    80

Thr Gly Asn Pro Phe Ser Phe Ala Cys Ser Glu Thr Ser Gln Met Val  
                     85                    90                    95

Met Asp Arg Ile Leu Ser His Ser Gln Glu Val Ser Pro Arg Thr Ser  
                     100                    105                    110

Gly Arg Leu Ser His Ser Ser Gly Pro Leu Asn Gly Ser Leu Thr Asp  
                     115                    120                    125

Ser Pro Pro Val Ser Pro Pro Glu Ser Asp Asp Ile Lys Gln Phe Cys  
                     130                    135                    140



Arg Ala Asn Lys Asn Ser Leu Asn Ser Val Asn Ser Gln Phe Arg Ser  
 145 150 155 160  
 Thr Ala Ala Thr Pro Gly Pro Ile Thr Ala Thr Ala Thr Gln Ser Lys  
 165 170 175  
 Thr Val Gly Arg Trp Leu Lys Asp Arg Arg Glu Lys Lys Lys Glu Glu  
 180 185 190  
 Thr Arg Ala His Asn Ala Gln Ile His Ala Ala Val Ser Val Ala Gly  
 195 200 205  
 Val Ala Ala Ala Val Ala Ala Ile Ala Ala Ala Thr Ala Ala Ser Ser  
 210 215 220  
 Ser Cys Gly Lys Asp Glu Gln Met Ala Lys Thr Asp Met Ala Val Ala  
 225 230 235 240  
 Ser Ala Ala Thr Leu Val Ala Ala Gln Cys Val Glu Ala Ala Glu Val  
 245 250 255  
 Met Gly Ala Glu Arg Glu Tyr Leu Ala Ser Val Val Ser Ser Ala Val  
 260 265 270  
 Asn Val Arg Ser Ala Gly Asp Ile Met Thr Leu Thr Ala Gly Ala Ala  
 275 280 285  
 Thr Ala Leu Arg Gly Val Gln Thr Leu Lys Ala Arg Ala Met Lys Glu  
 290 295 300  
 Val Trp Asn Ile Ala Ser Val Ile Pro Met Asp Lys Gly Leu Thr Ser  
 305 310 315 320  
 Thr Gly Gly Ser Ser Asn Asn Val Asn Gly Ser Asn Gly Ser Ser Ser  
 325 330 335  
 Ser Ser His Ser Gly Glu Leu Val Gln Gln Glu Asn Phe Leu Gly Thr  
 340 345 350  
 Cys Ser Arg Glu Trp Leu Ala Arg Gly Cys Glu Leu Leu Lys Arg Thr  
 355 360 365  
 Arg Lys Gly Asp Leu His Trp Lys Ile Val Ser Val Tyr Ile Asn Lys  
 370 375 380



Met Asn Gln Val Met Leu Lys Met Lys Ser Arg His Val Gly Gly Thr  
385 390 395 400

Phe Thr Lys Lys Lys Lys Asn Ile Val Leu Asp Val Ile Lys Asn Val  
405 410 415

Pro Ala Trp Pro Gly Arg His Leu Leu Glu Gly Gly Asp Asp Leu Arg  
420 425 430

Tyr Phe Gly Leu Lys Thr Val Met Arg Gly Asp Val Glu Phe Glu Val  
435 440 445

Lys Ser Gln Arg Glu Tyr Glu Met Trp Thr Gln Gly Val Ser Arg Leu  
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Leu Val Leu Ala Ala Glu Arg Lys Phe Arg Met  
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48

Met Glu Ile Met Arg Pro Gly Val Ser Glu Asn Thr Leu Lys Gly Lys  
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ata aga atc aca acg cgg tgc atg tgg ctt gac aaa gga aga ctt tta  
96

Ile Arg Ile Thr Thr Arg Cys Met Trp Leu Asp Lys Gly Arg Leu Leu  
20 25 30

gat gca ctt cac aaa gca gct cat gct gct cta tca agt tgt cct gtg  
144

Asp Ala Leu His Lys Ala Ala His Ala Ala Leu Ser Ser Cys Pro Val  
35 40 45

aca tgt ccc ttg tct cac atg gaa aga aca gtc tcc gaa gtc ctg agg  
192

Thr Cys Pro Leu Ser His Met Glu Arg Thr Val Ser Glu Val Leu Arg  
50 55 60

aag att gta agg aag tac agt ggt aaa agg cct gaa gtc atc gct ata  
240

Lys Ile Val Arg Lys Tyr Ser Gly Lys Arg Pro Glu Val Ile Ala Ile  
65 70 75 80

gcc act gag aat cca atg gct gtc cga gct gat gag gtc agt gcg aga  
288

Ala Thr Glu Asn Pro Met Ala Val Arg Ala Asp Glu Val Ser Ala Arg  
85 90 95

ctg tot ggt gat cca agt gtt ggt tct gga gtt gca gct tta agg aaa  
336

Leu Ser Gly Asp Pro Ser Val Gly Ser Gly Val Ala Ala Leu Arg Lys



100	105	110
ggt ggt gaa gga aat gac aaa aga agt cgg gcg aag aaa gca cct tca 384		
Val Val Glu Gly Asn Asp Lys Arg Ser Arg Ala Lys Lys Ala Pro Ser 115	120	125
caa gaa gct tcc ccc aaa gaa gta gat cgc act ttg gaa gat gat atc 432		
Gln Glu Ala Ser Pro Lys Glu Val Asp Arg Thr Leu Glu Asp Asp Ile 130	135	140
att gat agt gca aga cta ctg gct gaa gaa gaa act gcg gca tca aca 480		
Ile Asp Ser Ala Arg Leu Leu Ala Glu Glu Glu Thr Ala Ala Ser Thr 145	150	155 160
tac acg gaa gaa gtt gat acg ccc gtt ggg agt tct tca gaa gag tca 528		
Tyr Thr Glu Glu Val Asp Thr Pro Val Gly Ser Ser Ser Glu Glu Ser 165	170	175
gac gat ttt tgg aaa tca ttc atc aat cca tca tcg tca cct tca ccg 576		
Asp Asp Phe Trp Lys Ser Phe Ile Asn Pro Ser Ser Ser Pro Ser Pro 180	185	190
agt gaa aca gaa aat atg aat aag gta gct gat acg gag cct aaa gca 624		
Ser Glu Thr Glu Asn Met Asn Lys Val Ala Asp Thr Glu Pro Lys Ala 195	200	205
gag ggt aag gaa aac agc aga gac gac gat gaa tta gct gat gct tca 672		
Glu Gly Lys Glu Asn Ser Arg Asp Asp Asp Glu Leu Ala Asp Ala Ser 210	215	220
gat tct gaa acc aag tca tca cca aaa cgt gtg agg aag aac aaa tgg 720		
Asp Ser Glu Thr Lys Ser Ser Pro Lys Arg Val Arg Lys Asn Lys Trp 225	230	235 240
aaa ccg gag gag ata aag aag gta atc aga atg cga gga gag ctg cac 768		
Lys Pro Glu Glu Ile Lys Lys Val Ile Arg Met Arg Gly Glu Leu His 245	250	255
agt aga ttt caa gtg gtg aaa ggt aga atg gca ttg tgg gaa gag atc 816		
Ser Arg Phe Gln Val Val Lys Gly Arg Met Ala Leu Trp Glu Glu Ile 260	265	270
tct tca aat cta tca gct gaa gga atc aat cga agc ccg gga caa tgc 864		
Ser Ser Asn Leu Ser Ala Glu Gly Ile Asn Arg Ser Pro Gly Gln Cys 275	280	285
aaa tct ctc tgg gca tca ctt att cag aaa tac gag gag agc aag gct 912		
Lys Ser Leu Trp Ala Ser Leu Ile Gln Lys Tyr Glu Glu Ser Lys Ala 290	295	300



gat gag aga agc aag acg agt tgg cca cat ttt gag gat atg aac aac  
960

Asp Glu Arg Ser Lys Thr Ser Trp Pro His Phe Glu Asp Met Asn Asn  
305 310 315 320

att ttg tca gag cta ggc aca cct gcg tct taa  
993

Ile Leu Ser Glu Leu Gly Thr Pro Ala Ser  
325 330

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114

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20 25 30

Asp Ala Leu His Lys Ala Ala His Ala Ala Leu Ser Ser Cys Pro Val  
35 40 45

Thr Cys Pro Leu Ser His Met Glu Arg Thr Val Ser Glu Val Leu Arg  
50 55 60

Lys Ile Val Arg Lys Tyr Ser Gly Lys Arg Pro Glu Val Ile Ala Ile  
65 70 75 80

Ala Thr Glu Asn Pro Met Ala Val Arg Ala Asp Glu Val Ser Ala Arg  
85 90 95

Leu Ser Gly Asp Pro Ser Val Gly Ser Gly Val Ala Ala Leu Arg Lys  
100 105 110

Val Val Glu Gly Asn Asp Lys Arg Ser Arg Ala Lys Lys Ala Pro Ser  
115 120 125

Gln Glu Ala Ser Pro Lys Glu Val Asp Arg Thr Leu Glu Asp Asp Ile  
130 135 140

Ile Asp Ser Ala Arg Leu Leu Ala Glu Glu Glu Thr Ala Ala Ser Thr  
145 150 155 160

Tyr Thr Glu Glu Val Asp Thr Pro Val Gly Ser Ser Ser Glu Glu Ser  
165 170 175

Asp Asp Phe Trp Lys Ser Phe Ile Asn Pro Ser Ser Ser Pro Ser Pro  
180 185 190



Ser Glu Thr Glu Asn Met Asn Lys Val Ala Asp Thr Glu Pro Lys Ala  
195 200 205

Glu Gly Lys Glu Asn Ser Arg Asp Asp Asp Glu Leu Ala Asp Ala Ser  
210 215 220

Asp Ser Glu Thr Lys Ser Ser Pro Lys Arg Val Arg Lys Asn Lys Trp  
225 230 235 240

Lys Pro Glu Glu Ile Lys Lys Val Ile Arg Met Arg Gly Glu Leu His  
245 250 255

Ser Arg Phe Gln Val Val Lys Gly Arg Met Ala Leu Trp Glu Glu Ile  
260 265 270

Ser Ser Asn Leu Ser Ala Glu Gly Ile Asn Arg Ser Pro Gly Gln Cys  
275 280 285

Lys Ser Leu Trp Ala Ser Leu Ile Gln Lys Tyr Glu Glu Ser Lys Ala  
290 295 300

Asp Glu Arg Ser Lys Thr Ser Trp Pro His Phe Glu Asp Met Asn Asn  
305 310 315 320

Ile Leu Ser Glu Leu Gly Thr Pro Ala Ser  
325 330

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112

Met Asp Gln Asp Gln His Pro Gln Tyr  
1 5

ggt ata ccg gag ctc cgg cag ctc atg aaa ggc gga gga agg acg act  
160

Gly Ile Pro Glu Leu Arg Gln Leu Met Lys Gly Gly Gly Arg Thr Thr  
10 15 20 25

act aca aca ccg tct act tct tct cat ttt ccc tct gat ttc ttc ggt  
208

Thr Thr Thr Pro Ser Thr Ser Ser His Phe Pro Ser Asp Phe Phe Gly  
30 35 40



ttt aac ctt gct ccg gtg cag cca ccg cca cac cgt ctt cat cag ttc  
 256  
 Phe Asn Leu Ala Pro Val Gln Pro Pro Pro His Arg Leu His Gln Phe  
                   45                                  50                                  55

act act gat caa gat atg ggt ttc ttg cca cgt ggc ata cat gga ttg  
 304  
 Thr Thr Asp Gln Asp Met Gly Phe Leu Pro Arg Gly Ile His Gly Leu  
           60                                  65                                  70

ggt gga ggt tct tca acg gct gga aat aac agt aac tta aac gcg agt  
 352  
 Gly Gly Gly Ser Ser Thr Ala Gly Asn Asn Ser Asn Leu Asn Ala Ser  
           75                                  80                                  85

act agt ggt gga gga gtt ggg ttt agt ggg ttt ctt gac ggt ggt ggt  
 400  
 Thr Ser Gly Gly Gly Val Gly Phe Ser Gly Phe Leu Asp Gly Gly Gly  
           90                                  95                                  100                                  105

ttc ggc agc gga gta gga gga gac ggt gga gga act gga agg tgg ccg  
 448  
 Phe Gly Ser Gly Val Gly Gly Asp Gly Gly Gly Thr Gly Arg Trp Pro  
                   110                                  115                                  120

aga caa gaa acc cta act ctg ttg gaa att aga tct cgt ctt gat cat  
 496  
 Arg Gln Glu Thr Leu Thr Leu Leu Glu Ile Arg Ser Arg Leu Asp His  
                   125                                  130                                  135

aaa ttc aaa gaa gct aat cat aaa gga cct ctt tgg gat gaa gtt tct  
 544  
 Lys Phe Lys Glu Ala Asn His Lys Gly Pro Leu Trp Asp Glu Val Ser  
           140                                  145                                  150

agg att atg tcc gag gaa cat gga tac caa agg agt ggg aag aaa tgc  
 592  
 Arg Ile Met Ser Glu Glu His Gly Tyr Gln Arg Ser Gly Lys Lys Cys  
           155                                  160                                  165

aga gag aag ttt gag aat ctg tac aaa tac tat agt aag act aaa gaa  
 640  
 Arg Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Ser Lys Thr Lys Glu  
           170                                  175                                  180                                  185

ggc gaa gcc gga aga caa gac gga aaa cat cac aga ttt ttc cgc cag  
 688  
 Gly Glu Ala Gly Arg Gln Asp Gly Lys His His Arg Phe Phe Arg Gln  
                   190                                  195                                  200

ctc caa gcg cta tac ggg gat tct aat aac ttg gtt tct tgt ccc aat  
 736  
 Leu Gln Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn  
                   205                                  210                                  215

cat aac acg cag ttc atg agc agt gct ctt cat ggt ttc cat act caa  
 784  
 His Asn Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln  
           220                                  225                                  230



aac cct atg aac gtt gct aca aca acg tcc aac atc cat aac gtt gat  
 832  
 Asn Pro Met Asn Val Ala Thr Thr Thr Ser Asn Ile His Asn Val Asp  
 235 240 245  
 agt gtt cat ggt ttt cat caa agc ctt agt ctt tct aac aac tac aac  
 880  
 Ser Val His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn  
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Ile Lys Lys Arg Leu Ile Lys Lys Gly Ile Asp Pro Val Thr His Lys  
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Gly Ile Thr Ser Gly Thr Asp Lys Ser Glu Asn Leu Pro Glu Lys Gln  
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Lys Lys Asn Asn Lys Asn Phe Gly Leu Ser Ser Ala Ser Phe Leu Asn  
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Lys Val Ala Asn Arg Phe Gly Lys Arg Ile Asn Gln Ser Val Leu Ser  
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Glu Ile Ile Gly Ser Gly Gly Pro Leu Ala Ser Thr Ser His Thr Thr  
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20 25 30

Glu Arg Phe Leu Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg  
35 40 45

Ile Glu Glu His Ile Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His  
50 55 60

Ala Gln Lys Phe Phe Thr Lys Leu Glu Lys Glu Ala Glu Val Lys Gly  
65 70 75 80

Ile Pro Val Cys Gln Ala Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro  
85 90 95

Lys Arg Lys Pro Asn Thr Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly  
100 105 110

Thr Ser Ser Ser Gln Val Ser Ser Ala Lys Asp Ala Lys Leu Val Ser  
115 120 125

Ser Ala Ser Ser Ser Gln Leu Asn Gln Ala Phe Leu Asp Leu Glu Lys  
130 135 140

Met Pro Phe Ser Glu Lys Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu  
145 150 155 160

Asn Cys Ser Gly Val Ser Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys  
165 170 175



Gln Val Ser Gly Asp Ile Glu Thr Ser Lys Thr Ser Thr Val Asp Asn  
 180 185 190

Ala Val Gln Asp Val Pro Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp  
 195 200 205

Gly Thr Thr Val His Ser Met Gln Asn Tyr Pro Trp His Phe His Ala  
 210 215 220

Asp Ile Val Asn Gly Asn Ile Ala Lys Cys Pro Gln Asn His Pro Ser  
 225 230 235 240

Gly Met Val Ser Gln Asp Phe Met Phe His Pro Met Arg Glu Glu Thr  
 245 250 255

His Gly His Ala Asn Leu Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr  
 260 265 - 270

Ala Ser His Gln Ala Phe Pro Ala Cys His Ser Gln Asp Asp Tyr Arg  
 275 280 285

Ser Phe Leu Gln Ile Ser Ser Thr Phe Ser Asn Leu Ile Met Ser Thr  
 290 295 300

Leu Leu Gln Asn Pro Ala Ala His Ala Ala Thr Phe Ala Ala Ser  
 305 310 315 320

Val Trp Pro Tyr Ala Ser Val Gly Asn Ser Gly Asp Ser Ser Thr Pro  
 325 330 335

Met Ser Ser Ser Pro Pro Ser Ile Thr Ala Ile Ala Ala Thr Val  
 340 345 350

Ala Ala Ala Thr Ala Trp Trp Ala Ser His Gly Leu Leu Pro Val Cys  
 355 360 365

Ala Pro Ala Pro Ile Thr Cys Val Pro Phe Ser Thr Val Ala Val Pro  
 370 375 380

Thr Pro Ala Met Thr Glu Met Asp Thr Val Glu Asn Thr Gln Pro Phe  
 385 390 395 400

Glu Lys Gln Asn Thr Ala Leu Gln Asp Gln Thr Leu Ala Ser Lys Ser  
 405 410 415



Pro Ala Ser Ser Ser Asp Asp Ser Asp Glu Thr Gly Val Thr Lys Leu  
                   420                  425                  430

Asn Ala Asp Ser Lys Thr Asn Asp Asp Lys Ile Glu Glu Val Val Val  
                   435                  440                  445

Thr Ala Ala Val His Asp Ser Asn Thr Ala Gln Lys Lys Asn Leu Val  
                   450                  455                  460

Asp Arg Ser Ser Cys Gly Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu  
 465                  470                  475                  480

Thr Asp Ala Leu Asp Lys Met Glu Lys Asp Lys Glu Asp Val Lys Glu  
                   485                  490                  495

Thr Asp Glu Asn Gln Pro Asp Val Ile Glu Leu Asn Asn Arg Lys Ile  
                   500                  505                  510

Lys Met Arg Asp Asn Asn Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp  
                   515                  520                  525

Lys Glu Val Ser Glu Glu Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala  
                   530                  535                  540

Arg Glu Arg Leu Pro Gln Ser Phe Ser Pro Pro Gln Val Ala Glu Asn  
 545                  550                  555                  560

Val Asn Arg Lys Gln Ser Asp Thr Ser Met Pro Leu Ala Pro Asn Phe  
                   565                  570                  575

Lys Ser Gln Asp Ser Cys Ala Ala Asp Gln Glu Gly Val Val Met Ile  
                   580                  585                  590

Gly Val Gly Thr Cys Lys Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys  
                   595                  600                  605

Pro Tyr Lys Arg Cys Ser Met Glu Val Lys Glu Ser Gln Val Gly Asn  
                   610                  615                  620

Ile Asn Asn Gln Ser Asp Glu Lys Val Cys Lys Arg Leu Arg Leu Glu  
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Gly Glu Ala Ser Thr  
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 180

tttaccgcgt gaagggtttt ttttctttct attttctttc atttcctctc cttctacttc  
 240

ttcttctcca gttctcatct gggttcttca atg gcg agt gtt gaa ggt gat gat  
 294

Met Ala Ser Val Glu Gly Asp Asp  
 1 5

gat ttc gga agt tct tcg tca agg tct tat caa gat caa cta tac aca  
 342

Asp Phe Gly Ser Ser Ser Ser Arg Ser Tyr Gln Asp Gln Leu Tyr Thr  
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gag cta tgg aaa gtt tgt gca ggt cca tta gtg gaa gtt cct cgt gct  
 390

Glu Leu Trp Lys Val Cys Ala Gly Pro Leu Val Glu Val Pro Arg Ala  
 25 30 35 40

caa gag aga gtt ttc tac ttc cct cag ggt cac atg gaa caa ctt gtg  
 438

Gln Glu Arg Val Phe Tyr Phe Pro Gln Gly His Met Glu Gln Leu Val  
 45 50 55

gcg tca act aat caa gga atc aat tca gaa gaa ata cct gtt ttt gat  
 486

Ala Ser Thr Asn Gln Gly Ile Asn Ser Glu Glu Ile Pro Val Phe Asp  
 60 65 70

ctt cct cca aag ata ctt tgt cga gtt ctt gat gtc act tta aag gcg  
 534

Leu Pro Pro Lys Ile Leu Cys Arg Val Leu Asp Val Thr Leu Lys Ala  
 75 80 85

gag cat gaa aca gat gag gtt tac gct cag atc aca tta caa cca gag  
 582

Glu His Glu Thr Asp Glu Val Tyr Ala Gln Ile Thr Leu Gln Pro Glu  
 90 95 100

gaa gat caa agt gaa cca aca agt ctt gat cca cct att gtt gga cca  
 630

Glu Asp Gln Ser Glu Pro Thr Ser Leu Asp Pro Pro Ile Val Gly Pro  
 105 110 115 120

act aag caa gag ttt cat tcg ttt gtt aag att tta acg gct tca gat  
 678

Thr Lys Gln Glu Phe His Ser Phe Val Lys Ile Leu Thr Ala Ser Asp  
 125 130 135



aca agc act cat ggt gga ttc tct gtt ctt cgt aaa cac gcc act gaa  
 726  
 Thr Ser Thr His Gly Gly Phe Ser Val Leu Arg Lys His Ala Thr Glu  
 140 145 150  
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 774  
 Cys Leu Pro Ser Leu Asp Met Thr Gln Ala Thr Pro Thr Gln Glu Leu  
 155 160 165  
 gtg act aga gat ctt cat ggc ttt gaa tgg agg ttt aag cat ata ttc  
 822  
 Val Thr Arg Asp Leu His Gly Phe Glu Trp Arg Phe Lys His Ile Phe  
 170 175 180  
 aga gga caa cca cgg agg cat ttg ctt act acg ggt tgg agt aca ttt  
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 Arg Gly Gln Pro Arg Arg His Leu Leu Thr Thr Gly Trp Ser Thr Phe  
 185 190 195 200  
 gta tcc tcg aaa aga ctt gta gct gga gat gct ttt gtg ttc ttg agg  
 918  
 Val Ser Ser Lys Arg Leu Val Ala Gly Asp Ala Phe Val Phe Leu Arg  
 205 210 215  
 ggt gag aat ggg gat tta cgg gtt gga gtg aga cga tta gct cgg cat  
 966  
 Gly Glu Asn Gly Asp Leu Arg Val Gly Val Arg Arg Leu Ala Arg His  
 220 225 230  
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 Gln Ser Thr Met Pro Thr Ser Val Ile Ser Ser Gln Ser Met His Leu  
 235 240 245  
 gga gtt ctt gct aca gct tct cat gct gtg cgt aca aca aca atc ttt  
 1062  
 Gly Val Leu Ala Thr Ala Ser His Ala Val Arg Thr Thr Thr Ile Phe  
 250 255 260  
 gtt gtc ttt tac aag cct agg ata agc caa ttc ata gtt ggg gtg aac  
 1110  
 Val Val Phe Tyr Lys Pro Arg Ile Ser Gln Phe Ile Val Gly Val Asn  
 265 270 275 280  
 aag tat atg gaa gct ata aag cat gga ttt tct ctc ggt acc cga ttc  
 1158  
 Lys Tyr Met Glu Ala Ile Lys His Gly Phe Ser Leu Gly Thr Arg Phe  
 285 290 295  
 aga atg agg ttt gaa gga gaa gag tct cct gag aga ata ttt act ggt  
 1206  
 Arg Met Arg Phe Glu Gly Glu Glu Ser Pro Glu Arg Ile Phe Thr Gly  
 300 305 310  
 acg att gtg gga agt gga gat cta tct tca caa tgg cca gct tct aaa  
 1254  
 Thr Ile Val Gly Ser Gly Asp Leu Ser Ser Gln Trp Pro Ala Ser Lys  
 315 320 325



tgg agg tca ttg cag gta caa tgg gat gag cca aca aca gtt cag aga  
 1302  
 Trp Arg Ser Leu Gln Val Gln Trp Asp Glu Pro Thr Thr Val Gln Arg  
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cca gat aaa gtc tca cca tgg gag ata gag cct ttc ttg gca act tcc  
 1350  
 Pro Asp Lys Val Ser Pro Trp Glu Ile Glu Pro Phe Leu Ala Thr Ser  
 345 350 355 360

cca att tca act cct gct caa caa cca caa tcg aaa tgc aag cgg tca  
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 Pro Ile Ser Thr Pro Ala Gln Gln Pro Gln Ser Lys Cys Lys Arg Ser  
 365 370 375

aga ccc atc gag cca tca gtt aaa aca cca gcc cca cct agt ttc ttg  
 1446  
 Arg Pro Ile Glu Pro Ser Val Lys Thr Pro Ala Pro Pro Ser Phe Leu  
 380 385 390

tac agc ctc cct cag agc caa gat tcc att aat gca tcc ctt aaa ctg  
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 Tyr Ser Leu Pro Gln Ser Gln Asp Ser Ile Asn Ala Ser Leu Lys Leu  
 395 400 405

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 Phe Gln Asp Pro Ser Leu Glu Arg Ile Ser Gly Gly Tyr Ser Ser Asn  
 410 415 420

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 1590  
 Asn Ser Phe Lys Pro Glu Thr Pro Pro Pro Pro Thr Asn Cys Ser Tyr  
 425 430 435 440

agg ttg ttt gga ttt gat ctc aca agc aat tct cct gct cca atc cct  
 1638  
 Arg Leu Phe Gly Phe Asp Leu Thr Ser Asn Ser Pro Ala Pro Ile Pro  
 445 450 455

caa gac aag caa ccg atg gat act tgt gga gct gcc aag tgt caa gaa  
 1686  
 Gln Asp Lys Gln Pro Met Asp Thr Cys Gly Ala Ala Lys Cys Gln Glu  
 460 465 470

ccc atc act cca acc tca atg agt gag cag aag aag caa caa aca tca  
 1734  
 Pro Ile Thr Pro Thr Ser Met Ser Glu Gln Lys Lys Gln Gln Thr Ser  
 475 480 485

aga agt cga act aaa gtg caa atg caa ggc att gcg gtt ggt cgt gcg  
 1782  
 Arg Ser Arg Thr Lys Val Gln Met Gln Gly Ile Ala Val Gly Arg Ala  
 490 495 500

gtt gat tta aca ctg ttg aaa tct tac gat gaa ctg att gat gag ctt  
 1830  
 Val Asp Leu Thr Leu Leu Lys Ser Tyr Asp Glu Leu Ile Asp Glu Leu  
 505 510 515 520



gag gag atg ttt gag att caa gga cag ctt ctt gcc cga gac aaa tgg  
1878

Glu Glu Met Phe Glu Ile Gln Gly Gln Leu Leu Ala Arg Asp Lys Trp  
525 530 535

atc gtt gtc ttc act gat gat gaa gga gat atg atg ctt gct ggt gat  
1926

Ile Val Val Phe Thr Asp Asp Glu Gly Asp Met Met Leu Ala Gly Asp  
540 545 550

gat ccg tgg aat gag ttt tgc aag atg gca aag aag ata ttt ata tat  
1974

Asp Pro Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Ile Phe Ile Tyr  
555 560 565

tcg agc gat gag gtt aag aaa atg aca acg aaa ctg aag att tct tcg  
2022

Ser Ser Asp Glu Val Lys Lys Met Thr Thr Lys Leu Lys Ile Ser Ser  
570 575 580

tcg tta gag aat gag gaa tat ggt aat gaa tca ttc gaa aat cgt agt  
2070

Ser Leu Glu Asn Glu Glu Tyr Gly Asn Glu Ser Phe Glu Asn Arg Ser  
585 590 595 600

agg ggg tga gagttttagc tgtaattaa ggtaattcg ggcacgtcgt  
2119

Arg Gly

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2179

tttttcattgt caatttttca agttggcgat ttaatatattc ggttttggga cagtgggtga  
2239

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2299

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35 40 45

Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Ile Asn  
50 55 60

Ser Glu Glu Ile Pro Val Phe Asp Leu Pro Pro Lys Ile Leu Cys Arg  
65 70 75 80



Val Leu Asp Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val Tyr  
85 90 95

Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr Ser  
100 105 110

Leu Asp Pro Pro Ile Val Gly Pro Thr Lys Gln Glu Phe His Ser Phe  
115 120 125

Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe Ser  
130 135 140

Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met Thr  
145 150 155 160

Gln Ala Thr Pro Thr Gln Glu Leu Val Thr Arg Asp Leu His Gly Phe  
165 170 175

Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His Leu  
180 185 190

Leu Thr Thr Gly Trp Ser Thr Phe Val Ser Ser Lys Arg Leu Val Ala  
195 200 205

Gly Asp Ala Phe Val Phe <sup>1</sup>Leu Arg Gly Glu Asn Gly Asp Leu Arg Val  
210 215 220

Gly Val Arg Arg Leu Ala Arg His Gln Ser Thr Met Pro Thr Ser Val  
225 230 235 240

Ile Ser Ser Gln Ser Met His Leu Gly Val Leu Ala Thr Ala Ser His  
245 250 255

Ala Val Arg Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg Ile  
260 265 270

Ser Gln Phe Ile Val Gly Val Asn Lys Tyr Met Glu Ala Ile Lys His  
275 280 285

Gly Phe Ser Leu Gly Thr Arg Phe Arg Met Arg Phe Glu Gly Glu Glu  
290 295 300

Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Val Gly Ser Gly Asp Leu  
305 310 315 320



Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Val Gln Trp  
 325 330 335  
 Asp Glu Pro Thr Thr Val Gln Arg Pro Asp Lys Val Ser Pro Trp Glu  
 340 345 350  
 Ile Glu Pro Phe Leu Ala Thr Ser Pro Ile Ser Thr Pro Ala Gln Gln  
 355 360 365  
 Pro Gln Ser Lys Cys Lys Arg Ser Arg Pro Ile Glu Pro Ser Val Lys  
 370 375 380  
 Thr Pro Ala Pro Pro Ser Phe Leu Tyr Ser Leu Pro Gln Ser Gln Asp  
 385 390 395 400  
 Ser Ile Asn Ala Ser Leu Lys Leu Phe Gln Asp Pro Ser Leu Glu Arg  
 405 410 415  
 Ile Ser Gly Gly Tyr Ser Ser Asn Asn Ser Phe Lys Pro Glu Thr Pro  
 420 425 430  
 Pro Pro Pro Thr Asn Cys Ser Tyr Arg Leu Phe Gly Phe Asp Leu Thr  
 435 440 445  
 Ser Asn Ser Pro Ala Pro Ile Pro Gln Asp Lys Gln Pro Met Asp Thr  
 450 455 460  
 Cys Gly Ala Ala Lys Cys Gln Glu Pro Ile Thr Pro Thr Ser Met Ser  
 465 470 475 480  
 Glu Gln Lys Lys Gln Gln Thr Ser Arg Ser Arg Thr Lys Val Gln Met  
 485 490 495  
 Gln Gly Ile Ala Val Gly Arg Ala Val Asp Leu Thr Leu Leu Lys Ser  
 500 505 510  
 Tyr Asp Glu Leu Ile Asp Glu Leu Glu Glu Met Phe Glu Ile Gln Gly  
 515 520 525  
 Gln Leu Leu Ala Arg Asp Lys Trp Ile Val Val Phe Thr Asp Asp Glu  
 530 535 540  
 Gly Asp Met Met Leu Ala Gly Asp Asp Pro Trp Asn Glu Phe Cys Lys  
 545 550 555 560



Met Ala Lys Lys Ile Phe Ile Tyr Ser Ser Asp Glu Val Lys Lys Met  
 565 570 575

Thr Thr Lys Leu Lys Ile Ser Ser Ser Leu Glu Asn Glu Glu Tyr Gly  
 580 585 590

Asn Glu Ser Phe Glu Asn Arg Ser Arg Gly  
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 96  
 Ala Phe Asn Thr Arg Thr Ile Lys Asn Glu Glu Glu Thr His Pro Pro  
 20 25 30  
 gag caa gaa gcc aca ata gcc gtt aga tca tca toa tca tcg gat ctg  
 144  
 Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu  
 35 40 45  
 acg gcc gag aag cgt ccg gat aag atc ata gca tgt cca aga tgc aag  
 192  
 Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys  
 50 55 60  
 agc atg gag aca aag ttc tgt tac ttc aac aac tac aac ggt aat cag  
 240  
 Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln  
 65 70 75 80  
 cct cga cac ttt tgt aaa ggc tgc cac cgt tac tgg acc gcc ggt ggt  
 288  
 Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly  
 85 90 95  
 gca ctc cgg aac gtt ccc gtc ggc gcc ggt cgt cgg aag tcc aaa cca  
 336  
 Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro  
 100 105 110  
 cct ggt cgt gtc gtg gtt ggt atg ctt gga gat gga aat ggt gtt cgc  
 384  
 Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg  
 115 120 125  
 caa gtc gag ctt ata aat ggc ttg ctc gtt gag gag tgg cag cat gcc  
 432  
 Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala  
 130 135 140



gca gcc gca gct cac ggt agt ttc cgg cat gat ttt ccc atg aag cgg  
 480  
 Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg  
 145 150 155 160

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 165 170

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Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu  
 35 40 45

Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys  
 50 55 60

Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln  
 65 70 75 80

Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly  
 85 90 95

Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro  
 100 105 110

Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg  
 115 120 125

Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala  
 130 135 140

Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg  
 145 150 155 160

Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys  
 165 170

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115

Met Met Met Glu Thr Arg  
1 5

gat cca gct att aag ctt ttc ggt atg aaa atc cct ttt ccg tcg gtt  
163

Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile Pro Phe Pro Ser Val  
10 15 20

ttt gaa tcg gca gtt acg gtg gag gat gac gaa gaa gat gac tgg agc  
211

Phe Glu Ser Ala Val Thr Val Glu Asp Asp Glu Glu Asp Asp Trp Ser  
25 30 35

ggc gga gat gac aaa tca cca gag aag gta act cca gag tta tca gat  
259

Gly Gly Asp Asp Lys Ser Pro Glu Lys Val Thr Pro Glu Leu Ser Asp  
40 45 50

aag aac aac aac aac tgt aac gac aac agt ttt aac aat tcg aaa ccc  
307

Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser Phe Asn Asn Ser Lys Pro  
55 60 65 70

gaa acc ttg gac aaa gag gaa gcg aca tca act gat cag ata gag agt  
355

Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser Thr Asp Gln Ile Glu Ser  
75 80 85

agt gac acg cct gag gat aat cag cag acg aca cct gat ggt aaa acc  
403

Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr Thr Pro Asp Gly Lys Thr  
90 95 100

cta aag aaa ccg act aag att cta ccg tgt ccg aga tgc aaa agc atg  
451

Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Lys Ser Met  
105 110 115

gag acc aag ttc tgt tat tac aac aac tac aac ata aac cag cct cgt  
499

Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Ile Asn Gln Pro Arg  
120 125 130

cat ttc tgc aag gct tgt cag aga tat tgg act gct gga ggg act atg  
547

His Phe Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ala Gly Gly Thr Met  
135 140 145 150

agg aat gtt cct gtg ggg gca gga cgt cgt aag aac aaa agc tca tct  
595

Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Asn Lys Ser Ser Ser  
155 160 165

tct cat tac cgt cac atc act att tcc gag gct ctt gag gct gcg agg  
643



Ser His Tyr Arg His Ile Thr Ile Ser Glu Ala Leu Glu Ala Ala Arg  
 170 175 180  
 ctt gac ccg ggc tta cag gca aac aca agg gtc ttg agt ttt ggt ctc  
 691  
 Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg Val Leu Ser Phe Gly Leu  
 185 190 195  
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 739  
 Glu Ala Gln Gln Gln His Val Ala Ala Pro Met Thr Pro Val Met Lys  
 200 205 210  
 cta caa gaa gat caa aag gtc tca aac ggt gct agg aac agg ttt cac  
 787  
 Leu Gln Glu Asp Gln Lys Val Ser Asn Gly Ala Arg Asn Arg Phe His  
 215 220 225 230  
 ggg tta gcg gat caa cgg ctt gta gct cgg gta gag aat gga gat gat  
 835  
 Gly Leu Ala Asp Gln Arg Leu Val Ala Arg Val Glu Asn Gly Asp Asp  
 235 240 245  
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 883  
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 250 255 260  
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 931  
 Glu Ser Arg Ala Gln Ser Gly Ser Val Val Glu Ala Gln Met Asn Asn  
 265 270 275  
 aac aac aac aat aac atg aat ggt tat gct tgc atc cca ggt gtt cca  
 979  
 Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala Cys Ile Pro Gly Val Pro  
 280 285 290  
 tgg cct tac acg tgg aat cca gcg atg cct cca cca ggt ttt tac ccg  
 1027  
 Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro Pro Pro Gly Phe Tyr Pro  
 295 300 305 310  
 cct cca ggg tat cca atg ccg ttt tac cct tac tgg acc atc cca atg  
 1075  
 Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro Tyr Trp Thr Ile Pro Met  
 315 320 325  
 cta cca ccg cat caa tcc tca tcg cct ata agc caa aag tgt tca aat  
 1123  
 Leu Pro Pro His Gln Ser Ser Ser Pro Ile Ser Gln Lys Cys Ser Asn  
 330 335 340  
 aca aac tct ccg act ctc gga aag cat ccg aga gat gaa gga tca tcg  
 1171  
 Thr Asn Ser Pro Thr Leu Gly Lys His Pro Arg Asp Glu Gly Ser Ser  
 345 350 355  
 aaa aag gac aat gag aca gag cga aaa cag aag gcc ggg tgc gtt ctg  
 1219  
 Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln Lys Ala Gly Cys Val Leu



360                      365                      370  
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 1267  
 Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu Ala Ala Lys Ser  
 375                      380                      385                      390  
 tcg ata tgg aca aca ttg gga atc aag aac gag gcg atg tgc aaa gcc  
 1315  
 Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Ala Met Cys Lys Ala  
 395                      400                      405  
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 1363  
 Gly Gly Met Phe Lys Gly Phe Asp His Lys Thr Lys Met Tyr Asn Asn  
 410                      415                      420  
 gac aaa gct gag aac tcc cct gtt ctt tct gct aac cct gct gct cta  
 1411  
 Asp Lys Ala Glu Asn Ser Pro Val Leu Ser Ala Asn Pro Ala Ala Leu  
 425                      430                      435  
 tca aga tca cac aat ttc cat gaa cag att tag agttacatat gtatatgtat  
 1464  
 Ser Arg Ser His Asn Phe His Glu Gln Ile  
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 1524  
 aactcttttc ttctttctag tgattgcctt tattccttta catgttttgg ttctctgtac  
 1584  
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 20                      25                      30  
 Glu Glu Asp Asp Trp Ser Gly Gly Asp Asp Lys Ser Pro Glu Lys Val  
 35                      40                      45  
 Thr Pro Glu Leu Ser Asp Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser  
 50                      55                      60



Phe Asn Asn Ser Lys Pro Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser  
65 70 75 80

Thr Asp Gln Ile Glu Ser Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr  
85 90 95

Thr Pro Asp Gly Lys Thr Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys  
100 105 110

Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr  
115 120 125

Asn Ile Asn Gln Pro Arg His Phe Cys Lys Ala Cys Gln Arg Tyr Trp  
130 135 140

Thr Ala Gly Gly Thr Met Arg Asn Val Pro Val Gly Ala Gly Arg Arg  
145 150 155 160

Lys Asn Lys Ser Ser Ser Ser His Tyr Arg His Ile Thr Ile Ser Glu  
165 170 175

Ala Leu Glu Ala Ala Arg Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg  
180 185 190

Val Leu Ser Phe Gly Leu Glu Ala Gln Gln Gln His Val Ala Ala Pro  
195 200 205

Met Thr Pro Val Met Lys Leu Gln Glu Asp Gln Lys Val Ser Asn Gly  
210 215 220

Ala Arg Asn Arg Phe His Gly Leu Ala Asp Gln Arg Leu Val Ala Arg  
225 230 235 240

Val Glu Asn Gly Asp Asp Cys Ser Ser Gly Ser Ser Val Thr Thr Ser  
245 250 255

Asn Asn His Ser Val Asp Glu Ser Arg Ala Gln Ser Gly Ser Val Val  
260 265 270

Glu Ala Gln Met Asn Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala  
275 280 285

Cys Ile Pro Gly Val Pro Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro  
290 295 300



Pro Pro Gly Phe Tyr Pro Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro  
305 310 315 320

Tyr Trp Thr Ile Pro Met Leu Pro Pro His Gln Ser Ser Ser Pro Ile  
325 330 335

Ser Gln Lys Cys Ser Asn Thr Asn Ser Pro Thr Leu Gly Lys His Pro  
340 345 350

Arg Asp Glu Gly Ser Ser Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln  
355 360 365

Lys Ala Gly Cys Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro  
370 375 380

Asn Glu Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn  
385 390 395 400

Glu Ala Met Cys Lys Ala Gly Gly Met Phe Lys Gly Phe Asp His Lys  
405 410 415

Thr Lys Met Tyr Asn Asn Asp Lys Ala Glu Asn Ser Pro Val Leu Ser  
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118

Met Lys Met  
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gaa aat ggt atg tat aaa aag aaa gga gtg tgc gac tct tgt gtc tcg  
166  
Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val Ser  
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214  
Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu Pro  
20 25 30 35

cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat ctt ctc  
262  
Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu Leu



40 45 50  
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 310  
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 55 60 65  
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 358  
 Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu Tyr  
 70 75 80  
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 406  
 Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala Val  
 85 90 95  
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 454  
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 100 105 110 115  
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 502  
 Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg  
 120 125 130  
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 550  
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 135 140 145  
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 598  
 Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile  
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 646  
 Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro His  
 165 170 175  
 tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat tac  
 694  
 Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr Tyr  
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Met Glu Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn  
35 40 45

Asp Leu Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His  
50 55 60

Leu Met Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp  
65 70 75 80

Glu Glu Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met  
85 90 95

Ile Ala Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys  
100 105 110

Pro Asn Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val  
115 120 125

Ala Arg Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys  
130 135 140

Arg Ile Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp  
145 150 155 160

Glu Ala Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu  
165 170 175

Gln Pro His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu  
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Cys Tyr Tyr His Asn Ser Gln Pro  
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120



cgagaagggtt ttggagatag aatcttttgt tcttcttttg tccctccttg ctcgattttt  
180

gttacgtgtg aagcaataaa aaaaaactga tatagctaaa tcttccatcc attcagaggc  
240

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291

Met Glu Gln Val Phe Ala Asp Trp Asn Phe Glu  
1 5 10

gat aat ttt cac atg tcc act aat aaa aga tca atc aga cca gaa gat  
339

Asp Asn Phe His Met Ser Thr Asn Lys Arg Ser Ile Arg Pro Glu Asp  
15 20 25

gaa tta gtg gag cta ttg tgg aga gat ggt caa gtg gtt tta caa agc  
387

Glu Leu Val Glu Leu Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser  
30 35 40

caa gct cgt aga gaa ccg tca gtc caa gtc caa acc cac aaa caa gaa  
435

Gln Ala Arg Arg Glu Pro Ser Val Gln Val Gln Thr His Lys Gln Glu  
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acc cta aga aaa ccc aac aat att ttt ctt gac aac caa gaa aca gta  
483

Thr Leu Arg Lys Pro Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val  
60 65 70 75

caa aag cct aac tac gct gct cta gat gat caa gaa acc gtc tcc tgg  
531

Gln Lys Pro Asn Tyr Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp  
80 85 90

ata caa tac cct ccg gat gac gtc atc gac cct ttc gaa tcc gag ttc  
579

Ile Gln Tyr Pro Pro Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe  
95 100 105

tcc tct cat ttc ttc tct tcg atc gat cac ctc gga ggt cct gag aag  
627

Ser Ser His Phe Phe Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys  
110 115 120

cca cga acg atc gaa gag aca gtt aag cat gag gct caa gcc atg gct  
675

Pro Arg Thr Ile Glu Glu Thr Val Lys His Glu Ala Gln Ala Met Ala  
125 130 135

cct cct aag ttt aga tcc tcg gtt ata aca gtc gga ccg agt cat tgc  
723

Pro Pro Lys Phe Arg Ser Ser Val Ile Thr Val Gly Pro Ser His Cys  
140 145 150 155

ggc agc aac cag tca aca aat att cat cag gcc act aca ctt ccg gtt  
771

Gly Ser Asn Gln Ser Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val  
160 165 170



tct atg agt gat aga agc aag aac gtc gaa gaa aga ctt gac act tcg  
819

Ser Met Ser Asp Arg Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser  
175 180 185

tca ggt ggc tcc tcc ggt tgc agc tat gga agg aac aac aaa gaa acc  
867

Ser Gly Gly Ser Ser Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr  
190 195 200

gtt agt gga aca agt gta acc att gac cgt aaa aga aaa cat gtt atg  
915

Val Ser Gly Thr Ser Val Thr Ile Asp Arg Lys Arg Lys His Val Met  
205 210 215

gat gct gat caa gaa tct gtg tct caa tca gat ata ggt ttg acc tca  
963

Asp Ala Asp Gln Glu Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser  
220 225 230 235

acc gat gat caa acc atg ggt aac aaa tcg agc caa cgg tca gga tct  
1011

Thr Asp Asp Gln Thr Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser  
240 245 250

act cga aga agc cgt gca gct gaa gtt cat aat ctc tca gaa agg agg  
1059

Thr Arg Arg Ser Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg  
255 260 265

agg aga gat cgg atc aat gaa aga atg aaa gct ctt caa gaa ctc ata  
1107

Arg Arg Asp Arg Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile  
270 275 280

cct cac tgc agc aga aca gat aaa gct tcg ata ttg gat gaa gca att  
1155

Pro His Cys Ser Arg Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile  
285 290 295

gat tac tta aaa tca ctt caa atg caa ctc caa gtg atg tgg atg gga  
1203

Asp Tyr Leu Lys Ser Leu Gln Met Gln Leu Gln Val Met Trp Met Gly  
300 305 310 315

agt gga atg gcg gcg gcg gca gca gca gca gca agt ccg atg atg ttt  
1251

Ser Gly Met Ala Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe  
320 325 330

ccc ggg gta caa tca tct cca tac att aat cag atg gct atg caa agt  
1299

Pro Gly Val Gln Ser Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser  
335 340 345

cag atg caa ttg tct caa ttc ccg gtt atg aac ccg tcc gct ccg cag  
1347

Gln Met Gln Leu Ser Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln  
350 355 360



aac cat ccc ggt tta gta tgt caa aac ccg gta cag ttg cag ctc caa  
 1395  
 Asn His Pro Gly Leu Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln  
 365 370 375

gca cag aac caa atc tta tcg gag cag ctc gct agg tac atg ggc ggg  
 1443  
 Ala Gln Asn Gln Ile Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly  
 380 385 390 395

att ccc cag atg ccg ccg gcg gga aat cag atg cag acc gtg caa caa  
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 400 405 410

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 415 420 425

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 Gly

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 1703

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 1763

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Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser Gln Ala Arg Arg Glu  
 35 40 45



Pro Ser Val Gln Val Gln Thr His Lys Gln Glu Thr Leu Arg Lys Pro  
50 55 60

Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val Gln Lys Pro Asn Tyr  
65 70 75 80

Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro  
85 90 95

Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe Ser Ser His Phe Phe  
100 105 110

Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys Pro Arg Thr Ile Glu  
115 120 125

Glu Thr Val Lys His Glu Ala Gln Ala Met Ala Pro Pro Lys Phe Arg  
130 135 140

Ser Ser Val Ile Thr Val Gly Pro Ser His Cys Gly Ser Asn Gln Ser  
145 150 155 160

Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val Ser Met Ser Asp Arg  
165 170 175

Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser Ser Gly Gly Ser Ser  
180 185 190

Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr Val Ser Gly Thr Ser  
195 200 205

Val Thr Ile Asp Arg Lys Arg Lys His Val Met Asp Ala Asp Gln Glu  
210 215 220

Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser Thr Asp Asp Gln Thr  
225 230 235 240

Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser Thr Arg Arg Ser Arg  
245 250 255

Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile  
260 265 270

Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Arg  
275 280 285

Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser



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 305                      310                      315                      320  
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 325                      330                      335  
 Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser Gln Met Gln Leu Ser  
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 Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln Asn His Pro Gly Leu  
 355                      360                      365  
 Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln Ala Gln Asn Gln Ile  
 370                      375                      380  
 Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly Ile Pro Gln Met Pro  
 385                      390                      395                      400  
 Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln Gln Pro Ala Asp Met  
 405                      410                      415  
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 Met Val  
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 226  
 Ser Pro Glu Asn Ala Asn Trp Ile Cys Asp Leu Ile Asp Ala Asp Tyr  
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Gly Ser Phe Thr Ile Gln Gly Pro Gly Phe Ser Trp Pro Val Gln Gln  
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 Gly Asn Ser Glu Ala Ser Lys Glu Pro Gly Ser Lys Lys Arg Gly Arg  
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 418  
 Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu Lys Gln  
 70 75 80  
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 466  
 Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala Ile Leu  
 85 90 95  
 gag cct gga aat cct ccc aaa aca gac aag gct gct atc ttg gtt gat  
 514  
 Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu Val Asp  
 100 105 110  
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 562  
 Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys Leu Lys  
 115 120 125 130  
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 610  
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 135 140 145  
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 658  
 Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu Lys Glu  
 150 155 160  
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 Lys Leu Glu Gln Gln Leu Lys Ala Met Asn Ala Pro Gln Pro Ser Phe  
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 754  
 Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala Gln Gly  
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 Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro Gly Val  
 195 200 205 210  
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215 220 225  
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 His Val Leu Arg Pro Pro Val Ala  
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 Gly Arg Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu  
 65 70 75 80  
 Lys Gln Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala  
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 Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu  
 100 105 110  
 Val Asp Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys  
 115 120 125  
 Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys  
 130 135 140  
 Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu  
 145 150 155 160



Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Met Asn Ala Pro Gln Pro  
 165 170 175

Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala  
 180 185 190

Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro  
 195 200 205

Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser  
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 101  
 Asn Gly Ile Ile Val Glu Gln Thr Ser Asn Lys Gly Pro Leu Asn Ala  
 10 15 20 25

gtt aag aaa cca ccg tct aaa gat cga cac agc aaa gtt gac gga aga  
 149  
 Val Lys Lys Pro Pro Ser Lys Asp Arg His Ser Lys Val Asp Gly Arg  
 30 35 40

gga aga agg att cgt atg cca atc att tgc gca gct cga gtt ttt caa  
 197  
 Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe Gln  
 45 50 55

ttg acc aga gag tta ggt cac aag tcc gat ggt caa acc ata gag tgg  
 245  
 Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu Trp  
 60 65 70

ctt ctc cgt caa gct gag cct tct atc ata gcc gcc act gga act ggc  
 293  
 Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly  
 75 80 85

act act ccg gcg agt ttc tcc act gct tct ctc tcc act tct tct ccg  
 341  
 Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Leu Ser Thr Ser Ser Pro  
 90 95 100 105



ttt act ctc ggg aaa cgt gtc gtc aga gcg gag gaa gga gaa tcc ggc  
389

Phe Thr Leu Gly Lys Arg Val Val Arg Ala Glu Glu Gly Glu Ser Gly  
110 115 120

ggc gga gga gga gga ggg tta aca gtg gga cac aca atg ggg act tcg  
437

Gly Gly Gly Gly Gly Gly Leu Thr Val Gly His Thr Met Gly Thr Ser  
125 130 135

tta atg ggt ggt ggt ggt tct ggt ggg ttt tgg gct gtt ccg gcg agg  
485

Leu Met Gly Gly Gly Gly Ser Gly Gly Phe Trp Ala Val Pro Ala Arg  
140 145 150

ccg gat ttc gga caa gtc tgg agc ttt gca acc gga gct cca ccg gaa  
533

Pro Asp Phe Gly Gln Val Trp Ser Phe Ala Thr Gly Ala Pro Pro Glu  
155 160 165

atg gtt ttt gcg cag cag cag caa cca gct aca ctc ttc gtc cgc cac  
581

Met Val Phe Ala Gln Gln Gln Gln Pro Ala Thr Leu Phe Val Arg His  
170 175 180 185

cag cag caa cag caa gct tcc gcc gcc gca gca gct gca atg ggt gag  
629

Gln Gln Gln Gln Gln Ala Ser Ala Ala Ala Ala Ala Ala Met Gly Glu  
190 195 200

gct tca gca gct aga gtt ggg aat tat ctt ccg ggt cat cat ctc aat  
677

Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His His Leu Asn  
205 210 215

ttg ctt gct tct ttg tct ggt gga gct aac ggg tcg ggt cgg agg gaa  
725

Leu Leu Ala Ser Leu Ser Gly Gly Ala Asn Gly Ser Gly Arg Arg Glu  
220 225 230

gac gac cac gaa cca cgt tga gaaatggtat tgtctttttg gtaatgtata  
776

Asp Asp His Glu Pro Arg  
235

gaaaaattcc tatgttttat gtcacgaaa gtgttttagaa agtacctcta atttgcggtt  
836

tcttttgctc cttttttact taatttaagc ttattgcttg tttgattagg gttttagggt  
896

ttaagaatat ttggtctcgt taatttggtt cggagagtga tagaaagaga gagagattga  
956

ttgattgttg tacctaaaac gctataaaaag ctctgttttt actagcgaaa aaa  
1009

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134



Met Ala Asp Asn Asp Gly Ala Val Ser Asn Gly Ile Ile Val Glu Gln  
1 5 10 15

Thr Ser Asn Lys Gly Pro Leu Asn Ala Val Lys Lys Pro Pro Ser Lys  
20 25 30

Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met Pro  
35 40 45

Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly His  
50 55 60

Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu Pro  
65 70 75 80

Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe Ser  
85 90 95

Thr Ala Ser Leu Ser Thr Ser Ser Pro Phe Thr Leu Gly Lys Arg Val  
100 105 110

Val Arg Ala Glu Glu Gly Glu Ser Gly Gly Gly Gly Gly Gly Gly Leu  
115 120 125

Thr Val Gly His Thr Met Gly Thr Ser Leu Met Gly Gly Gly Gly Ser  
130 135 140

Gly Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp  
145 150 155 160

Ser Phe Ala Thr Gly Ala Pro Pro Glu Met Val Phe Ala Gln Gln Gln  
165 170 175

Gln Pro Ala Thr Leu Phe Val Arg His Gln Gln Gln Gln Gln Ala Ser  
180 185 190

Ala Ala Ala Ala Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly  
195 200 205

Asn Tyr Leu Pro Gly His His Leu Asn Leu Leu Ala Ser Leu Ser Gly  
210 215 220

Gly Ala Asn Gly Ser Gly Arg Arg Glu Asp Asp His Glu Pro Arg  
225 230 235



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ttccattttc ttgtgtgttt ttttcccat aatttataaa ttttataagc aat atg  
 116

Met  
 1

gag tcc cac aac aac aac cag agc aac aac aac acc act ggt tcg gcc  
 164

Glu Ser His Asn Asn Asn Gln Ser Asn Asn Asn Thr Thr Gly Ser Ala  
           5                          10                          15

cat ctg gtc cca tcc atg gga cca atc tcc ggt tca gtc tca tta acc  
 212

His Leu Val Pro Ser Met Gly Pro Ile Ser Gly Ser Val Ser Leu Thr  
           20                          25                          30

acc act gct cca aac tcc act acc acc acc gtc acc gcc gct aaa aca  
 260

Thr Thr Ala Pro Asn Ser Thr Thr Thr Thr Val Thr Ala Ala Lys Thr  
           35                          40                          45

ccc gca aaa cga ccg tcc aag gac cgt cac atc aaa gta gac gga cgt  
 308

Pro Ala Lys Arg Pro Ser Lys Asp Arg His Ile Lys Val Asp Gly Arg  
           50                          55                          60                          65

ggc cgg agg ata cgt atg ccg gct atc tgc gca gca cgt gtc ttc caa  
 356

Gly Arg Arg Ile Arg Met Pro Ala Ile Cys Ala Ala Arg Val Phe Gln  
           70                          75                          80

cta aca cgt gag tta caa cac aaa tcg gac ggc gag act ata gag tgg  
 404

Leu Thr Arg Glu Leu Gln His Lys Ser Asp Gly Glu Thr Ile Glu Trp  
           85                          90                          95

ctg ctc caa caa gcg gag cca gct atc atc gca gcc acc gga act gga  
 452

Leu Leu Gln Gln Ala Glu Pro Ala Ile Ile Ala Ala Thr Gly Thr Gly  
           100                          105                          110

acc ata ccg gcg aat atc tct act ttg aac atc tct ctt cga agc agt  
 500

Thr Ile Pro Ala Asn Ile Ser Thr Leu Asn Ile Ser Leu Arg Ser Ser  
           115                          120                          125

ggc tct act ctt tca gct cca ctg tct aaa tct ttc cac atg gga aga  
 548

Gly Ser Thr Leu Ser Ala Pro Leu Ser Lys Ser Phe His Met Gly Arg  
           130                          135                          140                          145

gcg gct caa aac gct gcc gtt ttt ggg ttc cag caa cag ctt tat cat  
 596

Ala Ala Gln Asn Ala Ala Val Phe Gly Phe Gln Gln Gln Leu Tyr His  
           150                          155                          160



cct cat cat atc acg aca gat tct tct tct tct tct ctt ccc aaa aca  
 644  
 Pro His His Ile Thr Thr Asp Ser Ser Ser Ser Ser Leu Pro Lys Thr  
 165 170 175  
 ttc cgt gaa gaa gat ctt ttt aaa gat cct aat ttt cta gat caa gaa  
 692  
 Phe Arg Glu Glu Asp Leu Phe Lys Asp Pro Asn Phe Leu Asp Gln Glu  
 180 185 190  
 ccc ggt tca aga tca cct aaa ccg gga tcc gaa gct cct gat caa gat  
 740  
 Pro Gly Ser Arg Ser Pro Lys Pro Gly Ser Glu Ala Pro Asp Gln Asp  
 195 200 205  
 ccg ggt tcg acc cgg tca aga aca caa aat atg ata ccg ccg atg tgg  
 788  
 Pro Gly Ser Thr Arg Ser Arg Thr Gln Asn Met Ile Pro Pro Met Trp  
 210 215 220 225  
 gca cta gcg cca acg cca gcc tcc aca aac gga ggt agt gct ttt tgg  
 836  
 Ala Leu Ala Pro Thr Pro Ala Ser Thr Asn Gly Gly Ser Ala Phe Trp  
 230 235 240  
 atg tta cca gtc gga gga gga gga ggt ccg gct aac gtt cag gat cca  
 884  
 Met Leu Pro Val Gly Gly Gly Gly Gly Pro Ala Asn Val Gln Asp Pro  
 245 250 255  
 tca cag cac atg tgg gcg ttt aat ccg ggt cat tac ccg ggt cga atc  
 932  
 Ser Gln His Met Trp Ala Phe Asn Pro Gly His Tyr Pro Gly Arg Ile  
 260 265 270  
 ggg tcg gtt cag cta ggg tct atg tta gtg gga ggt caa cag tta ggg  
 980  
 Gly Ser Val Gln Leu Gly Ser Met Leu Val Gly Gly Gln Gln Leu Gly  
 275 280 285  
 tta ggt gtt gca gaa aat aac aat ttg ggg cta ttt tcc ggc gga gga  
 1028  
 Leu Gly Val Ala Glu Asn Asn Asn Leu Gly Leu Phe Ser Gly Gly Gly  
 290 295 300 305  
 gga gac ggt ggt cgg gtt ggt ctc gga atg agt ctt gag caa aag cct  
 1076  
 Gly Asp Gly Gly Arg Val Gly Leu Gly Met Ser Leu Glu Gln Lys Pro  
 310 315 320  
 caa cat caa gtg agt gat cat gct act aga gac caa aat cct act ata  
 1124  
 Gln His Gln Val Ser Asp His Ala Thr Arg Asp Gln Asn Pro Thr Ile  
 325 330 335  
 gat ggt tct cct tga aagacttcat gatttctttg gtttttaaaa agtgtgaatg  
 1179  
 Asp Gly Ser Pro  
 340



tgtgatttat tgcaactttt gttgaggact ccaatgttaa tatgggtttt agggttggct  
1239

tttcgggatt gccaaattgt tatt  
1263

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Met Glu Ser His Asn Asn Asn Gln Ser Asn Asn Asn Thr Thr Gly Ser  
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Ala His Leu Val Pro Ser Met Gly Pro Ile Ser Gly Ser Val Ser Leu  
20 25 30

Thr Thr Thr Ala Pro Asn Ser Thr Thr Thr Thr Val Thr Ala Ala Lys  
35 40 45

Thr Pro Ala Lys Arg Pro Ser Lys Asp Arg His Ile Lys Val Asp Gly  
50 55 60

Arg Gly Arg Arg Ile Arg Met Pro Ala Ile Cys Ala Ala Arg Val Phe  
65 70 75 80

Gln Leu Thr Arg Glu Leu Gln His Lys Ser Asp Gly Glu Thr Ile Glu  
85 90 95

Trp Leu Leu Gln Gln Ala Glu Pro Ala Ile Ile Ala Ala Thr Gly Thr  
100 105 110

Gly Thr Ile Pro Ala Asn Ile Ser Thr Leu Asn Ile Ser Leu Arg Ser  
115 120 125

Ser Gly Ser Thr Leu Ser Ala Pro Leu Ser Lys Ser Phe His Met Gly  
130 135 140

Arg Ala Ala Gln Asn Ala Ala Val Phe Gly Phe Gln Gln Gln Leu Tyr  
145 150 155 160

His Pro His His Ile Thr Thr Asp Ser Ser Ser Ser Ser Leu Pro Lys  
165 170 175

Thr Phe Arg Glu Glu Asp Leu Phe Lys Asp Pro Asn Phe Leu Asp Gln  
180 185 190

Glu Pro Gly Ser Arg Ser Pro Lys Pro Gly Ser Glu Ala Pro Asp Gln  
195 200 205



Asp Pro Gly Ser Thr Arg Ser Arg Thr Gln Asn Met Ile Pro Pro Met  
 210 215 220

Trp Ala Leu Ala Pro Thr Pro Ala Ser Thr Asn Gly Gly Ser Ala Phe  
 225 230 235 240

Trp Met Leu Pro Val Gly Gly Gly Gly Gly Pro Ala Asn Val Gln Asp  
 245 250 255

Pro Ser Gln His Met Trp Ala Phe Asn Pro Gly His Tyr Pro Gly Arg  
 260 265 270

Ile Gly Ser Val Gln Leu Gly Ser Met Leu Val Gly Gly Gln Gln Leu  
 275 280 285

Gly Leu Gly Val Ala Glu Asn Asn Asn Leu Gly Leu Phe Ser Gly Gly  
 290 295 300

Gly Gly Asp Gly Gly Arg Val Gly Leu Gly Met Ser Leu Glu Gln Lys  
 305 310 315 320

Pro Gln His Gln Val Ser Asp His Ala Thr Arg Asp Gln Asn Pro Thr  
 325 330 335

Ile Asp Gly Ser Pro  
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ccacttcccc cccaccaaag cttcgatcat catcatcatc atcatc atg gat ccg  
 115

Met Asp Pro  
 1

gat ccg gat cat aac cat cga ccc aac ttc cct ctc cag ctt ctt gat  
 163

Asp Pro Asp His Asn His Arg Pro Asn Phe Pro Leu Gln Leu Leu Asp  
 5 10 15

tct tct acc tcc tcc tct tcc act tcc tta gcc atc atc tct act act  
 211

Ser Ser Thr Ser Ser Ser Ser Thr Ser Leu Ala Ile Ile Ser Thr Thr  
 20 25 30 35

tcc gaa cct aac tcc gaa cct aag aag cct cct cct aaa cga acc tct  
 259



Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys Arg Thr Ser  
 40 45 50  
 act aaa gac cga cac acc aaa gtc gaa ggc cga ggc cgt cgg atc cgt  
 307  
 Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg  
 55 60 65  
 atg cct gcc atg tgt gct gca cgt gtc ttt cag ctc aca cgt gag ctt  
 355  
 Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu  
 70 75 80  
 ggt cac aaa tcc gac ggt gaa act att gag tgg cta ctc caa caa gca  
 403  
 Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala  
 85 90 95  
 gaa cca gcg gtt ata gcc gct aca ggg act gga acc att ccg gct aac  
 451  
 Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn  
 100 105 110 115  
 ttc act tot tta aac atc tca ctt cgt agc tca aga tct tct ctc tct  
 499  
 Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser Ser Leu Ser  
 120 125 130  
 gct gct cat ctt cgt aca act cct agt agc tat tac ttt cat tca cca  
 547  
 Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe His Ser Pro  
 135 140 145  
 cat cag tcc atg act cat cat ctt caa cat cag cat cag gtt cgt ccc  
 595  
 His Gln Ser Met Thr His His Leu Gln His Gln His Gln Val Arg Pro  
 150 155 160  
 aag aac gag tca cat tct tcg tct tct tct tct tca cag ctt tta gat  
 643  
 Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln Leu Leu Asp  
 165 170 175  
 cac aac caa atg ggt aac tat cta gta caa tca act gct gga tct tta  
 691  
 His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala Gly Ser Leu  
 180 185 190 195  
 cct acg agt cag agt cct gca acg gca ccg ttt tgg agt agt ggt gac  
 739  
 Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser Ser Gly Asp  
 200 205 210  
 aac aca cag aat ctt tgg gct ttt aat att aat cct cat cat tcc ggt  
 787  
 Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His His Ser Gly  
 215 220 225  
 gtt gtc gcc gga gat gtt tac aac ccc aac agt ggt ggt agt ggc ggc  
 835  
 Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly Ser Gly Gly



230 235 240  
 ggt agt gga gtt cat ttg atg aat ttt gca gct cct att gct ttg ttt  
 883  
 Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile Ala Leu Phe  
 245 250 255  
 tct gga cag cct ttg gct tct ggt tat gga gga gga gga ggt ggc ggt  
 931  
 Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly Gly Gly  
 260 265 270 275  
 gga gaa cat agc cat tat gga gtt tta gcg gcg ttg aat gct gct tac  
 979  
 Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn Ala Ala Tyr  
 280 285 290  
 cga ccg gtg gcg gag acg ggg aac cat aac aac aac cag caa aac cgt  
 1027  
 Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln Gln Asn Arg  
 295 300 305  
 gac gga gat cat cat cac aac cat caa gaa gat gga agc acc agt cat  
 1075  
 Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser Thr Ser His  
 310 315 320  
 cat tcc tag gcaaacatac acaaacaaat atattctgtg agattttattt  
 1124  
 His Ser  
 325  
 ttcttttttt gtcccttcgt ttgtttgttt gttcttaaca agcgtgtttt ttttgcattg  
 1184  
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 20 25 30  
 Ser Thr Thr Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys  
 35 40 45  
 Arg Thr Ser Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg  
 50 55 60  
 Arg Ile Arg Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr  
 65 70 75 80



Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu  
 85 90 95

Gln Gln Ala Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile  
 100 105 110

Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser  
 115 120 125

Ser Leu Ser Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe  
 130 135 140

His Ser Pro His Gln Ser Met Thr His His Leu Gln His Gln His Gln  
 145 150 155 160

Val Arg Pro Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln  
 165 170 175

Leu Leu Asp His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala  
 180 185 190

Gly Ser Leu Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser  
 195 200 205

Ser Gly Asp Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His  
 210 215 220

His Ser Gly Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly  
 225 230 235 240

Ser Gly Gly Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile  
 245 250 255

Ala Leu Phe Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly  
 260 265 270

Gly Gly Gly Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn  
 275 280 285

Ala Ala Tyr Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln  
 290 295 300

Gln Asn Arg Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser  
 305 310 315 320



Thr Ser His His Ser  
325

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cagg atg atg aac ccg ttt ctc ccg gaa ggc tgc gat cca cca cca cca  
109

Met Met Asn Pro Phe Leu Pro Glu Gly Cys Asp Pro Pro Pro Pro  
1 5 10 15

cca caa cca atg gag ggt tta cac gaa aat gct cca cct cca ttt ctg  
157

Pro Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu  
20 25 30

acc aag aca ttt gag atg gtg gat gat cca aac act gac cac atc gta  
205

Thr Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val  
35 40 45

tct tgg aac aga gga gga aca agt ttt gtc gtc tgg gat ttg cat tct  
253

Ser Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser  
50 55 60

ttc tcc acg att cto ctt cct cgt cat ttc aaa cac agc aat ttc tca  
301

Phe Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser  
65 70 75

agt ttc atc aga caa ctc aat act tat ggt ttc aga aag ata gaa gca  
349

Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala  
80 85 90 95

gag aga tgg gaa ttt gca aac gaa gag ttt ttg tta gga caa aga cag  
397

Glu Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln  
100 105 110

ttg ttg aag aac atc aag agg aga aac cct ttt act cca tca tct tca  
445

Leu Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser  
115 120 125

cca agc cat gac gct tgc aac gag ctt cgc aga gag aag caa gtg cta  
493

Pro Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu  
130 135 140

atg atg gag ata gtg agt cta aga cag cag caa caa aca acg aaa agc  
541

Met Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser  
145 150 155



tac atc aaa gct atg gaa cag agg ata gaa gga aca gag agg aaa cag  
 589  
 Tyr Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln  
 160 165 170 175

aga caa atg atg tcg ttt ctg gct aga gca atg cag agt cct tcg ttt  
 637  
 Arg Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe  
 180 185 190

ttg cat cag ttg ttg aaa caa aga gat aaa aaa att aag gag ctt gag  
 685  
 Leu His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu  
 195 200 205

gat aat gag tca gca aag agg aaa aga ggt tct tct tcg atg tcg gaa  
 733  
 Asp Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu  
 210 215 220

ttg gaa gtt ttg gct ttg gag atg caa ggg cat gga aaa cag agg aat  
 781  
 Leu Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn  
 225 230 235

atg ttg gaa gaa gag gat cat caa ctg gtg gta gag aga gag ttg gat  
 829  
 Met Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp  
 240 245 250 255

gat ggt ttc tgg gaa gag ttg ctt agt gat gag agt ttg gct tcc acc  
 877  
 Asp Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr  
 260 265 270

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 Ser

tcattttctt ctgtcaca  
 952

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 1 5 10 15

Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu Thr  
 20 25 30

Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val Ser  
 35 40 45

Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser Phe  
 50 55 60



Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser Ser  
65 70 75 80

Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu  
85 90 95

Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln Leu  
100 105 110

Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser Pro  
115 120 125

Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu Met  
130 135 140

Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser Tyr  
145 150 155 160

Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln Arg  
165 170 175

Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe Leu  
180 185 190

His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu Asp  
195 200 205

Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu Leu  
210 215 220

Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn Met  
225 230 235 240

Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp Asp  
245 250 255

Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr Ser  
260 265 270

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120

ggaatttggg ttttaagata gcgtgatctg taataataag tggttcgcga tcgtgatcaa  
180

gaaactgggtg gctgatagtg atatgcatat ttgagag atg gtg ttc aag aga aag  
235

Met Val Phe Lys Arg Lys  
1 5

tta gat tgc ctt tcc gtg gga ttt gat ttt ccc aac att ccc aga gct  
283

Leu Asp Cys Leu Ser Val Gly Phe Asp Phe Pro Asn Ile Pro Arg Ala  
10 15 20

cct cgt tca tgc agg agg aag gtt cta aac aag agg att gat cat gat  
331

Pro Arg Ser Cys Arg Arg Lys Val Leu Asn Lys Arg Ile Asp His Asp  
25 30 35

gat gat aac act cag atc tgt gca att gac tta cta gct ttg gct gga  
379

Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp Leu Leu Ala Leu Ala Gly  
40 45 50

aag att cta cag gaa agc gag agt tcc tct gcg tct tct aat gca ttt  
427

Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser Ala Ser Ser Asn Ala Phe  
55 60 65 70

gaa gaa att aag caa gag aaa gta gaa aat tgc aag act att aaa tct  
475

Glu Glu Ile Lys Gln Glu Lys Val Glu Asn Cys Lys Thr Ile Lys Ser  
75 80 85

gag tct tct gac caa gga aac tct gtg tca aag cct act tat gat atc  
523

Glu Ser Ser Asp Gln Gly Asn Ser Val Ser Lys Pro Thr Tyr Asp Ile  
90 95 100

tct act gag aag tgt gtg gtg aac agt tgt ttt tca ttt ccg gat agt  
571

Ser Thr Glu Lys Cys Val Val Asn Ser Cys Phe Ser Phe Pro Asp Ser  
105 110 115

gac ggc gtt ttg gag cgg act ccg atg tct gat tac aag aag att cat  
619

Asp Gly Val Leu Glu Arg Thr Pro Met Ser Asp Tyr Lys Lys Ile His  
120 125 130

ggt ttg atg gat gta ggg tgt gaa aac aag aat gta aat aat ggg ttc  
667

Gly Leu Met Asp Val Gly Cys Glu Asn Lys Asn Val Asn Asn Gly Phe  
135 140 145 150

gag caa gga gaa gca acc gat cgc gtg ggt gat gga ggc tta gtc act  
715

Glu Gln Gly Glu Ala Thr Asp Arg Val Gly Asp Gly Gly Leu Val Thr  
155 160 165



gat act tgc aac tta gag gat gca act gcg tta ggt ctg cag ttt ccg  
763  
Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala Leu Gly Leu Gln Phe Pro  
170 175 180

aaa tca gtc tgt gtg ggt ggt gat tta aaa tca cca tcc acc ttg gat  
811  
Lys Ser Val Cys Val Gly Gly Asp Leu Lys Ser Pro Ser Thr Leu Asp  
185 190 195

atg acc cct aat ggt tcc tat gct aga cat ggg aac cat act aac cta  
859  
Met Thr Pro Asn Gly Ser Tyr Ala Arg His Gly Asn His Thr Asn Leu  
200 205 210

ggg aga aaa gat gat gat gaa aaa ttc tat agt tac cat aaa ctt agc  
907  
Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr Ser Tyr His Lys Leu Ser  
215 220 225 230

aat aaa ttt aag tcg tat agg tct cca aca att cga aga ata aga aag  
955  
Asn Lys Phe Lys Ser Tyr Arg Ser Pro Thr Ile Arg Arg Ile Arg Lys  
235 240 245

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Ser Met Ser Ser Lys Tyr Trp Lys Gln Val Pro Lys Asp Phe Gly Tyr  
250 255 260

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1051  
Ser Arg Ala Asp Val Gly Val Lys Thr Leu Tyr Arg Lys Arg Lys Ser  
265 270 275

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1099  
Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu Ile Ile Tyr Lys Arg Arg  
280 285 290

aga tca cct gac aga agc tcg gtc gta act tct gat gga gga ctc agt  
1147  
Arg Ser Pro Asp Arg Ser Ser Val Val Thr Ser Asp Gly Gly Leu Ser  
295 300 305 310

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1195  
Ser Gly Ser Val Ser Lys Leu Pro Lys Lys Gly Asp Thr Val Lys Leu  
315 320 325

agc att aag tcc ttt agg att cca gag ctt ttt att gaa gtt cca gaa  
1243  
Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu Phe Ile Glu Val Pro Glu  
330 335 340

act gca aca gta gga tca cta aag agg act gtg atg gag gct gtc agt  
1291  
Thr Ala Thr Val Gly Ser Leu Lys Arg Thr Val Met Glu Ala Val Ser  
345 350 355



gtt tta ctc agc gga gga ata cgt gtt ggg gtg tta atg cat ggg aag  
 1339  
 Val Leu Leu Ser Gly Gly Ile Arg Val Gly Val Leu Met His Gly Lys  
 360 365 370

aag gtt aga gat gaa agg aaa act ctg tcc cag act ggg atc tca tgt  
 1387  
 Lys Val Arg Asp Glu Arg Lys Thr Leu Ser Gln Thr Gly Ile Ser Cys  
 375 380 385 390

gat gaa aat cta gac aac ctt ggg ttc acc ttg gag cct agt ccc agc  
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 Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr Leu Glu Pro Ser Pro Ser  
 395 400 405

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 Lys Val Pro Leu Pro Leu Cys Ser Glu Asp Pro Ala Val Pro Thr Asp  
 410 415 420

cct aca agt ttg tct gaa cgg tct gcg gcg tct cct atg cta gat tct  
 1531  
 Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala Ser Pro Met Leu Asp Ser  
 425 430 435

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 1579  
 Gly Ile Pro His Ala Asp Asp Val Ile Asp Ser Arg Asn Ile Val Asp  
 440 445 450

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 1627  
 Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly Asp Ile Ser Val Asp Glu  
 455 460 465 470

cct tca tca gat tca aaa gag ctt gtc cca ctt cca gag ttg gaa gtc  
 1675  
 Pro Ser Ser Asp Ser Lys Glu Leu Val Pro Leu Pro Glu Leu Glu Val  
 475 480 485

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 Lys Ala Leu Ala Ile Val Pro Leu Asn Gln Lys Pro Lys Arg Thr Glu  
 490 495 500

cta gcc cag agg aga act agg aga ccc ttc tct gtg aca gag gta gaa  
 1771  
 Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe Ser Val Thr Glu Val Glu  
 505 510 515

gct ctt gta caa gca gtt gag gaa ctc ggg act gga aga tgg cgt gat  
 1819  
 Ala Leu Val Gln Ala Val Glu Glu Leu Gly Thr Gly Arg Trp Arg Asp  
 520 525 530

gta aaa ttg cgt gct ttc gag gat gca gat cat cgg act tac gtg gac  
 1867  
 Val Lys Leu Arg Ala Phe Glu Asp Ala Asp His Arg Thr Tyr Val Asp  
 535 540 545 550



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1915

Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala Ser Ile Ser Pro  
555 560 565

cag caa cga aga gga gag ccg gtg cca caa gaa ctg cta gac aga gtc  
1963

Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu Leu Asp Arg Val  
570 575 580

ttg agg gca tac ggg tat tgg tcg cag cac caa gga aaa cat cag gcg  
2011

Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His Gln Gly Lys His Gln Ala  
585 590 595

aga gga gcg tcc aaa gat cca gac atg aac aga ggt gga gct ttt gaa  
2059

Arg Gly Ala Ser Lys Asp Pro Asp Met Asn Arg Gly Gly Ala Phe Glu  
600 605 610

tca ggt gtt tca gtg taa aaaaggaggt acgcattggt gggtgggtgt  
2107

Ser Gly Val Ser Val  
615

acagaagcaa acaacacaat aaatggacaa ctcaatttct gcaaagtta attgtcttta  
2167

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Lys Arg Ile Asp His Asp Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp  
35 40 45

Leu Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser  
50 55 60

Ala Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn  
65 70 75 80

Cys Lys Thr Ile Lys Ser Glu Ser Ser Asp Gln Gly Asn Ser Val Ser  
85 90 95

Lys Pro Thr Tyr Asp Ile Ser Thr Glu Lys Cys Val Val Asn Ser Cys  
100 105 110



Phe Ser Phe Pro Asp Ser Asp Gly Val Leu Glu Arg Thr Pro Met Ser  
 115 120 125

Asp Tyr Lys Lys Ile His Gly Leu Met Asp Val Gly Cys Glu Asn Lys  
 130 135 140

Asn Val Asn Asn Gly Phe Glu Gln Gly Glu Ala Thr Asp Arg Val Gly  
 145 150 155 160

Asp Gly Gly Leu Val Thr Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala  
 165 170 175

Leu Gly Leu Gln Phe Pro Lys Ser Val Cys Val Gly Gly Asp Leu Lys  
 180 185 190

Ser Pro Ser Thr Leu Asp Met Thr Pro Asn Gly Ser Tyr Ala Arg His  
 195 200 205

Gly Asn His Thr Asn Leu Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr  
 210 215 220

Ser Tyr His Lys Leu Ser Asn Lys Phe Lys Ser Tyr Arg Ser Pro Thr  
 225 230 235 240

Ile Arg Arg Ile Arg Lys Ser Met Ser Ser Lys Tyr Trp Lys Gln Val  
 245 250 255

Pro Lys Asp Phe Gly Tyr Ser Arg Ala Asp Val Gly Val Lys Thr Leu  
 260 265 270

Tyr Arg Lys Arg Lys Ser Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu  
 275 280 285

Ile Ile Tyr Lys Arg Arg Arg Ser Pro Asp Arg Ser Ser Val Val Thr  
 290 295 300

Ser Asp Gly Gly Leu Ser Ser Gly Ser Val Ser Lys Leu Pro Lys Lys  
 305 310 315 320

Gly Asp Thr Val Lys Leu Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu  
 325 330 335

Phe Ile Glu Val Pro Glu Thr Ala Thr Val Gly Ser Leu Lys Arg Thr  
 340 345 350



Val Met Glu Ala Val Ser Val Leu Leu Ser Gly Gly Ile Arg Val Gly  
 355 360 365

Val Leu Met His Gly Lys Lys Val Arg Asp Glu Arg Lys Thr Leu Ser  
 370 375 380

Gln Thr Gly Ile Ser Cys Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr  
 385 390 395 400

Leu Glu Pro Ser Pro Ser Lys Val Pro Leu Pro Leu Cys Ser Glu Asp  
 405 410 415

Pro Ala Val Pro Thr Asp Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala  
 420 425 430

Ser Pro Met Leu Asp Ser Gly Ile Pro His Ala Asp Asp Val Ile Asp  
 435 440 445

Ser Arg Asn Ile Val Asp Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly  
 450 455 460

Asp Ile Ser Val Asp Glu Pro Ser Ser Asp Ser Lys Glu Leu Val Pro  
 465 470 475 480

Leu Pro Glu Leu Glu Val Lys Ala Leu Ala Ile Val Pro Leu Asn Gln  
 485 490 495

Lys Pro Lys Arg Thr Glu Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe  
 500 505 510

Ser Val Thr Glu Val Glu Ala Leu Val Gln Ala Val Glu Glu Leu Gly  
 515 520 525

Thr Gly Arg Trp Arg Asp Val Lys Leu Arg Ala Phe Glu Asp Ala Asp  
 530 535 540

His Arg Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His  
 545 550 555 560

Thr Ala Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln  
 565 570 575

Glu Leu Leu Asp Arg Val Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His  
 580 585 590



Gln Gly Lys His Gln Ala Arg Gly Ala Ser Lys Asp Pro Asp Met Asn  
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 116

Met Ser Asn  
 1

aat aat aat tct ccg acc acc gtg aat caa gaa acg acg acg tct cgt  
 164

Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr Thr Ser Arg  
 5 10 15

gaa gtc tca atc aca ttg cct act gat caa tct cct caa acc tca cca  
 212

Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln Thr Ser Pro  
 20 25 30 35

gga tca tct tct tct cct tca ccg aga cct tcc ggt gga tca ccg gcg  
 260

Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly Ser Pro Ala  
 40 45 50

aga aga acg gcg act gga tta tcc ggc aag cac tct att ttc agg ggg  
 308

Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile Phe Arg Gly  
 55 60 65

att cga cta cgt aac gga aaa tgg gta tcg gag att aga gag cca cgt  
 356

Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg  
 70 75 80

aaa acg aca aga att tgg ctc ggg act tat ccg gta ccg gag atg gct  
 404

Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro Glu Met Ala  
 85 90 95

gcc gcc gct tac gac gtg gct gcg tta gct tta aaa gga ccc gac gcc  
 452

Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Pro Asp Ala  
 100 105 110 115

gtt ttg aat ttt cct ggt tta gct ttg act tac gtg gct ccg gtt tca  
 500

Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala Pro Val Ser  
 120 125 130



aac tct gct gcg gat ata aga gcg gct gct agt aga gca gcg gag atg  
548

Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala Ala Glu Met  
135 140 145

aag caa ccg gat cag ggt ggg gat gag aag gta ttg gaa ccg gtt caa  
596

Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val Gln  
150 155 160

ccc ggc aaa gag gaa gaa tta gaa gaa gtg tcg tgt aac tcg tgt tcg  
644

Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys Ser  
165 170 175

ttg gag ttt atg gat gag gaa gcg atg ttg aat atg ccg act ttg ttg  
692

Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu Leu  
180 185 190 195

acg gag atg gct gaa ggg atg ttg atg agt cca ccg aga atg atg ata  
740

Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met Ile  
200 205 210

cat ccg acg atg gaa gat gat tcg ccg gag aat cat gaa gga gat aat  
788

His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp Asn  
215 220 225

ctt tgg agt tat aaa tga atccattgaa gctgctctct tttttattgt  
836

Leu Trp Ser Tyr Lys  
230

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890

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Thr Ser Pro Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly  
35 40 45

Ser Pro Ala Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile  
50 55 60

Phe Arg Gly Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg  
65 70 75 80



Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro  
85 90 95

Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly  
100 105 110

Pro Asp Ala Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala  
115 120 125

Pro Val Ser Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala  
130 135 140

Ala Glu Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu  
145 150 155 160

Pro Val Gln Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn  
165 170 175

Ser Cys Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro  
180 185 190

Thr Leu Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg  
195 200 205

Met Met Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu  
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118

Met  
1

gat cag tac tca tcc tct ttg gtc gat act tca tta gat ctc act att  
166  
Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile  
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ggc gtt act cgt atg cga gtt gaa gaa gat cca ccg aca agt gct ttg  
214  
Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu



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262		
Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser Glu		
35	40	45
atg cta act ttg atg tgt gac aac tac aac gtc ttg agg aag caa ctt		
310		
Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln Leu		
50	55	60
atg gaa tat gtt aac aag agc aac ata acc gag agg gat caa atc agc		
358		
Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile Ser		
	70	80
cct ccc aag aaa cgc aaa tcc ccg gcg aga gag gac gca ttc agc tgc		
406		
Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys		
	85	95
gcg gtt att ggc gga gtg tcg gag agt agc tca acg gat caa gat gag		
454		
Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp Glu		
	100	110
tat ttg tgt aag aag cag aga gaa gag act gtc gtg aag gag aaa gtc		
502		
Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val		
115	120	125
tca agg gtc tat tac aag acc gaa gct tct gac act acc ctc gtt gtg		
550		
Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val		
130	135	145
aaa gat ggg tat caa tgg agg aaa tat gga cag aaa gtg act aga gac		
598		
Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp		
	150	160
aat cca tct cca aga gct tac ttc aaa tgt gct tgt gct cca agc tgt		
646		
Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser Cys		
	165	175
tct gtc aaa aag aag gtt cag aga agt gtg gag gat cag tcc gtg tta		
694		
Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val Leu		
	180	190
gtt gca act tat gag ggt gaa cac aac cat cca atg cca tcg cag atc		
742		
Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln Ile		
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790		
Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser Ala		
210	215	225



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838

Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val  
230 235 240

act acc gta gat atg att gaa tcg aag aaa gtg acg agc cca acg tca  
886

Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser  
245 250 255

aga atc gat ttt ccc caa gtt cag aaa ctt ttg gtg gag caa atg gct  
934

Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala  
260 265 270

tct tcc tta acc aaa gat cct aac ttt aca gca gct tta gca gca gct  
982

Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Ala  
275 280 285

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1024

Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys  
290 295 300

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1084

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35 40 45

Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln  
50 55 60

Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile  
65 70 75 80

Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser  
85 90 95

Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp



100 105 110  
 Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys  
 115 120 125  
 Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val  
 130 135 140  
 Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg  
 145 150 155 160  
 Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser  
 165 170 175  
 Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val  
 180 185 190  
 Leu Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln  
 195 200 205  
 Ile Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser  
 210 215 220  
 Ala Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro  
 225 230 235 240  
 Val Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr  
 245 250 255  
 Ser Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met  
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 Val Cys Ser Ser Ala Pro Pro Phe Thr Glu Gly His Met Cys Ser Asp  
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 146  
 Ser His Thr Ala Leu Cys Asp Asp Leu Ser Ser Asp Glu Glu Met Glu  
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 194  
 Ile Glu Glu Leu Glu Lys Lys Ile Trp Arg Asp Lys Gln Arg Leu Lys  
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 80 85 90  
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 338  
 Tyr Lys Ala Gln Asp Gly Ile Leu Lys Tyr Met Ser Lys Thr Met Glu  
 95 100 105 110  
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 386  
 Arg Tyr Lys Ala Gln Gly Phe Val Tyr Gly Ile Val Leu Glu Asn Gly  
 115 120 125  
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 Lys Thr Val Ala Gly Ser Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp  
 130 135 140  
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 Lys Val Arg Phe Asp Arg Asn Gly Pro Ala Ala Ile Ile Lys His Gln  
 145 150 155  
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 530  
 Arg Asp Ile Asn Leu Ser Asp Gly Ser Asp Ser Gly Ser Glu Val Gly  
 160 165 170  
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 578  
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 175 180 185 190  
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 Ala Leu Leu Ser Ala Leu Phe Pro His Cys Asn Pro Pro Gln Arg Arg  
 195 200 205



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 674  
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 Glu Asp Trp Trp Asp Gln Leu Ser Leu Pro Val Asp Phe Arg Gly Val  
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 Pro Pro Pro Tyr Lys Lys Pro His Asp Leu Lys Lys Leu Trp Lys Ile  
 240 245 250

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 Gly Val Leu Ile Gly Val Ile Arg His Met Ala Ser Asp Ile Ser Asn  
 255 260 265 270

ata ccc aat ctc gtg aga cgg tct aga agt ttg cag gag aaa atg acg  
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 275 280 285

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 290 295 300

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 305 310 315

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 Phe Leu Val Pro Ala Thr Gly Gly Asp Pro Asp Val Leu Phe Pro Glu  
 320 325 330

tct aca gac tat gat gtt gaa ctg att ggt ggc act cat cgg acc aat  
 1058  
 Ser Thr Asp Tyr Asp Val Glu Leu Ile Gly Gly Thr His Arg Thr Asn  
 335 340 345 350

cag cag tat cct gaa ttt gaa aac aac tac aac tgt gtt tac aag aga  
 1106  
 Gln Gln Tyr Pro Glu Phe Glu Asn Asn Tyr Asn Cys Val Tyr Lys Arg  
 355 360 365

aag ttt gaa gaa gat ttt ggg atg cca atg cat cca aca ctc cta aca  
 1154  
 Lys Phe Glu Glu Asp Phe Gly Met Pro Met His Pro Thr Leu Leu Thr  
 370 375 380

tgt gag aac agt ctc tgt cct tat agc caa cca cat atg gga ttt ctt  
 1202  
 Cys Glu Asn Ser Leu Cys Pro Tyr Ser Gln Pro His Met Gly Phe Leu  
 385 390 395



gac agg aac tta aga gag aat cac caa atg act tgt cct tat aaa gtc  
1250

Asp Arg Asn Leu Arg Glu Asn His Gln Met Thr Cys Pro Tyr Lys Val  
400 405 410

act tcc ttc tac caa cca act aaa ccc tat ggt atg acg ggt tta atg  
1298

Thr Ser Phe Tyr Gln Pro Thr Lys Pro Tyr Gly Met Thr Gly Leu Met  
415 420 425 430

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1346

Val Pro Cys Pro Asp Tyr Asn Gly Met Gln Gln Gln Val Gln Ser Phe  
435 440 445

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1394

Gln Asp Gln Phe Asn His Pro Asn Asp Leu Tyr Arg Pro Lys Ala Pro  
450 455 460

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1442

Gln Arg Gly Asn Asp Asp Leu Val Glu Asp Leu Asn Pro Ser Pro Ser  
465 470 475

acg ctg aat cag aat ctt ggt tta gtc tta cct act gac ttc aat gga  
1490

Thr Leu Asn Gln Asn Leu Gly Leu Val Leu Pro Thr Asp Phe Asn Gly  
480 485 490

ggt gag gaa aca gta gga aca gag aac aat ctg cat aat caa ggg caa  
1538

Gly Glu Glu Thr Val Gly Thr Glu Asn Asn Leu His Asn Gln Gly Gln  
495 500 505 510

gag ttg ccc aca tct tgg att cag taa agaaagcttc agagttttct  
1585

Glu Leu Pro Thr Ser Trp Ile Gln  
515

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1645

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1722

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20 25 30



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 35 40 45

Glu Leu Glu Lys Lys Ile Trp Arg Asp Lys Gln Arg Leu Lys Arg Leu  
 50 55 60

Lys Glu Met Ala Lys Asn Gly Leu Gly Thr Arg Leu Leu Leu Lys Gln  
 65 70 75 80

Gln His Asp Asp Phe Pro Glu His Ser Ser Lys Arg Thr Met Tyr Lys  
 85 90 95

Ala Gln Asp Gly Ile Leu Lys Tyr Met Ser Lys Thr Met Glu Arg Tyr  
 100 105 110

Lys Ala Gln Gly Phe Val Tyr Gly Ile Val Leu Glu Asn Gly Lys Thr  
 115 120 125

Val Ala Gly Ser Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val  
 130 135 140

Arg Phe Asp Arg Asn Gly Pro Ala Ala Ile Ile Lys His Gln Arg Asp  
 145 150 155 160

Ile Asn Leu Ser Asp Gly Ser Asp Ser Gly Ser Glu Val Gly Asp Ser  
 165 170 175

Thr Ala Gln Lys Leu Leu Glu Leu Gln Asp Thr Thr Leu Gly Ala Leu  
 180 185 190

Leu Ser Ala Leu Phe Pro His Cys Asn Pro Pro Gln Arg Arg Phe Pro  
 195 200 205

Leu Glu Lys Gly Val Thr Pro Pro Trp Trp Pro Thr Gly Lys Glu Asp  
 210 215 220

Trp Trp Asp Gln Leu Ser Leu Pro Val Asp Phe Arg Gly Val Pro Pro  
 225 230 235 240

Pro Tyr Lys Lys Pro His Asp Leu Lys Lys Leu Trp Lys Ile Gly Val  
 245 250 255

Leu Ile Gly Val Ile Arg His Met Ala Ser Asp Ile Ser Asn Ile Pro  
 260 265 270

Asn Leu Val Arg Arg Ser Arg Ser Leu Gln Glu Lys Met Thr Ser Arg



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 Glu Gly Ala Leu Trp Leu Ala Ala Leu Tyr Arg Glu Lys Ala Ile Val  
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 Asp Gln Ile Ala Met Ser Arg Glu Asn Asn Asn Thr Ser Asn Phe Leu  
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 Asp Tyr Asp Val Glu Leu Ile Gly Gly Thr His Arg Thr Asn Gln Gln  
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 Tyr Pro Glu Phe Glu Asn Asn Tyr Asn Cys Val Tyr Lys Arg Lys Phe  
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 Phe Tyr Gln Pro Thr Lys Pro Tyr Gly Met Thr Gly Leu Met Val Pro  
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 Cys Pro Asp Tyr Asn Gly Met Gln Gln Gln Val Gln Ser Phe Gln Asp  
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 Gln Phe Asn His Pro Asn Asp Leu Tyr Arg Pro Lys Ala Pro Gln Arg  
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 Gly Asn Asp Asp Leu Val Glu Asp Leu Asn Pro Ser Pro Ser Thr Leu  
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 Asn Gln Asn Leu Gly Leu Val Leu Pro Thr Asp Phe Asn Gly Gly Glu  
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 116

Met Gly Asp Leu Ala  
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atg tcc gta gca gac atc agg atg gag aat gag cct gat gat tta gct  
 164

Met Ser Val Ala Asp Ile Arg Met Glu Asn Glu Pro Asp Asp Leu Ala  
 10 15 20

agt gat aat gtt gct gag att gat gtg agt gat gaa gag att gat gct  
 212

Ser Asp Asn Val Ala Glu Ile Asp Val Ser Asp Glu Glu Ile Asp Ala  
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gac gac ctt gag aga cgg atg tgg aaa gat cgt gtc agg ctt aaa aga  
 260

Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg Val Arg Leu Lys Arg  
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atc aaa gag cga caa aaa gct ggc tct caa gga gct caa acg aag gag  
 308

Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly Ala Gln Thr Lys Glu  
 55 60 65

aca cct aag aaa atc tct gat caa gct cag agg aag aaa atg tct aga  
 356

Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg Lys Lys Met Ser Arg  
 70 75 80 85

gct caa gat ggt atc ctt aag tac atg ttg aag ctt atg gaa gtc tgc  
 404

Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Leu Met Glu Val Cys  
 90 95 100

aaa gtt cgc ggg ttt gtc tat ggt ata ata ccg gaa aag ggc aag cct  
 452

Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro  
 105 110 115

gtg agt ggt tcc tct gac aat ata aga gct tgg tgg aaa gag aaa gtg  
 500

Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp Trp Lys Glu Lys Val  
 120 125 130

aag ttt gat aag aac ggt cct gct gct att gct aaa tac gaa gag gag  
 548

Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala Lys Tyr Glu Glu Glu  
 135 140 145

tgt tta gcg ttt ggg aaa tct gat ggg aat agg aat tca cag ttt gtt  
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Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg Asn Ser Gln Phe Val  
 150 155 160 165  
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 644  
 Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser Leu Leu Ser Ser Leu  
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 atg caa cat tgt gat cct cct caa agg aag tat ccg ttg gag aaa ggg  
 692  
 Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr Pro Leu Glu Lys Gly  
 185 190 195  
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 Thr Pro Pro Pro Trp Trp Pro Thr Gly Asn Glu Glu Trp Trp Val Lys  
 200 205 210  
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 Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr Arg Lys Pro His Asp  
 215 220 225  
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 836  
 Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr Ala Val Ile Asn His  
 230 235 240 245  
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 884  
 Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His Val Arg Gln Ser Lys  
 250 255 260  
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 Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Ile Trp Leu Ala  
 265 270 275  
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 Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln Pro Ser Ser Asp Asn  
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 1028  
 Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg Gly Asn Asn Ala Asp  
 295 300 305  
 agg agg aaa cct gtg gtc aac agt gac agt gac tat gat gtt gat ggg  
 1076  
 Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp Tyr Asp Val Asp Gly  
 310 315 320 325  
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 1124  
 Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys Asp Ser Arg Arg Asn  
 330 335 340  
 cag att caa aaa gaa caa cca aca gcc atc tca cat tca gta aga gat  
 1172  
 Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser His Ser Val Arg Asp



345	350	355
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1220		
Gln Asp Lys Ala Glu Lys His	Arg Arg Arg Lys Arg	Pro Arg Ile Arg
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1268		
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375	380	385
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1316		
Arg Asn Ile Leu Pro Asp Met Asn His Val	Asp Ala Pro Leu Leu Glu	
390	395	405
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1364		
Tyr Asn Ile Asn Gly Thr His Gln	Glu Asp Asp Val Val Asp	Pro Asn
410	415	420
att gcc tta gga cca gag gat aat ggt ctg gaa cta gtg gtt cct gag		
1412		
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425	430	435
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1460		
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1508		
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455	460	465
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1556		
Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr	Asn Pro Ser Ala Val	
470	475	485
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1604		
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490	495	500
aat aca caa gca cca cct cac aac agt ggg ttc gag gag gcc cca gga		
1652		
Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe Glu Glu Ala	Pro Gly	
505	510	515
gga gta ctt caa ccc ctt ggt tta ctc gga aat gaa gac ggt gta aca		
1700		
Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn Glu Asp Gly Val Thr		
520	525	530
ggg agt gag ttg cct cag tat cag agt ggc att ctg tct cca ttg act		
1748		
Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile Leu Ser Pro Leu Thr		
535	540	545



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1796

Asp Leu Asp Phe Asp Tyr Gly Gly Phe Gly Asp Asp Phe Ser Trp Phe  
550 555 560 565

gga gct tag tgtcttgcca ttttttttgg gagattacat agttcaaaag  
1845

Gly Ala

gacatggcaa tagtctggct agtacagtta ctttctcttc ttcattttct ctgatcttat  
1905

attcttcctc tttttttctt ataatatattt cttagatttg ttaagagaaa caattttcct  
1965

tttgaataag ttgccagaag aactgctttg cccgttgtaa tggctctctag ggaaagcagt  
2025

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Glu Glu Ile Asp Ala Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg  
35 40 45

Val Arg Leu Lys Arg Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly  
50 55 60

Ala Gln Thr Lys Glu Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg  
65 70 75 80

Lys Lys Met Ser Arg Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys  
85 90 95

Leu Met Glu Val Cys Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro  
100 105 110

Glu Lys Gly Lys Pro Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp  
115 120 125

Trp Lys Glu Lys Val Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala  
130 135 140



Lys Tyr Glu Glu Glu Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg  
 145 150 155 160  
 Asn Ser Gln Phe Val Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser  
 165 170 175  
 Leu Leu Ser Ser Leu Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr  
 180 185 190  
 Pro Leu Glu Lys Gly Thr Pro Pro Pro Trp Trp Pro Thr Gly Asn Glu  
 195 200 205  
 Glu Trp Trp Val Lys Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr  
 210 215 220  
 Arg Lys Pro His Asp Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr  
 225 230 235 240  
 Ala Val Ile Asn His Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His  
 245 250 255  
 Val Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser  
 260 265 270  
 Ala Ile Trp Leu Ala Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln  
 275 280 285  
 Pro Ser Ser Asp Asn Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg  
 290 295 300  
 Gly Asn Asn Ala Asp Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp  
 305 310 315 320  
 Tyr Asp Val Asp Gly Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys  
 325 330 335  
 Asp Ser Arg Arg Asn Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser  
 340 345 350  
 His Ser Val Arg Asp Gln Asp Lys Ala Glu Lys His Arg Arg Arg Lys  
 355 360 365  
 Arg Pro Arg Ile Arg Ser Gly Thr Val Asn Arg Gln Glu Glu Glu Gln  
 370 375 380



Pro Glu Ala Gln Gln Arg Asn Ile Leu Pro Asp Met Asn His Val Asp  
385 390 395 400

Ala Pro Leu Leu Glu Tyr Asn Ile Asn Gly Thr His Gln Glu Asp Asp  
405 410 415

Val Val Asp Pro Asn Ile Ala Leu Gly Pro Glu Asp Asn Gly Leu Glu  
420 425 430

Leu Val Val Pro Glu Phe Asn Asn Asn Tyr Thr Tyr Leu Pro Leu Val  
435 440 445

Asn Glu Gln Thr Met Met Pro Val Asp Glu Arg Pro Met Leu Tyr Gly  
450 455 460

Pro Asn Pro Asn Gln Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr  
465 470 475 480

Asn Pro Ser Ala Val Phe Val His Asn Gln Glu Asp Asp Ile Leu His  
485 490 495

Thr Gln Ile Glu Met Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe  
500 505 510

Glu Glu Ala Pro Gly Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn  
515 520 525

Glu Asp Gly Val Thr Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile  
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Asp Phe Ser Trp Phe Gly Ala  
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105  
Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser Trp Val



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Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile Trp Leu Gly Thr
      25              30              35

ttt gag aca gcg gag gat gca gca agg gcc tac gac gag gcg gct agg
201
Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Glu Ala Ala Arg
      40              45              50

cta atg tgt ggc ccg aga gct cgt act aat ttc cca tac aac cct aat
249
Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro Tyr Asn Pro Asn
      55              60              65

gcc att cct act tcc tct tcc aag ctt cta tca gca act ctt acc gct
297
Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala Thr Leu Thr Ala
      70              75              80

aaa ctc cac aaa tgc tac atg gct tct ctt caa atg acc aag caa acg
345
Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met Thr Lys Gln Thr
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caa aca caa acg caa acg cag acc gca aga tca caa tcc gcg gac agt
393
Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln Ser Ala Asp Ser
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gac ggt gtg acg gct aac gaa agt cat ttg aac aga gga gta acg gag
441
Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg Gly Val Thr Glu
      120              125              130

acg aca gag atc aag tgg gaa gat gga aat gcg aat atg caa cag aat
489
Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn Met Gln Gln Asn
      135              140              145

ttt agg cca ttg gag gaa gat cat atc gag caa atg att gag gag ctg
537
Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met Ile Glu Glu Leu
      150              155              160

ctt cac tac ggt tcc att gag ctt tgc tct gtt tta cca act cag acg
585
Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu Pro Thr Gln Thr
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641
Leu

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701

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aaaaaaaaaa aa  
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35 40 45

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50 55 60

Tyr Asn Pro Asn Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala  
65 70 75 80

Thr Leu Thr Ala Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met  
85 90 95

Thr Lys Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln  
100 105 110

Ser Ala Asp Ser Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg  
115 120 125

Gly Val Thr Glu Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn  
130 135 140

Met Gln Gln Asn Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met  
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Pro Thr Gln Thr Leu  
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 107

Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser  
 1 5 10 15

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 155

Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala  
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cca agg cct aaa cga gcc aaa agg gct aag aaa tct tct cct tct ggt  
 203

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly  
 35 40 45

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 251

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser  
 50 55 60

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Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala  
 65 70 75 80

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 347

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly  
 85 90 95

aaa caa gtt tat ctg gga gca tat gac agt gaa gaa gca gca gca cat  
 395

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His  
 100 105 110

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 443

Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu  
 115 120 125

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 491

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg  
 130 135 140

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Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly  
 145 150 155 160

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 587

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His  
 165 170 175



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 635  
 Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr  
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 683  
 Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr  
 195 200 205  
 gac atg gct gcg att gag tat cga ggc gca aac gcg gtt act aat ttc  
 731  
 Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe  
 210 215 220  
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 Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro  
 225 230 235 240  
 ttc cct gtg aac caa gct aac cat caa gag ggt att ctt gtt gaa gcc  
 827  
 Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala  
 245 250 255  
 aaa caa gaa gtt gaa acg aga gaa gcg aag gaa gag cct aga gaa gaa  
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 Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu  
 260 265 270  
 gtg aaa caa cag tac gtg gaa gaa cca ccg caa gaa gaa gaa gag aag  
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 Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Lys  
 275 280 285  
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 971  
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 290 295 300  
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 1019  
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 305 310 315 320  
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 1067  
 Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys  
 325 330 335  
 atg atg gat aca ggg ttt tct ccg ttt ttg act gat cag aat ctc gcg  
 1115  
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 340 345 350  
 aat gag aat ccc ata gag tat ccg gag cta ttc aat gag tta gca ttt  
 1163  
 Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe  
 355 360 365



gag gac aac atc gac ttc atg ttc gat gat ggg aag cac gag tgc ttg  
 1211  
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu  
 370 375 380

aac ttg gaa aat ctg gat tgt tgc gtg gtg gga aga gag agc cca ccc  
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 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro  
 385 390 395 400

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 Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser  
 405 410 415

aca aca aca aca aca acc tcg gtt tct tgt aac tat ttg gtc tga  
 1352  
 Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val  
 420 425 430

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tcttttggtg gggtctgctt aggggttgta ttccagtttc agggcttggt cggttggtct  
 1472

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Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly  
 35 40 45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser  
 50 55 60

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala  
 65 70 75 80

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly  
 85 90 95

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His  
 100 105 110



Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu  
 115 120 125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg  
 130 135 140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly  
 145 150 155 160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His  
 165 170 175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr  
 180 185 190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr  
 195 200 205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe  
 210 215 220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro  
 225 230 235 240

Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala  
 245 250 255

Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu  
 260 265 270

Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Lys  
 275 280 285

Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser  
 290 295 300

Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met  
 305 310 315 320

Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys  
 325 330 335

Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala  
 340 345 350

Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe



355                      360                      365  
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu  
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 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro  
     385                      390                      395                      400  
 Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser  
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 tgg acc gag gaa gaa gac gct aag atc ctt gct tat gtt gct atc cat  
 96  
 Trp Thr Glu Glu Glu Asp Ala Lys Ile Leu Ala Tyr Val Ala Ile His  
                     20                      25                      30  
 ggt gta gga aac tgg agc ttg atc ccc aaa aaa gca ggt ctg aat cga  
 144  
 Gly Val Gly Asn Trp Ser Leu Ile Pro Lys Lys Ala Gly Leu Asn Arg  
                     35                      40                      45  
 tgt gga aag agc tgt aga cta aga tgg act aat tac tta aga cct gac  
 192  
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp  
                     50                      55                      60  
 ctt aaa cat gac agc ttc tct acc caa gaa gaa gag ctt atc att gag  
 240  
 Leu Lys His Asp Ser Phe Ser Thr Gln Glu Glu Glu Leu Ile Ile Glu  
     65                      70                      75                      80  
 tgt cat aga gcc att ggc agc agg tgg tct tcc att gca cga aag ctt  
 288  
 Cys His Arg Ala Ile Gly Ser Arg Trp Ser Ser Ile Ala Arg Lys Leu  
                     85                      90                      95  
 cca gga aga acg gat aat gat gtg aag aat cac tgg aac aca aag ctg  
 336  
 Pro Gly Arg Thr Asp Asn Asp Val Lys Asn His Trp Asn Thr Lys Leu  
                     100                      105                      110  
 aag aag aag ctg atg aaa atg ggg ata gac ccg gtg act cat aaa ccg  
 384  
 Lys Lys Lys Leu Met Lys Met Gly Ile Asp Pro Val Thr His Lys Pro



115	120	125
gtt tct caa ctc ctt gca gaa ttc aga aac att agc ggc cat gga aat 432		
Val Ser Gln Leu Leu Ala Glu Phe Arg Asn Ile Ser Gly His Gly Asn 130 135 140		
gca tcc ttc aaa aca gaa cca tct aac aac tct ata ctc aca caa tcc 480		
Ala Ser Phe Lys Thr Glu Pro Ser Asn Asn Ser Ile Leu Thr Gln Ser 145 150 155 160		
aac tca gct tgg gaa atg atg aga aac aca aca aca aac cat gag agt 528		
Asn Ser Ala Trp Glu Met Met Arg Asn Thr Thr Thr Asn His Glu Ser 165 170 175		
tat tac acc aac tct cca atg atg ttt aca aat tcc tct gag tac caa 576		
Tyr Tyr Thr Asn Ser Pro Met Met Phe Thr Asn Ser Ser Glu Tyr Gln 180 185 190		
act act cca ttt cat ttc tat agc cat cca aat cat ctg ctc aat gga 624		
Thr Thr Pro Phe His Phe Tyr Ser His Pro Asn His Leu Leu Asn Gly 195 200 205		
acc aca tct tca tgc tct tcc tca tca tct tct act agt atc act cag 672		
Thr Thr Ser Ser Cys Ser Ser Ser Ser Ser Ser Thr Ser Ile Thr Gln 210 215 220		
cca aac caa gta cct caa aca ccg gtt act aac ttc tac tgg agc gat 720		
Pro Asn Gln Val Pro Gln Thr Pro Val Thr Asn Phe Tyr Trp Ser Asp 225 230 235 240		
ttc ctt ctc tcg gac ccg gtt cct caa gta gtg gga tcc tca gct act 768		
Phe Leu Leu Ser Asp Pro Val Pro Gln Val Val Gly Ser Ser Ala Thr 245 250 255		
agc gac ctc act ttt acg cag aac gaa cat cat ttc aac atc gaa gcc 816		
Ser Asp Leu Thr Phe Thr Gln Asn Glu His His Phe Asn Ile Glu Ala 260 265 270		
gaa tac atc tct caa aac atc gat tca aag gcc tcg gga aca tgt cat 864		
Glu Tyr Ile Ser Gln Asn Ile Asp Ser Lys Ala Ser Gly Thr Cys His 275 280 285		
tcc gcg agt tcc ttc gtt gac gaa ata cta gat aaa gac caa gag atg 912		
Ser Ala Ser Ser Phe Val Asp Glu Ile Leu Asp Lys Asp Gln Glu Met 290 295 300		
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20 25 30

Gly Val Gly Asn Trp Ser Leu Ile Pro Lys Lys Ala Gly Leu Asn Arg  
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp  
50 55 60

Leu Lys His Asp Ser Phe Ser Thr Gln Glu Glu Glu Leu Ile Ile Glu  
65 70 75 80

Cys His Arg Ala Ile Gly Ser Arg Trp Ser Ser Ile Ala Arg Lys Leu  
85 90 95

Pro Gly Arg Thr Asp Asn Asp Val Lys Asn His Trp Asn Thr Lys Leu  
100 105 110

Lys Lys Lys Leu Met Lys Met Gly Ile Asp Pro Val Thr His Lys Pro  
115 120 125

Val Ser Gln Leu Leu Ala Glu Phe Arg Asn Ile Ser Gly His Gly Asn  
130 135 140

Ala Ser Phe Lys Thr Glu Pro Ser Asn Asn Ser Ile Leu Thr Gln Ser  
145 150 155 160

Asn Ser Ala Trp Glu Met Met Arg Asn Thr Thr Thr Asn His Glu Ser  
165 170 175

Tyr Tyr Thr Asn Ser Pro Met Met Phe Thr Asn Ser Ser Glu Tyr Gln  
180 185 190

Thr Thr Pro Phe His Phe Tyr Ser His Pro Asn His Leu Leu Asn Gly  
195 200 205

Thr Thr Ser Ser Cys Ser Ser Ser Ser Ser Thr Ser Ile Thr Gln  
210 215 220



Pro Asn Gln Val Pro Gln Thr Pro Val Thr Asn Phe Tyr Trp Ser Asp  
225 230 235 240

Phe Leu Leu Ser Asp Pro Val Pro Gln Val Val Gly Ser Ser Ala Thr  
245 250 255

Ser Asp Leu Thr Phe Thr Gln Asn Glu His His Phe Asn Ile Glu Ala  
260 265 270

Glu Tyr Ile Ser Gln Asn Ile Asp Ser Lys Ala Ser Gly Thr Cys His  
275 280 285

Ser Ala Ser Ser Phe Val Asp Glu Ile Leu Asp Lys Asp Gln Glu Met  
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gac tct tct cga gat aag aag atg aaa aat ccg cga ttt tcg ttt cgc  
103

Asp Ser Ser Arg Asp Lys Lys Met Lys Asn Pro Arg Phe Ser Phe Arg  
10 15 20

aca aag agt gat gca gat att ctc gat gat ggt tat cga tgg aga aag  
151

Thr Lys Ser Asp Ala Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys  
25 30 35

tac ggt cag aaa tcc gtc aag aac agc ttg tat ccc agg agc tat tat  
199

Tyr Gly Gln Lys Ser Val Lys Asn Ser Leu Tyr Pro Arg Ser Tyr Tyr  
40 45 50

aga tgc aca caa cac atg tgt aac gtg aag aag caa gtt cag agg ctg  
247

Arg Cys Thr Gln His Met Cys Asn Val Lys Lys Gln Val Gln Arg Leu  
55 60 65

tcg aag gag acg agc att gtg gag aca act tat gaa gga atc cat aac  
295

Ser Lys Glu Thr Ser Ile Val Glu Thr Thr Tyr Glu Gly Ile His Asn  
70 75 80 85

cat cct tgt gag gag ctc atg caa acc cta act cct ctt ctt cat caa  
343

His Pro Cys Glu Glu Leu Met Gln Thr Leu Thr Pro Leu Leu His Gln



90 95 100  
 ttg cag ttc ctc tct aag ttc acc taa ttatgtttgt atatatttta  
 390  
 Leu Gln Phe Leu Ser Lys Phe Thr  
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 476  
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 Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys Asn Ser Leu Tyr  
 35 40 45  
 Pro Arg Ser Tyr Tyr Arg Cys Thr Gln His Met Cys Asn Val Lys Lys  
 50 55 60  
 Gln Val Gln Arg Leu Ser Lys Glu Thr Ser Ile Val Glu Thr Thr Tyr  
 65 70 75 80  
 Glu Gly Ile His Asn His Pro Cys Glu Glu Leu Met Gln Thr Leu Thr  
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 cttccacact tcctttttac taggcagtgt taaccaattg agagagaaaa atg atg  
 176  
 Met  
 1



gtt gat gaa aat gtg gaa acc aag gcc tct act tta gtg gca agt gtt  
 224  
 Val Asp Glu Asn Val Glu Thr Lys Ala Ser Thr Leu Val Ala Ser Val  
 5 10 15

gat cat ggg ttt gga tcc ggg tcg ggt cat gat cat cat ggg tta tcg  
 272  
 Asp His Gly Phe Gly Ser Gly Ser Gly His Asp His His Gly Leu Ser  
 20 25 30

gcg tct gtg cct ctt ctt ggt gtt aac tgg aag aag aga agg atg cct  
 320  
 Ala Ser Val Pro Leu Leu Gly Val Asn Trp Lys Lys Arg Arg Met Pro  
 35 40 45

aga cag aga cga tct tct tct tcc ttt aac ctt ctc tct ttc cct cct  
 368  
 Arg Gln Arg Arg Ser Ser Ser Ser Phe Asn Leu Leu Ser Phe Pro Pro  
 50 55 60 65

cct atg cct cct att tcc cac gtg cca act cct ctc ccc gca cgt aaa  
 416  
 Pro Met Pro Pro Ile Ser His Val Pro Thr Pro Leu Pro Ala Arg Lys  
 70 75 80

att gac cca aga aag cta aga ttc ctc ttc caa aag gaa ctc aag aac  
 464  
 Ile Asp Pro Arg Lys Leu Arg Phe Leu Phe Gln Lys Glu Leu Lys Asn  
 85 90 95

agt gac gtc agc tct ctc cga cgt atg ata ctc ccg aag aaa gcc gcg  
 512  
 Ser Asp Val Ser Ser Leu Arg Arg Met Ile Leu Pro Lys Lys Ala Ala  
 100 105 110

gag gct cac ttg ccg gca ctt gaa tgc aag gaa ggg att cct ata aga  
 560  
 Glu Ala His Leu Pro Ala Leu Glu Cys Lys Glu Gly Ile Pro Ile Arg  
 115 120 125

atg gaa gat ttg gac ggt ttt cac gtt tgg acc ttc aag tat agg tac  
 608  
 Met Glu Asp Leu Asp Gly Phe His Val Trp Thr Phe Lys Tyr Arg Tyr  
 130 135 140 145

tgg cca aac aac aat agc aga atg tac gtg cta gaa aac aca ggc gat  
 656  
 Trp Pro Asn Asn Asn Ser Arg Met Tyr Val Leu Glu Asn Thr Gly Asp  
 150 155 160

ttt gtg aat gct cat ggt ctg cag cta ggt gac ttc atc atg gtt tac  
 704  
 Phe Val Asn Ala His Gly Leu Gln Leu Gly Asp Phe Ile Met Val Tyr  
 165 170 175

caa gat ctc tac tca aac aat tac gtt ata caa gca aga aaa gca tcg  
 752  
 Gln Asp Leu Tyr Ser Asn Asn Tyr Val Ile Gln Ala Arg Lys Ala Ser  
 180 185 190



gaa gaa gaa gaa gta gac gta atc aat ctt gaa gaa gac gac gtt tac  
 800  
 Glu Glu Glu Glu Val Asp Val Ile Asn Leu Glu Glu Asp Asp Val Tyr  
 195 200 205  
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 848  
 Thr Asn Leu Thr Arg Ile Glu Asn Thr Val Val Asn Asp Leu Leu Leu  
 210 215 220 225  
 caa gat ttt aat cat cac aac aac aac aac aac aac agc aac agc  
 896  
 Gln Asp Phe Asn His His Asn Asn Asn Asn Asn Asn Ser Asn Ser  
 230 235 240  
 aac agc aac aaa tgt tct tac tat tat cca gtc ata gat gat gtc acc  
 944  
 Asn Ser Asn Lys Cys Ser Tyr Tyr Tyr Pro Val Ile Asp Asp Val Thr  
 245 250 255  
 aca aac aca gag tct ttt gtc tac gac acg acg gct ctt acc tcc aac  
 992  
 Thr Asn Thr Glu Ser Phe Val Tyr Asp Thr Thr Ala Leu Thr Ser Asn  
 260 265 270  
 gat act cct ctc gat ttt ttg ggt gga cat acg acg act act aat aat  
 1040  
 Asp Thr Pro Leu Asp Phe Leu Gly Gly His Thr Thr Thr Thr Asn Asn  
 275 280 285  
 tat tac tcc aag ttc gga aca ttc gat ggt ttg ggc tcc gtt gag aat  
 1088  
 Tyr Tyr Ser Lys Phe Gly Thr Phe Asp Gly Leu Gly Ser Val Glu Asn  
 290 295 300 305  
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 1142  
 Ile Ser Leu Asp Asp Phe Tyr  
 310  
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 Ser Ala Ser Val Pro Leu Leu Gly Val Asn Trp Lys Lys Arg Arg Met  
 35 40 45



Pro Arg Gln Arg Arg Ser Ser Ser Ser Phe Asn Leu Leu Ser Phe Pro  
 50 55 60

Pro Pro Met Pro Pro Ile Ser His Val Pro Thr Pro Leu Pro Ala Arg  
 65 70 75 80

Lys Ile Asp Pro Arg Lys Leu Arg Phe Leu Phe Gln Lys Glu Leu Lys  
 85 90 95

Asn Ser Asp Val Ser Ser Leu Arg Arg Met Ile Leu Pro Lys Lys Ala  
 100 105 110

Ala Glu Ala His Leu Pro Ala Leu Glu Cys Lys Glu Gly Ile Pro Ile  
 115 120 125

Arg Met Glu Asp Leu Asp Gly Phe His Val Trp Thr Phe Lys Tyr Arg  
 130 135 140

Tyr Trp Pro Asn Asn Asn Ser Arg Met Tyr Val Leu Glu Asn Thr Gly  
 145 150 155 160

Asp Phe Val Asn Ala His Gly Leu Gln Leu Gly Asp Phe Ile Met Val  
 165 170 175

Tyr Gln Asp Leu Tyr Ser Asn Asn Tyr Val Ile Gln Ala Arg Lys Ala  
 180 185 190

Ser Glu Glu Glu Glu Val Asp Val Ile Asn Leu Glu Glu Asp Asp Val  
 195 200 205

Tyr Thr Asn Leu Thr Arg Ile Glu Asn Thr Val Val Asn Asp Leu Leu  
 210 215 220

Leu Gln Asp Phe Asn His His Asn Asn Asn Asn Asn Asn Ser Asn  
 225 230 235 240

Ser Asn Ser Asn Lys Cys Ser Tyr Tyr Tyr Pro Val Ile Asp Asp Val  
 245 250 255

Thr Thr Asn Thr Glu Ser Phe Val Tyr Asp Thr Thr Ala Leu Thr Ser  
 260 265 270

Asn Asp Thr Pro Leu Asp Phe Leu Gly Gly His Thr Thr Thr Thr Asn  
 275 280 285



Asn Tyr Tyr Ser Lys Phe Gly Thr Phe Asp Gly Leu Gly Ser Val Glu  
 290 295 300

Asn Ile Ser Leu Asp Asp Phe Tyr  
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 104

Met Leu Glu Ser Arg Asn Ser Met Arg Ala Ser Asn Ser Val Pro Asp  
 5 10 15

ctg tct ctt cag atc agt ctt cct aac tat cac gcc gga aaa cct ctt  
 152

Leu Ser Leu Gln Ile Ser Leu Pro Asn Tyr His Ala Gly Lys Pro Leu  
 20 25 30

cac gcc ggt gac cgg agc tcc aca agc agt gat tct gga agc agc ctc  
 200

His Gly Gly Asp Arg Ser Ser Thr Ser Ser Asp Ser Gly Ser Ser Leu  
 35 40 45 50

agt gac ctg agc cat gag aac aac ttc ttc aac aaa cct ctc ttg agc  
 248

Ser Asp Leu Ser His Glu Asn Asn Phe Phe Asn Lys Pro Leu Leu Ser  
 55 60 65

tta gga ttt gac cat cat cat caa agg cgc tca aac atg ttc caa cct  
 296

Leu Gly Phe Asp His His His Gln Arg Arg Ser Asn Met Phe Gln Pro  
 70 75 80

caa atc tac ggt cga gat ttc aag aga agc tca tca tca atg gtt ggt  
 344

Gln Ile Tyr Gly Arg Asp Phe Lys Arg Ser Ser Ser Ser Met Val Gly  
 85 90 95

ctt aaa cga agc att cgt gct cca aga atg aga tgg act tct act ctt  
 392

Leu Lys Arg Ser Ile Arg Ala Pro Arg Met Arg Trp Thr Ser Thr Leu  
 100 105 110

cat gct cac ttc gtc cat gct gtt caa ctt ctt ggc ggc cat gaa aga  
 440

His Ala His Phe Val His Ala Val Gln Leu Leu Gly Gly His Glu Arg  
 115 120 125 130

gca acg cct aaa tca gtg ttg gag ctc atg aat gtg aag gat cta acc  
 488

Ala Thr Pro Lys Ser Val Leu Glu Leu Met Asn Val Lys Asp Leu Thr  
 135 140 145



cta gct cat gtc aag agt cac ttg cag atg tat aga aca gtg aaa tgc  
536

Leu Ala His Val Lys Ser His Leu Gln Met Tyr Arg Thr Val Lys Cys  
150 155 160

act gat aaa gga tca cca gga gaa gga aag gta gag aaa gag gca gag  
584

Thr Asp Lys Gly Ser Pro Gly Glu Gly Lys Val Glu Lys Glu Ala Glu  
165 170 175

cag agg ata gag gac aat aat aat aat gaa gaa gct gat gaa gga act  
632

Gln Arg Ile Glu Asp Asn Asn Asn Asn Glu Glu Ala Asp Glu Gly Thr  
180 185 190

gac aca aat tcg cca aac tca tca tct gtg caa aag acc caa aga gct  
680

Asp Thr Asn Ser Pro Asn Ser Ser Ser Val Gln Lys Thr Gln Arg Ala  
195 200 205 210

tca tgg tca tcg aca aag gaa gta tct agg agc ata tct aca caa gca  
728

Ser Trp Ser Ser Thr Lys Glu Val Ser Arg Ser Ile Ser Thr Gln Ala  
215 220 225

tat tct cac ttg gga aca act cat cac act aag gcc aat gaa gag aaa  
776

Tyr Ser His Leu Gly Thr Thr His His Thr Lys Ala Asn Glu Glu Lys  
230 235 240

gag gat acc aac att cat ctc aat ttg gat ttc aca ttg ggc ggc cta  
824

Glu Asp Thr Asn Ile His Leu Asn Leu Asp Phe Thr Leu Gly Gly Leu  
245 250 255

gtt ggg gga tgg aat atg cgg aac cct cca gtg att taa cccttctcaa  
873

Val Gly Gly Trp Asn Met Arg Asn Pro Pro Val Ile  
260 265 270

gtgctaattg ccttaagcta caacaaataa gtcagcttag gttaccagtt ttaacataat  
933

tttaacttgt ttgatcata tgagcttcgg aagaatcata ttatcatcat atatgaactt  
993

ctttccaaga atgttctatg agttttttga tatgtataat caagagaatc gtttgaagta  
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1057

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20 25 30

Pro Leu His Gly Gly Asp Arg Ser Ser Thr Ser Ser Asp Ser Gly Ser  
35 40 45

Ser Leu Ser Asp Leu Ser His Glu Asn Asn Phe Phe Asn Lys Pro Leu  
50 55 60

Leu Ser Leu Gly Phe Asp His His His Gln Arg Arg Ser Asn Met Phe  
65 70 75 80

Gln Pro Gln Ile Tyr Gly Arg Asp Phe Lys Arg Ser Ser Ser Ser Met  
85 90 95

Val Gly Leu Lys Arg Ser Ile Arg Ala Pro Arg Met Arg Trp Thr Ser  
100 105 110

Thr Leu His Ala His Phe Val His Ala Val Gln Leu Leu Gly Gly His  
115 120 125

Glu Arg Ala Thr Pro Lys Ser Val Leu Glu Leu Met Asn Val Lys Asp  
130 135 140

Leu Thr Leu Ala His Val Lys Ser His Leu Gln Met Tyr Arg Thr Val  
145 150 155 160

Lys Cys Thr Asp Lys Gly Ser Pro Gly Glu Gly Lys Val Glu Lys Glu  
165 170 175

Ala Glu Gln Arg Ile Glu Asp Asn Asn Asn Asn Glu Glu Ala Asp Glu  
180 185 190

Gly Thr Asp Thr Asn Ser Pro Asn Ser Ser Ser Val Gln Lys Thr Gln  
195 200 205

Arg Ala Ser Trp Ser Ser Thr Lys Glu Val Ser Arg Ser Ile Ser Thr  
210 215 220

Gln Ala Tyr Ser His Leu Gly Thr Thr His His Thr Lys Ala Asn Glu  
225 230 235 240

Glu Lys Glu Asp Thr Asn Ile His Leu Asn Leu Asp Phe Thr Leu Gly  
245 250 255

Gly Leu Val Gly Gly Trp Asn Met Arg Asn Pro Pro Val Ile



260

265

270

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Met Gly Gly Gly Gly Asp Thr Thr Asp Thr  
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aat atg atg cag aga gtt aat tct tct tct ggt aca tcg tct tct tcg  
 100

Asn Met Met Gln Arg Val Asn Ser Ser Ser Gly Thr Ser Ser Ser Ser  
 15 20 25

atc cct aaa cac aat ctt cac ttg aat cct gct ctt atc cgc tct cac  
 148

Ile Pro Lys His Asn Leu His Leu Asn Pro Ala Leu Ile Arg Ser His  
 30 35 40

cat cac ttc cgt cac cct ttc acc gga gct cct cca ccg ccg att cca  
 196

His His Phe Arg His Pro Phe Thr Gly Ala Pro Pro Pro Pro Ile Pro  
 45 50 55

ccc att tct cct tac tct cag atc ccg gcg act tta caa cct aga cat  
 244

Pro Ile Ser Pro Tyr Ser Gln Ile Pro Ala Thr Leu Gln Pro Arg His  
 60 65 70

tct cgc tct atg tcg caa ccg tct tct ttc ttc tcc ttt gat tca ttg  
 292

Ser Arg Ser Met Ser Gln Pro Ser Ser Phe Phe Ser Phe Asp Ser Leu  
 75 80 85 90

ccg ccg tta aat cct tct gct ccg tcg gtt tcg gtg tcg gtg gag gag  
 340

Pro Pro Leu Asn Pro Ser Ala Pro Ser Val Ser Val Ser Val Glu Glu  
 95 100 105

aaa acc ggt gcc gga ttt agt cct tcg ttg cct ccg tca ccg ttt acg  
 388

Lys Thr Gly Ala Gly Phe Ser Pro Ser Leu Pro Pro Ser Pro Phe Thr  
 110 115 120

atg tgt cat tct tct agc tct agg aac gcc gga gat gga gag aat cta  
 436

Met Cys His Ser Ser Ser Ser Arg Asn Ala Gly Asp Gly Glu Asn Leu  
 125 130 135

cct ccg aga aag tcg cat agg cgt tcg aat agt gat gtt act ttt ggg  
 484

Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Val Thr Phe Gly  
 140 145 150

ttt agt tca atg atg tct cag aat caa aag tct cct cct ttg agt tct  
 532

Phe Ser Ser Met Met Ser Gln Asn Gln Lys Ser Pro Pro Leu Ser Ser  
 155 160 165 170



ttg gag aga tcg atc tct ggt gaa gat aca tca gat tgg tct aat ttg  
580

Leu Glu Arg Ser Ile Ser Gly Glu Asp Thr Ser Asp Trp Ser Asn Leu  
175 180 185

gtg aag aaa gaa ccg aga gaa ggc ttc tac aag gga aga aaa cca gag  
628

Val Lys Lys Glu Pro Arg Glu Gly Phe Tyr Lys Gly Arg Lys Pro Glu  
190 195 200

gtt gaa gca gct atg gac gat gtt ttc acg gct tat atg aat ctt gat  
676

Val Glu Ala Ala Met Asp Asp Val Phe Thr Ala Tyr Met Asn Leu Asp  
205 210 215

aac att gat gtc ttg aat tct ttt gga ggt gaa gat ggc aag aat ggg  
724

Asn Ile Asp Val Leu Asn Ser Phe Gly Gly Glu Asp Gly Lys Asn Gly  
220 225 230

aat gag aat gtg gag gag atg gag agt agt aga ggt agt ggt aca aag  
772

Asn Glu Asn Val Glu Glu Met Glu Ser Ser Arg Gly Ser Gly Thr Lys  
235 240 245 250

aag acg aat ggt gga agt agt agt gat tct gaa gga gat agc agt gcg  
820

Lys Thr Asn Gly Gly Ser Ser Ser Asp Ser Glu Gly Asp Ser Ser Ala  
255 260 265

agt ggg aat gtg aag gtt gcg ttg agt tct tct tct tca ggc gtg aag  
868

Ser Gly Asn Val Lys Val Ala Leu Ser Ser Ser Ser Ser Gly Val Lys  
270 275 280

aga aga gca ggt gga gat att gct cct act ggt aga cat tac agg agt  
916

Arg Arg Ala Gly Gly Asp Ile Ala Pro Thr Gly Arg His Tyr Arg Ser  
285 290 295

gtt tct atg gac agt tgt ttc atg ggg aag ttg aat ttc ggc gac gaa  
964

Val Ser Met Asp Ser Cys Phe Met Gly Lys Leu Asn Phe Gly Asp Glu  
300 305 310

tca tcg cta aag ctt ccg cct tct tca tca gct aaa gtt tcc cca acc  
1012

Ser Ser Leu Lys Leu Pro Pro Ser Ser Ser Ala Lys Val Ser Pro Thr  
315 320 325 330

aat tca ggt gaa ggg aat tca agt gct tat agt gtt gaa ttt gga aac  
1060

Asn Ser Gly Glu Gly Asn Ser Ser Ala Tyr Ser Val Glu Phe Gly Asn  
335 340 345

agt gag ttt act gca gct gaa atg aag aag att gca gct gat gag aaa  
1108

Ser Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Ala Ala Asp Glu Lys  
350 355 360



ctc gct gag att gta atg gct gac cct aag cgt gtt aaa aga atc ttg  
 1156  
 Leu Ala Glu Ile Val Met Ala Asp Pro Lys Arg Val Lys Arg Ile Leu  
 365 370 375

gcg aac cgc gta tct gct gca cgt tca aag gag cgg aag acg cga tac  
 1204  
 Ala Asn Arg Val Ser Ala Ala Arg Ser Lys Glu Arg Lys Thr Arg Tyr  
 380 385 390

atg gca gag ttg gaa cac aag gtg cag aca ctt cag act gaa gct act  
 1252  
 Met Ala Glu Leu Glu His Lys Val Gln Thr Leu Gln Thr Glu Ala Thr  
 395 400 405 410

aca tta tcg gct cag ctc aca cat ttg cag aga gat tct atg ggg ttg  
 1300  
 Thr Leu Ser Ala Gln Leu Thr His Leu Gln Arg Asp Ser Met Gly Leu  
 415 420 425

aca aac cag aac agt gag ctg aag ttt cgt ctt caa gct atg gag cag  
 1348  
 Thr Asn Gln Asn Ser Glu Leu Lys Phe Arg Leu Gln Ala Met Glu Gln  
 430 435 440

caa gca caa ctc cgc gat gct ctg tca gag aaa ctg aat gaa gaa gtc  
 1396  
 Gln Ala Gln Leu Arg Asp Ala Leu Ser Glu Lys Leu Asn Glu Glu Val  
 445 450 455

cag cgg ttg aaa ctg gtg ata ggg gag ccg aac cgc agg caa agt ggg  
 1444  
 Gln Arg Leu Lys Leu Val Ile Gly Glu Pro Asn Arg Arg Gln Ser Gly  
 460 465 470

agc agc agc agc gaa tca aag atg tca cta aac ccg gag atg ttt cag  
 1492  
 Ser Ser Ser Ser Glu Ser Lys Met Ser Leu Asn Pro Glu Met Phe Gln  
 475 480 485 490

cag ctt agc ata agt cag tta caa cac caa cag atg cag cat tcc aat  
 1540  
 Gln Leu Ser Ile Ser Gln Leu Gln His Gln Gln Met Gln His Ser Asn  
 495 500 505

cag tgt agc aca atg aaa gca aag cac act tca aac gac tag  
 1582  
 Gln Cys Ser Thr Met Lys Ala Lys His Thr Ser Asn Asp  
 510 515

ggtaagtaaa actgcgatcc gcagttgtct agttacatat atgataagaa tcttttgtgc  
 1642

agagttctgt ttttgaagt tttaaagaaa catatataaa gattatgtcc gggaaatttg  
 1702

atcatatttc ctgaaacata cacacatata tatagtggta atggaggact ttctttctgg  
 1762

acca  
 1766



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164

Met Gly Gly Gly Gly Asp Thr Thr Asp Thr Asn Met Met Gln Arg Val  
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Asn Ser Ser Ser Gly Thr Ser Ser Ser Ser Ile Pro Lys His Asn Leu  
20 25 30

His Leu Asn Pro Ala Leu Ile Arg Ser His His His Phe Arg His Pro  
35 40 45

Phe Thr Gly Ala Pro Pro Pro Pro Ile Pro Pro Ile Ser Pro Tyr Ser  
50 55 60

Gln Ile Pro Ala Thr Leu Gln Pro Arg His Ser Arg Ser Met Ser Gln  
65 70 75 80

Pro Ser Ser Phe Phe Ser Phe Asp Ser Leu Pro Pro Leu Asn Pro Ser  
85 90 95

Ala Pro Ser Val Ser Val Ser Val Glu Lys Thr Gly Ala Gly Phe  
100 105 110

Ser Pro Ser Leu Pro Pro Ser Pro Phe Thr Met Cys His Ser Ser Ser  
115 120 125

Ser Arg Asn Ala Gly Asp Gly Glu Asn Leu Pro Pro Arg Lys Ser His  
130 135 140

Arg Arg Ser Asn Ser Asp Val Thr Phe Gly Phe Ser Ser Met Met Ser  
145 150 155 160

Gln Asn Gln Lys Ser Pro Pro Leu Ser Ser Leu Glu Arg Ser Ile Ser  
165 170 175

Gly Glu Asp Thr Ser Asp Trp Ser Asn Leu Val Lys Lys Glu Pro Arg  
180 185 190

Glu Gly Phe Tyr Lys Gly Arg Lys Pro Glu Val Glu Ala Ala Met Asp  
195 200 205

Asp Val Phe Thr Ala Tyr Met Asn Leu Asp Asn Ile Asp Val Leu Asn  
210 215 220



Ser Phe Gly Gly Glu Asp Gly Lys Asn Gly Asn Glu Asn Val Glu Glu  
 225 230 235 240

Met Glu Ser Ser Arg Gly Ser Gly Thr Lys Lys Thr Asn Gly Gly Ser  
 245 250 255

Ser Ser Asp Ser Glu Gly Asp Ser Ser Ala Ser Gly Asn Val Lys Val  
 260 265 270

Ala Leu Ser Ser Ser Ser Ser Gly Val Lys Arg Arg Ala Gly Gly Asp  
 275 280 285

Ile Ala Pro Thr Gly Arg His Tyr Arg Ser Val Ser Met Asp Ser Cys  
 290 295 300

Phe Met Gly Lys Leu Asn Phe Gly Asp Glu Ser Ser Leu Lys Leu Pro  
 305 310 315 320

Pro Ser Ser Ser Ala Lys Val Ser Pro Thr Asn Ser Gly Glu Gly Asn  
 325 330 335

Ser Ser Ala Tyr Ser Val Glu Phe Gly Asn Ser Glu Phe Thr Ala Ala  
 340 345 350

Glu Met Lys Lys Ile Ala Ala Asp Glu Lys Leu Ala Glu Ile Val Met  
 355 360 365

Ala Asp Pro Lys Arg Val Lys Arg Ile Leu Ala Asn Arg Val Ser Ala  
 370 375 380

Ala Arg Ser Lys Glu Arg Lys Thr Arg Tyr Met Ala Glu Leu Glu His  
 385 390 395 400

Lys Val Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu  
 405 410 415

Thr His Leu Gln Arg Asp Ser Met Gly Leu Thr Asn Gln Asn Ser Glu  
 420 425 430

Leu Lys Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Gln Leu Arg Asp  
 435 440 445

Ala Leu Ser Glu Lys Leu Asn Glu Glu Val Gln Arg Leu Lys Leu Val  
 450 455 460

Ile Gly Glu Pro Asn Arg Arg Gln Ser Gly Ser Ser Ser Ser Glu Ser



292



cat cat cat cac agc atc aac ggc aat gtg ggt ccc acg cgt tca tcc  
 506  
 His His His His Ser Ile Asn Gly Asn Val Gly Pro Thr Arg Ser Ser  
 110 115 120  
 tcc aac acc tcc acg ccg tcc gat cat aat agc ctt agc gac gac gac  
 554  
 Ser Asn Thr Ser Thr Pro Ser Asp His Asn Ser Leu Ser Asp Asp Asp  
 125 130 135  
 aac aac aaa gaa gca cca ccg tcc gat cat gat cat cac atg gac aat  
 602  
 Asn Asn Lys Glu Ala Pro Pro Ser Asp His Asp His His Met Asp Asn  
 140 145 150 155  
 aat gta gcc aat caa aac aac gcc gcc ggt aac aat tac aac gaa tca  
 650  
 Asn Val Ala Asn Gln Asn Asn Ala Ala Gly Asn Asn Tyr Asn Glu Ser  
 160 165 170  
 gac gag gtc caa agc cag tgc aag acg gag cca caa gat ggt ccg tcg  
 698  
 Asp Glu Val Gln Ser Gln Cys Lys Thr Glu Pro Gln Asp Gly Pro Ser  
 175 180 185  
 gcg aat caa aac tcc ggt gga agc tcc ggt aat cgt att cac gac cct  
 746  
 Ala Asn Gln Asn Ser Gly Gly Ser Ser Gly Asn Arg Ile His Asp Pro  
 190 195 200  
 aaa agg gta aaa aga att tta gca aat agg caa tca gca cag aga tca  
 794  
 Lys Arg Val Lys Arg Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser  
 205 210 215  
 agg gtg agg aaa ttg caa tac ata tca gag ctt gaa agg agc gtt act  
 842  
 Arg Val Arg Lys Leu Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr  
 220 225 230 235  
 tca ttg cag act gaa gtg tca gtg tta tcg cca aga gtt gcg ttt ttg  
 890  
 Ser Leu Gln Thr Glu Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu  
 240 245 250  
 gat cat cag cga ttg ctt ctc aac gtc gac aat agt gct atc aag caa  
 938  
 Asp His Gln Arg Leu Leu Leu Asn Val Asp Asn Ser Ala Ile Lys Gln  
 255 260 265  
 cga atc gca gct tta gca caa gat aag att ttc aaa gac gct cat caa  
 986  
 Arg Ile Ala Ala Leu Ala Gln Asp Lys Ile Phe Lys Asp Ala His Gln  
 270 275 280  
 gaa gca ttg aag aga gaa ata gag aga ctt cga caa gta tat cat caa  
 1034  
 Glu Ala Leu Lys Arg Glu Ile Glu Arg Leu Arg Gln Val Tyr His Gln  
 285 290 295



caa agc ctc aag aag atg gag aat aat gtc tcc gat caa tct ccg gcc  
1082

Gln Ser Leu Lys Lys Met Glu Asn Asn Val Ser Asp Gln Ser Pro Ala  
300 305 310 315

gat atc aaa ccg tcc gtt gag aag gaa cag ctc ctc aat gtc taa  
1127

Asp Ile Lys Pro Ser Val Glu Lys Glu Gln Leu Leu Asn Val  
320 325

agctgttcgt tcactaagat ctttcttttc atggcgaaaa gattcttgac tataaaacct  
1187

ctttgtgtca agaaattaat ttatcaaaga agatggcctt ttttatttga tctaatacaca  
1247

tttttttaag ttgtgatgaa ttgtcttttg atgtatctgt tttttttttt ttttttt  
1304

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Met Ala Gln Leu Pro Pro Lys Ile Pro Thr Met Thr Thr Pro Asn Trp  
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Pro Asp Phe Ser Ser Gln Lys Leu Pro Ser Ile Ala Ala Thr Ala Ala  
20 25 30

Ala Ala Ala Thr Ala Gly Pro Gln Gln Gln Asn Pro Ser Trp Met Asp  
35 40 45

Glu Phe Leu Asp Phe Ser Ala Thr Arg Arg Gly Thr His Arg Arg Ser  
50 55 60

Ile Ser Asp Ser Ile Ala Phe Leu Glu Pro Pro Ser Ser Gly Val Gly  
65 70 75 80

Asn His His Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met Phe  
85 90 95

Asn Asp Asp Val His Asn Asn Asn His Asn His His His His His Ser  
100 105 110

Ile Asn Gly Asn Val Gly Pro Thr Arg Ser Ser Ser Asn Thr Ser Thr  
115 120 125

Pro Ser Asp His Asn Ser Leu Ser Asp Asp Asp Asn Asn Lys Glu Ala  
130 135 140

Pro Pro Ser Asp His Asp His His Met Asp Asn Asn Val Ala Asn Gln  
145 150 155 160



Asn Asn Ala Ala Gly Asn Asn Tyr Asn Glu Ser Asp Glu Val Gln Ser  
 165 170 175

Gln Cys Lys Thr Glu Pro Gln Asp Gly Pro Ser Ala Asn Gln Asn Ser  
 180 185 190

Gly Gly Ser Ser Gly Asn Arg Ile His Asp Pro Lys Arg Val Lys Arg  
 195 200 205

Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys Leu  
 210 215 220

Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Thr Glu  
 225 230 235 240

Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg Leu  
 245 250 255

Leu Leu Asn Val Asp Asn Ser Ala Ile Lys Gln Arg Ile Ala Ala Leu  
 260 265 270

Ala Gln Asp Lys Ile Phe Lys Asp Ala His Gln Glu Ala Leu Lys Arg  
 275 280 285

Glu Ile Glu Arg Leu Arg Gln Val Tyr His Gln Gln Ser Leu Lys Lys  
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Met Glu Asn Asn Val Ser Asp Gln Ser Pro Ala Asp Ile Lys Pro Ser  
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Val Glu Lys Glu Gln Leu Leu Asn Val  
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 120

tctctttctc tcatcatcaa tcatcaatca tccaaaagaa aaaaccctaa aatttcactt  
 180

gtaagctttt caccagtttc tctccatacc cattttatca gcttctccat atctttctct  
 240



atg gat tct gac ata atg aac atg atg atg cat cag atg gag aag ctt  
 288  
 Met Asp Ser Asp Ile Met Asn Met Met Met His Gln Met Glu Lys Leu  
 1 5 10 15  
 cct gag ttt tgt aac cct aat tcc tct ttc ttc tct ccc gac cac aac  
 336  
 Pro Glu Phe Cys Asn Pro Asn Ser Ser Phe Phe Ser Pro Asp His Asn  
 20 25 30  
 aac act tac cct ttt ctc ttt aac tcc act cat tac cag tcc gat cac  
 384  
 Asn Thr Tyr Pro Phe Leu Phe Asn Ser Thr His Tyr Gln Ser Asp His  
 35 40 45  
 tca atg acc aac gaa cca ggt ttc cgc tac ggt tcc ggt tta ctc act  
 432  
 Ser Met Thr Asn Glu Pro Gly Phe Arg Tyr Gly Ser Gly Leu Leu Thr  
 50 55 60  
 aac cct tct tct atc tct ccc aac aca gct tac tct tcc gtt ttt ctt  
 480  
 Asn Pro Ser Ser Ile Ser Pro Asn Thr Ala Tyr Ser Ser Val Phe Leu  
 65 70 75 80  
 gac aaa aga aac aac agt aac aac aac aat aat ggc acg aac atg gca  
 528  
 Asp Lys Arg Asn Asn Ser Asn Asn Asn Asn Asn Gly Thr Asn Met Ala  
 85 90 95  
 gct atg cga gag atg atc ttc cgt atc gcc gtg atg caa ccg atc cat  
 576  
 Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His  
 100 105 110  
 atc gat ccc gag gcg gtt aag cca ccg aag agg agg aac gtc agg atc  
 624  
 Ile Asp Pro Glu Ala Val Lys Pro Pro Lys Arg Arg Asn Val Arg Ile  
 115 120 125  
 tct aaa gat cct caa agc gtg gcg gct agg cat aga agg gag aga ata  
 672  
 Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile  
 130 135 140  
 agc gag agg att cgg att ttg caa cgg ctt gtt cct ggt ggg acg aag  
 720  
 Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys  
 145 150 155 160  
 atg gat aca gct tcg atg ctc gat gaa gca att cat tat gtg aag ttt  
 768  
 Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe  
 165 170 175  
 tta aag aaa cag gtg cag tct ctg gag gag cag gcg gtg gtt act ggc  
 816  
 Leu Lys Lys Gln Val Gln Ser Leu Glu Glu Gln Ala Val Val Thr Gly  
 180 185 190



gga ggg gga gga gga gga gga agg gtt ttg atc ggt gga ggt gga atg  
864  
Gly Gly Gly Gly Gly Gly Arg Val Leu Ile Gly Gly Gly Gly Met  
195 200 205

acg gcg gcg agt ggt ggt ggt ggc ggc ggg gga gtg gtt atg aaa ggg  
912  
Thr Ala Ala Ser Gly Gly Gly Gly Gly Gly Val Val Met Lys Gly  
210 215 220

tgt gga aca gtg ggg act cat cag atg gtg ggc aat gca cag att ctt  
960  
Cys Gly Thr Val Gly Thr His Gln Met Val Gly Asn Ala Gln Ile Leu  
225 230 235 240

aga tga tgatgatttt taattttatt attattatat taatgttgga gaaaaagaga  
1016  
Arg

aaaatgattc tggagaggga agccaagtaa tttatgtgag agtctttaat ttaactttat  
1076

tttcttggtt agataatgtg taatgatggt ttttaaagcc aaagactctc catggttggt  
1136

ggagcgagtt tg  
1148

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168

Met Asp Ser Asp Ile Met Asn Met Met Met His Gln Met Glu Lys Leu  
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20 25 30

Asn Thr Tyr Pro Phe Leu Phe Asn Ser Thr His Tyr Gln Ser Asp His  
35 40 45

Ser Met Thr Asn Glu Pro Gly Phe Arg Tyr Gly Ser Gly Leu Leu Thr  
50 55 60

Asn Pro Ser Ser Ile Ser Pro Asn Thr Ala Tyr Ser Ser Val Phe Leu  
65 70 75 80

Asp Lys Arg Asn Asn Ser Asn Asn Asn Asn Gly Thr Asn Met Ala  
85 90 95

Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His  
100 105 110



Ile Asp Pro Glu Ala Val Lys Pro Pro Lys Arg Arg Asn Val Arg Ile  
 115 120 125

Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile  
 130 135 140

Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys  
 145 150 155 160

Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe  
 165 170 175

Leu Lys Lys Gln Val Gln Ser Leu Glu Glu Gln Ala Val Val Thr Gly  
 180 185 190

Gly Gly Gly Gly Gly Gly Gly Arg Val Leu Ile Gly Gly Gly Gly Met  
 195 200 205

Thr Ala Ala Ser Gly Gly Gly Gly Gly Gly Gly Val Val Met Lys Gly  
 210 215 220

Cys Gly Thr Val Gly Thr His Gln Met Val Gly Asn Ala Gln Ile Leu  
 225 230 235 240

Arg

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 117

Met Gln Lys Pro  
 1

aca tca agt atc tta aat gtc ata atg gac ggt gga gac agc gtc gga  
 165  
 Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly Asp Ser Val Gly  
 5 10 15 20

gga gga gga gga gat gat cac cac cgt cac ctc cac cat cac cac cgc  
 213  
 Gly Gly Gly Gly Asp Asp His His Arg His Leu His His His His Arg  
 25 30 35

cct act ttc cct ttt caa cta ctc gga aaa cac gac ccc gac gac aac  
 261  
 Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp Pro Asp Asp Asn



40	45	50
cat caa caa caa cct tcc cct tcc tcc tcc tcc tct cta ttt tct ctc		
309		
His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser Ser Leu Phe Ser Leu		
55	60	65
cat caa cac caa caa tta tct caa tcg caa cct caa tcg caa tcg caa		
357		
His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln Ser Gln Ser Gln		
70	75	80
aag tca caa ccg cag aca acg caa aaa gag tta tta caa acg caa gag		
405		
Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu Gln Thr Gln Glu		
85	90	95
gaa tct gcg gtg gtg gca gct aaa aag cca ccg ttg aaa cga gcg tcg		
453		
Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu Lys Arg Ala Ser		
105	110	115
acg aaa gac cga cac acg aaa gta gac gga aga ggg agg aga ata agg		
501		
Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly Arg Arg Ile Arg		
120	125	130
atg ccg gcg tta tgt gca gct agg gtt ttt cag cta acg cga gag cta		
549		
Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu		
135	140	145
ggt cat aaa tcc gac ggt gag aca ata gag tgg ctt ctt caa caa gct		
597		
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala		
150	155	160
gaa cca tct gta atc gcc gcc acc gga acc gga aca atc ccg gcg aat		
645		
Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn		
165	170	175
ttc act tct tta aac atc tct ctc cgt tct tca ggc tct tcc atg tct		
693		
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly Ser Ser Met Ser		
185	190	195
ctt cct tct cat ttc cgc tcc gcc gct tcc act ttt agc cct aat aac		
741		
Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe Ser Pro Asn Asn		
200	205	210
ata ttt tct ccg gcg atg ctt caa caa caa caa caa caa caa cgt ggt		
789		
Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln Gln Gln Arg Gly		
215	220	225
ggt ggt gtt ggg ttt cat cat ccc cat cta cag gga cgt gca cct acg		
837		
Gly Gly Val Gly Phe His His Pro His Leu Gln Gly Arg Ala Pro Thr		
230	235	240



tcg tct ttg ttt cct ggt att gat aac ttc aca cca acg acg tcg ttt  
 885  
 Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro Thr Thr Ser Phe  
 245 250 255 260  
 ttg aac ttt cat aat cca aca aag caa gaa gga gat caa gat tct gaa  
 933  
 Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp Gln Asp Ser Glu  
 265 270 275  
 gag tta aac tcg gag aag aaa aga aga atc caa acg acg tcg gat ttg  
 981  
 Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr Thr Ser Asp Leu  
 280 285 290  
 cat caa caa caa caa caa cac caa cat gat caa atc gga gga tat aca  
 1029  
 His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile Gly Gly Tyr Thr  
 295 300 305  
 ctt caa tct agc aac agt gga tct acg gcc acc gca gcc gcc gcg caa  
 1077  
 Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala Ala Ala Ala Gln  
 310 315 320  
 caa ata ccg gga aat ttc tgg atg gtt gcg gcg gct gcg gct gca ggt  
 1125  
 Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala Ala Ala Ala Gly  
 325 330 335 340  
 ggt ggt ggt ggt aat aac aac caa aca ggt ggt ctt atg aca gct tct  
 1173  
 Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu Met Thr Ala Ser  
 345 350 355  
 att ggt act ggt ggc ggc ggt gga gag cct gtt tgg acg ttt cct tcc  
 1221  
 Ile Gly Thr Gly Gly Gly Gly Gly Glu Pro Val Trp Thr Phe Pro Ser  
 360 365 370  
 att aac acg gca gcg gca gcg tta tat aga agt ggc gtt tcg ggc gtt  
 1269  
 Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly Val Ser Gly Val  
 375 380 385  
 cca agc ggc gcg gtt tct agc ggt tta cat ttt atg aat ttc gca gcg  
 1317  
 Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met Asn Phe Ala Ala  
 390 395 400  
 cca atg gca ttt ctt act gga caa caa cag cta gca aca act agt aat  
 1365  
 Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala Thr Thr Ser Asn  
 405 410 415 420  
 cat gag att aat gaa gat agt aat aat aat gaa gga gga aga agt gac  
 1413  
 His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly Gly Arg Ser Asp  
 425 430 435



ggt ggt ggt gat cat cat aat aca cag aga cat cat cat cat caa caa  
1461

Gly Gly Gly Asp His His Asn Thr Gln Arg His His His His Gln Gln  
440 445 450

caa cat cat cat aat att ctc tcc ggc ttg aac cag tac gga cgg caa  
1509

Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln Tyr Gly Arg Gln  
455 460 465

ggt tcc ggc gac tct caa gct agt gga tca ctt gga ggt ggt gat gag  
1557

Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly Gly Gly Asp Glu  
470 475 480

gag gat cag caa gat tag acacacacaa aaacatttta atggtgggat  
1605

Glu Asp Gln Gln Asp  
485

tttctgccga cggcggtagc ggtgacggcg ttcggcggct gtgtaaaact tttgttttca  
1665

ccgttaattt tttttatttt ctgtagtaat tttttttgct aagtaaaaaa aaaaaaaaaa  
1725

aaa  
1728

<210> 170 <211> 489 <212> PRT <213> Arabidopsis thaliana <400>  
170

Met Gln Lys Pro Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly  
1 5 10 15

Asp Ser Val Gly Gly Gly Gly Gly Asp Asp His His Arg His Leu His  
20 25 30

His His His Arg Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp  
35 40 45

Pro Asp Asp Asn His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser  
50 55 60

Leu Phe Ser Leu His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln  
65 70 75 80

Ser Gln Ser Gln Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu  
85 90 95

Gln Thr Gln Glu Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu  
100 105 110



Lys Arg Ala Ser Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly  
115 120 125

Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu  
130 135 140

Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu  
145 150 155 160

Leu Gln Gln Ala Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr  
165 170 175

Ile Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly  
180 185 190

Ser Ser Met Ser Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe  
195 200 205

Ser Pro Asn Asn Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln  
210 215 220

Gln Gln Arg Gly Gly Gly Val Gly Phe His His Pro His Leu Gln Gly  
225 230 235 240

Arg Ala Pro Thr Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro  
245 250 255

Thr Thr Ser Phe Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp  
260 265 270

Gln Asp Ser Glu Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr  
275 280 285

Thr Ser Asp Leu His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile  
290 295 300

Gly Gly Tyr Thr Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala  
305 310 315 320

Ala Ala Ala Gln Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala  
325 330 335

Ala Ala Ala Gly Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu  
340 345 350

Met Thr Ala Ser Ile Gly Thr Gly Gly Gly Gly Gly Glu Pro Val Trp



355                      360                      365  
 Thr Phe Pro Ser Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly  
 370                      375                      380  
 Val Ser Gly Val Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met  
 385                      390                      395                      400  
 Asn Phe Ala Ala Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala  
 405                      410                      415  
 Thr Thr Ser Asn His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly  
 420                      425                      430  
 Gly Arg Ser Asp Gly Gly Gly Asp His His Asn Thr Gln Arg His His  
 435                      440                      445  
 His His Gln Gln Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln  
 450                      455                      460  
 Tyr Gly Arg Gln Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly  
 465                      470                      475                      480  
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 atgcaaagaa gaagctactt ctttctcttg cctaattaa tctacctaac tagggtttcc  
 120  
 tcttaccttt catgagagag atcatttaac ataagtcacc tttttatat cttttgcttc  
 180  
 gtctttaatt tagttctgtt cttggtctgt ttctatattt tgtcggttg cgtaaccgat  
 240  
 cacaccttaa tgctttagct attgtttcct caaaatcatg agttttgact tctcgatctg  
 300  
 agttttcttt ttctctcttt acgctcttct tcacctagct accaatatat gaacgagcag  
 360  
 gatcaagaat cgagaaattg atttgagctg gcgaataagc agtggtggga tagggaatta  
 420



gtagatgcgg cggcgc atg gaa ggc ggt tac gag caa ggc ggt gga gct tct  
471

Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser  
1 5 10

aga tac ttc cat aac ctc ttt aga ccg gag att cac cac caa cag ctt  
519

Arg Tyr Phe His Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu  
15 20 25

caa ccg cag ggc ggg atc aat ctt atc gac cag cat cat cat cag cac  
567

Gln Pro Gln Gly Gly Ile Asn Leu Ile Asp Gln His His His Gln His  
30 35 40

cag caa cat caa caa caa caa ccg tcg gat gat tca aga gaa tct  
615

Gln Gln His Gln Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser  
45 50 55 60

gac cat tca aac aaa gat cat cat caa cag ggt cga ccc gat tca gac  
663

Asp His Ser Asn Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp  
65 70 75

ccg aat aca tca agc tca gca ccg gga aaa cgt cca cgt gga cgt cca  
711

Pro Asn Thr Ser Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro  
80 85 90

cca gga tct aag aac aaa gcc aag cca ccg atc ata gta act cgt gat  
759

Pro Gly Ser Lys Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp  
95 100 105

agc ccc aac gcg ctt aga tct cac gtt ctt gaa gta tct cct gga gct  
807

Ser Pro Asn Ala Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala  
110 115 120

gac ata gtt gag agt gtt tcc acg tac gct agg agg aga ggg aga ggc  
855

Asp Ile Val Glu Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly  
125 130 135 140

gtc tcc gtt tta gga gga aac ggc acc gta tct aac gtc act ctc cgt  
903

Val Ser Val Leu Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg  
145 150 155

cag cca gtc act cct gga aat ggc ggt ggt gtg tcc gga gga gga gga  
951

Gln Pro Val Thr Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Gly  
160 165 170

gtt gtg act tta cat gga agg ttt gag att ctt tcg cta acg ggg act  
999

Val Val Thr Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr  
175 180 185



gtt ttg cca cct cct gca ccg cct ggt gcc ggt ggt ttg tct ata ttt  
1047

Val Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe  
190 195 200

tta gcc gga ggg caa ggt cag gtg gtc gga gga agc gtt gtg gct ccc  
1095

Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro  
205 210 215 220

ctt att gca tca gct ccg gtt ata cta atg gcg gct tcg ttc tca aat  
1143

Leu Ile Ala Ser Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn  
225 230 235

gcg gtt ttc gag aga cta ccg att gag gag gag gaa gaa gaa ggt ggt  
1191

Ala Val Phe Glu Arg Leu Pro Ile Glu Glu Glu Glu Glu Glu Gly Gly  
240 245 250

ggt ggc gga gga gga gga gga gga gga cca ccg cag atg caa caa gct  
1239

Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala  
255 260 265

cca tca gca tct ccg ccg tct gga gtg acc ggt cag gga cag tta gga  
1287

Pro Ser Ala Ser Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly  
270 275 280

ggt aat gtg ggt ggt tat ggg ttt tct ggt gat cct cat ttg ctt gga  
1335

Gly Asn Val Gly Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly  
285 290 295 300

tgg gga gct gga aca cct tca aga cca cct ttt taa ttgaatttta  
1381

Trp Gly Ala Gly Thr Pro Ser Arg Pro Pro Phe  
305 310

atgtccggaa atttatgtgt ttttatcatc ttgaggagtc gtctttcctt tgggatattt  
1441

ggtgtttaat gtttagttga tatgcatatt tt  
1473

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172

Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser Arg Tyr Phe His  
1 5 10 15

Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu Gln Pro Gln Gly  
20 25 30

Gly Ile Asn Leu Ile Asp Gln His His His Gln His Gln Gln His Gln  
35 40 45



Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser Asp His Ser Asn  
 50 55 60

Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp Pro Asn Thr Ser  
 65 70 75 80

Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys  
 85 90 95

Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp Ser Pro Asn Ala  
 100 105 110

Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala Asp Ile Val Glu  
 115 120 125

Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly Val Ser Val Leu  
 130 135 140

Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg Gln Pro Val Thr  
 145 150 155 160

Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Gly Val Val Thr Leu  
 165 170 175

His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr Val Leu Pro Pro  
 180 185 190

Pro Ala Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe Leu Ala Gly Gly  
 195 200 205

Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro Leu Ile Ala Ser  
 210 215 220

Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn Ala Val Phe Glu  
 225 230 235 240

Arg Leu Pro Ile Glu Glu Glu Glu Glu Glu Gly Gly Gly Gly Gly Gly  
 245 250 255

Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala Pro Ser Ala Ser  
 260 265 270

Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly Gly Asn Val Gly  
 275 280 285



Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly Trp Gly Ala Gly  
 290 295 300

Thr Pro Ser Arg Pro Pro Phe  
 305 310

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 <221> CDS <222> (170)..(1144) <223> G1070

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gttttgacag caaaataaga agcaaaaaaa aggtcaacta aaaaagatct gttcttagat  
 120

cactctcttc ttcttttttt gatccaattc caccattgaa tcatagatc atg.gat cca  
 178

Met Asp Pro  
 1

gta caa tct cat gga tca caa agc tct cta cct cct cct ttc cac gca  
 226

Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro Phe His Ala  
 5 10 15

aga gac ttt caa tta cat ctt caa caa cag caa caa gag ttc ttc ctc  
 274

Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln Glu Phe Phe Leu  
 20 25 30 35

cac cat cac cag caa caa aga aac caa acc gat ggt gac caa caa gga  
 322

His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp Gln Gln Gly  
 40 45 50

gga tca gga gga aac cga caa atc aag atg gat cgt gaa gag aca agc  
 370

Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu Glu Thr Ser  
 55 60 65

gac aac ata gac aac ata gct aac aac agc ggt agt gaa ggt aaa gac  
 418

Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu Gly Lys Asp  
 70 75 80

ata gat ata cac ggt ggt tca gga gaa gga ggt ggt ggc tcc gga gga  
 466

Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly Ser Gly Gly  
 85 90 95

gat cat cag atg aca aga aga cca aga gga aga cca gcg gga tcc aag  
 514

Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys  
 100 105 110 115

aac aaa cca aaa cca ccg att atc atc aca cgg gac agc gca aac gcg  
 562

Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala



	120		125		130
ctt aga acc cac gtg atg gag atc gga gat ggc tgc gac tta gtc gaa					
610					
Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Leu Val Glu					
	135		140		145
agc gtt gcc act ttt gca cga aga cgc caa cgc ggc gtt tgc gtt atg					
658					
Ser Val Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met					
	150		155		160
agc ggt act gga aat gtt act aac gtc act ata cgt cag cct gga tct					
706					
Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser					
	165		170		175
cat cct tct cct ggc tgc gta gtt agt ctt cac gga agg ttc gag att					
754					
His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile					
	180		185		190
cta tct ctc tca gga tct ttt ctc cct cct ccg gct cct cct aca gcc					
802					
Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Thr Ala					
	200		205		210
acc gga ttg agt gtt tac ctc gct gga gga caa gga cag gtg gtt gga					
850					
Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly					
	215		220		225
gga agc gta gtt ggt ccg ttg tta tgt gct ggt cct gtc gtt gtc atg					
898					
Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val Val Val Met					
	230		235		240
gct gcg tct ttt agc aat gcg gcg tac gaa agg ttg cct tta gag gaa					
946					
Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu					
	245		250		255
gat gag atg cag acg ccg gtt cat ggc gga gga gga gga tca ttg					
994					
Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly Gly Ser Leu					
	260		265		270
gag tgc ccg cca atg atg gga caa caa ctg caa cat cag caa caa gct					
1042					
Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln Gln Gln Ala					
	280		285		290
atg tca ggt cat caa ggg tta cca cct aat ctt ctt ggt tgc gtt cag					
1090					
Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln					
	295		300		305
ttg cag cag caa cat gat cag tct tat tgg tca acg gga cga cca ccg					
1138					
Leu Gln Gln Gln His Asp Gln Ser Tyr Trp Ser Thr Gly Arg Pro Pro					
	310		315		320



tat tga tcaaataac acacacactc ataatcgttg ctagctagct aacgatgaat  
 1194  
 Tyr

catgagttta gtggatatat atatgattaa aagagggttag cttatgaaca ttaataagag  
 1254

tttgattct atcgagcttc attatgtttg ggtcatcggt c  
 1295

<210> 174 <211> 324 <212> PRT <213> Arabidopsis thaliana <400>  
 174

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro  
 1 5 10 15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Glu  
 20 25 30

Phe Phe Leu His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp  
 35 40 45

Gln Gln Gly Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu  
 50 55 60

Glu Thr Ser Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu  
 65 70 75 80

Gly Lys Asp Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly  
 85 90 95

Ser Gly Gly Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala  
 100 105 110

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser  
 115 120 125

Ala Asn Ala Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp  
 130 135 140

Leu Val Glu Ser Val Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val  
 145 150 155 160

Cys Val Met Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln  
 165 170 175

Pro Gly Ser His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg



180                      185                      190  
 Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro  
                     195                      200                      205  
 Pro Thr Ala Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln  
                     210                      215                      220  
 Val Val Gly Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val  
                     225                      230                      235                      240  
 Val Val Met Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro  
                     245                      250                      255  
 Leu Glu Glu Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly  
                     260                      265                      270  
 Gly Ser Leu Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln  
                     275                      280                      285  
 Gln Gln Ala Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly  
                     290                      295                      300  
 Ser Val Gln Leu Gln Gln Gln His Asp Gln Ser Tyr Trp Ser Thr Gly  
                     305                      310                      315                      320  
 Arg Pro Pro Tyr

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                     Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg  
                     1                      5                      10  
 tac gtc cac aac gtc gat ggt ggc ggc ggc gga cag ttc acc acc gac  
 99  
 Tyr Val His Asn Val Asp Gly Gly Gly Gly Gly Gln Phe Thr Thr Asp  
                     15                      20                      25  
 aac cac cac gaa gat gac ggt ggc gct gga gga aac cac cat cat cac  
 147  
 Asn His His Glu Asp Asp Gly Gly Ala Gly Gly Asn His His His His  
                     30                      35                      40  
 cat cat aat cat aat cac cat caa ggt tta gat tta ata gct tct aat  
 195  
 His His Asn His Asn His His Gln Gly Leu Asp Leu Ile Ala Ser Asn



45	50	55
gat aac tct gga cta ggc ggc ggt gga gga gga ggg agc ggt gac ctc		
243		
Asp Asn Ser Gly Leu Gly Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu	65	70 75
60		
gtc atg cgt cgg cca cgt ggc cgt cca gct gga tog aag aac aaa ccg		
291		
Val Met Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro	80	85 90
aag ccg ccg gtg att gtc acg cgc gag agc gca aac act ctt agg gct		
339		
Lys Pro Pro Val Ile Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala	95	100 105
cac att ctt gaa gtt gga agt ggc tgc gac gtt ttc gaa tgt atc tcc		
387		
His Ile Leu Glu Val Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser	110	115 120
act tac gct cgt cgg aga cag cgc ggg att tgc gtt tta tcc ggg acg		
435		
Thr Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr	125	130 135
gga acc gtc act aac gtc agc atc cgt cag cct acg gcg gcc gga gct		
483		
Gly Thr Val Thr Asn Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala	140	145 150 155
gtt gtg act ctg cgg ggt act ttt gag att ctt tcc ctc tcc gga tct		
531		
Val Val Thr Leu Arg Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser	160	165 170
ttt ctt ccg cca cct gct cct cca ggg gcg act agc ttg acg ata ttc		
579		
Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe	175	180 185
ctc gct gga gct caa gga cag gtc gtc gga ggt aac gta gtt ggt gag		
627		
Leu Ala Gly Ala Gln Gly Gln Val Val Gly Gly Asn Val Val Gly Glu	190	195 200
tta atg gcg gcg ggg ccg gta atg gtc atg gca gcg tct ttt aca aac		
675		
Leu Met Ala Ala Gly Pro Val Met Val Met Ala Ala Ser Phe Thr Asn	205	210 215
gtg gct tac gaa agg ttg cct ttg gac gag cat gag gag cac ttg caa		
723		
Val Ala Tyr Glu Arg Leu Pro Leu Asp Glu His Glu Glu His Leu Gln	220	225 230 235
agt ggc ggc ggc gga ggt gga ggg aat atg tac tog gaa gcc act ggc		
771		
Ser Gly Gly Gly Gly Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly	240	245 250



ggt ggc gga ggg ttg cct ttc ttt aat ttg ccg atg agt atg cct cag  
819

Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Ser Met Pro Gln  
255 260 265

att gga gtt gaa agt tgg cag ggg aat cac gcc ggc gcc ggt agg gct  
867

Ile Gly Val Glu Ser Trp Gln Gly Asn His Ala Gly Ala Gly Arg Ala  
270 275 280

ccg ttt tag caatttaaga aactttaatt gttttttcca cttttttgtt  
916

Pro Phe  
285

tttctccgaa ttttatgaaa ttatgattta agaaaaaaaa cgatattgtt catgtattga  
976

ccctcttact gcatggttgc ttctattggg ttaattggct agctcataag aattgtttaa  
1036

tttggttatt gtcacaaat ttgcccacat ataaagcttc tagcaaat  
1084

<210> 176 <211> 285 <212> PRT <213> Arabidopsis thaliana <400>  
176

Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg Tyr Val His Asn Val  
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Asp Gly Gly Gly Gly Gly Gln Phe Thr Thr Asp Asn His His Glu Asp  
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Asp Gly Gly Ala Gly Gly Asn His His His His His Asn His Asn  
35 40 45

His His Gln Gly Leu Asp Leu Ile Ala Ser Asn Asp Asn Ser Gly Leu  
50 55 60

Gly Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu Val Met Arg Arg Pro  
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Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Ile  
85 90 95

Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His Ile Leu Glu Val  
100 105 110

Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser Thr Tyr Ala Arg Arg  
115 120 125



Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr Gly Thr Val Thr Asn  
130 135 140

Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala Val Val Thr Leu Arg  
145 150 155 160

Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro  
165 170 175

Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu Ala Gly Ala Gln  
180 185 190

Gly Gln Val Val Gly Gly Asn Val Val Gly Glu Leu Met Ala Ala Gly  
195 200 205

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210 215 220

Leu Pro Leu Asp Glu His Glu Glu His Leu Gln Ser Gly Gly Gly Gly  
225 230 235 240

Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly Gly Gly Gly Gly Leu  
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102

Glu Asn Glu Glu Ala Val Thr Arg Cys Lys Glu Arg Lys Gln Leu Met  
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aaa gac gcc gtc act gct cgt aac gct ttc gcc gcc gct cac tca gct  
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Lys Asp Ala Val Thr Ala Arg Asn Ala Phe Ala Ala Ala His Ser Ala  
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198



Tyr Ala Met Ala Leu Lys Asn Thr Gly Ala Ala Leu Ser Asp Tyr Ser  
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 His Gly Glu Phe Leu Val Ser Asn His Ser Ser Ser Ser Ala Ala Ala  
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 Pro Ser Ser Thr Ala Pro Val Ser Asn Ser Thr Ala Ser Ser Ser Ser  
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 Gly Arg Ser Gly Gly Gly His Ala Gly Ser Gly Leu Asn Gly Ile Glu  
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 Glu Asp Gly Ala Leu Asp Asn Asp Asp Asp Asp Asp Asp Asp Asp  
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1446

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1494

Gly Gly His Ser Asp Ser Leu Glu Arg Ala Lys Ala Val Ser His  
475 480 485

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1542

Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser Met Asp Ser Thr Val  
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1590

Ser Glu Ile Asn Arg Leu Arg Asp Glu Gln Leu Tyr Leu Lys Leu Val  
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cac ctt gtt gag gcg atg ggg aag atg tgg gaa atg atg caa ata cat  
1638

His Leu Val Glu Ala Met Gly Lys Met Trp Glu Met Met Gln Ile His  
525 530 535

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1686

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1734

Ser Gln Ala Val Lys Glu Thr Asn Asp His His His Glu Arg Thr Ile  
555 560 565

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Gln Leu Leu Ala Val Val Gln Glu Trp His Thr Gln Phe Cys Arg Met  
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1830

Ile Asp His Gln Lys Glu Tyr Ile Lys Ala Leu Gly Gly Trp Leu Lys  
585 590 595 600

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1878

Leu Asn Leu Ile Pro Ile Glu Ser Thr Leu Lys Glu Lys Val Ser Ser  
605 610 615

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1926

Pro Pro Arg Val Pro Asn Pro Ala Ile Gln Lys Leu Leu His Ala Trp  
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tat gac cgt tta gac aaa atc ccc gac gaa atg gct aaa agt gcc ata  
1974

Tyr Asp Arg Leu Asp Lys Ile Pro Asp Glu Met Ala Lys Ser Ala Ile  
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2070

Glu Ile Ser Leu Arg Asn Lys Cys Glu Glu Thr Arg Lys Glu Leu Gly  
665 670 675 680

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2118

Arg Lys Ile Arg Gln Phe Glu Asp Trp Tyr His Lys Tyr Ile Gln Lys  
685 690 695

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2166

Arg Gly Pro Glu Gly Met Asn Pro Asp Glu Ala Asp Asn Asp His Asn  
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Glu Lys Ser Leu Ala Ser Leu Arg Thr Arg Leu Pro Glu Leu Phe Gln  
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Ala Met Ser Glu Val Ala Tyr Ser Cys Ser Asp Met Tyr Arg Ala Ile  
765 770 775

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His Ser Ser Ser Ser Ala Ala Ala Ala Ile Ala Ser Thr Ser Ser Leu  
65 70 75 80

Pro Thr Ala Ile Ser Pro Pro Leu Pro Ser Ser Thr Ala Pro Val Ser  
85 90 95

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115 120 125

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Arg Thr Thr Ile Glu Asp His His Leu Gln Glu Glu Lys Ala Pro Pro  
195 200 205



Pro Pro Pro Leu Ala Asn Ser Arg Pro Ile Pro Pro Pro Arg Gln His  
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Val Lys Ala Gly Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ala  
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Arg Ala Lys Ala Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp  
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Met Trp Glu Met Met Gln Ile His His Gln Arg Gln Ala Glu Ile Ser  
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Asp His His His Glu Arg Thr Ile Gln Leu Leu Ala Val Val Gln Glu  
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Trp His Thr Gln Phe Cys Arg Met Ile Asp His Gln Lys Glu Tyr Ile  
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Lys Ala Leu Gly Gly Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser  
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Thr Leu Lys Glu Lys Val Ser Ser Pro Pro Arg Val Pro Asn Pro Ala  
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Glu Glu Thr Arg Lys Glu Leu Gly Arg Lys Ile Arg Gln Phe Glu Asp  
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Trp Tyr His Lys Tyr Ile Gln Lys Arg Gly Pro Glu Gly Met Asn Pro



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 Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe  
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 Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg  
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 Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His  
 85                      90                      95



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336

Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val  
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384

Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser  
115 120 125

aag aac tct caa gaa tgc tct gtt tgt tta aac gag ttt caa gaa gac  
432

Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp  
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480

Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp  
145 150 155 160

tgc att gat atc tgg ctt cag ggc aac gca aat tgt ccc ttg tgc aga  
528

Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg  
165 170 175

acc agc gtt tct tgc gaa gca agt ttc act ctt gac cta atc tct gca  
576

Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala  
180 185 190

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624

Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu  
195 200 205

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672

Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu  
210 215 220

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720

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225 230 235 240

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768

Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly  
245 250 255

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816

Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg  
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Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly  
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Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe  
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Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg  
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Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His  
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Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val  
 100 105 110



Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser  
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 Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu  
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 Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu  
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 Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile  
 20 25 30

cgt tca gct cca gcg act tgg ctt gaa gct tta ctt gag gaa gat gaa  
 204  
 Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu  
 35 40 45

gaa gag tct ttg aaa cct aat ctt ggt ctc acc gat ttg ctt acc ggg  
 252  
 Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly  
 50 55 60

aac tcg aac gat tta ccg aca agt cgc ggc tcg ttc gag ttc ccg att  
 300  
 Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile  
 65 70 75 80

cct gtt gag caa ggg ttg tat caa caa ggt ggg ttt cac cga cag aat  
 348  
 Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn  
 85 90 95

agt act ccg gcg gat ttt ctt agt ggt tct gat gga ttt atc caa agc  
 396  
 Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser  
 100 105 110

ttt ggg att cag gcg aat tac gat tac tta tcg ggg aat atc gat gtt  
 444  
 Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val  
 115 120 125

tct ccg gga agt aag ccg tct aga gaa atg gaa gca ctc ttc tct tct  
 492  
 Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser  
 130 135 140



cct gag ttt act tct caa atg aaa gga gag caa agc agc ggt caa gtt  
540

Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val  
145 150 155 160

cct acc gga gta tca agc atg tcg gat atg aac atg gag aac ctt atg  
588

Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met  
165 170 175

gag gac tct gtt gct ttt agg gtt cgg gct aaa cgt ggt tgc gca act  
636

Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr  
180 185 190

cat ccc cgc agc att gcc gag agg gta cga agg acg cgg att agt gat  
684

His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp  
195 200 205

cgg ata agg aag cta caa gag ctt gta cct aac atg gac aag caa acc  
732

Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr  
210 215 220

aac act gca gac atg tta gaa gaa gca gta gaa tac gtg aaa gtt ctt  
780

Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu  
225 230 235 240

caa agg cag atc cag gag tta aca gaa gaa cag aag agg tgc aca tgc  
828

Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys  
245 250 255

ata cct aag gaa gaa caa taa ggtttgctcc tgatttggtt tatatttgct  
879

Ile Pro Lys Glu Glu Gln  
260

taacggcaat gatctgatcg aaaaattcga aagatgatct tagcttgaat ttagatggat  
939

gtcatgttga aaagtatatt atttgataaa tggatgtagg tgtaataataa aatttttgta  
999

caataatgaa gaaagttaaa aagaattaat gaaaacatat attctttatg atataaaaaa  
1059

aaaaa  
1064

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182

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1 5 10 15

Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile



20	25	30
Arg Ser Ala Pro Ala Thr Trp 35	Leu Glu Ala Leu Leu 40	Glu Glu Asp Glu 45
Glu Glu Ser Leu Lys Pro Asn 50	Leu Gly Leu Thr 55	Asp Leu Leu Thr Gly 60
Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile 65	70	75 80
Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn 85	90	95
Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser 100	105	110
Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val 115	120	125
Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser 130	135	140
Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val 145	150	155 160
Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met 165	170	175
Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr 180	185	190
His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp 195	200	205
Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr 210	215	220
Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu 225	230	235 240
Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys 245	250	255
Ile Pro Lys Glu Glu Gln 260		



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acc tca gat cag atg ttg tac tcg ttt ctt gcc gga aac gaa gtc ggc  
 105  
 Thr Ser Asp Gln Met Leu Tyr Ser Phe Leu Ala Gly Asn Glu Val Gly  
 5 10 15 20

ggt gga ggg tac tgc gtc tcc ggc gac tac atg acg act atg cag agc  
 153  
 Gly Gly Gly Tyr Cys Val Ser Gly Asp Tyr Met Thr Thr Met Gln Ser  
 25 30 35

tta tgt ggg tct tcg tcg tcg acg tca tcg tat tac cca ctg gcg atc  
 201  
 Leu Cys Gly Ser Ser Ser Ser Thr Ser Ser Tyr Tyr Pro Leu Ala Ile  
 40 45 50

tcc ggc atc gga gaa acg atg gct caa gac aga gct tta gct gct ttg  
 249  
 Ser Gly Ile Gly Glu Thr Met Ala Gln Asp Arg Ala Leu Ala Ala Leu  
 55 60 65

agg aac cac aaa gaa gct gag aga aga agg aga gag agg atc aat tct  
 297  
 Arg Asn His Lys Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn Ser  
 70 75 80

cat ctc aac aag ctt cgt aac gta ctc tct tgt aat tct aag acc gat  
 345  
 His Leu Asn Lys Leu Arg Asn Val Leu Ser Cys Asn Ser Lys Thr Asp  
 85 90 95 100

aaa gcc aca ctg ctc gcc aaa gta gtt caa cga gtc aga gaa ctt aaa  
 393  
 Lys Ala Thr Leu Leu Ala Lys Val Val Gln Arg Val Arg Glu Leu Lys  
 105 110 115

cag caa acc cta gag acc tcc gac tcc gac caa aca tta tta cca tca  
 441  
 Gln Gln Thr Leu Glu Thr Ser Asp Ser Asp Gln Thr Leu Leu Pro Ser  
 120 125 130

gag acc gac gaa att agt gtt cta cac ttt gga gac tat tca aac gac  
 489  
 Glu Thr Asp Glu Ile Ser Val Leu His Phe Gly Asp Tyr Ser Asn Asp  
 135 140 145

ggt cat ata atc ttc aaa gcc tct cta tgt tgt gaa gat aga tca gat  
 537  
 Gly His Ile Ile Phe Lys Ala Ser Leu Cys Cys Glu Asp Arg Ser Asp  
 150 155 160



ctc ttg ccg gac ctt atg gag att ctc aag tct ctt aac atg aag act  
585

Leu Leu Pro Asp Leu Met Glu Ile Leu Lys Ser Leu Asn Met Lys Thr  
165 170 175 180

ctc cga gct gag atg gta acc att ggt ggt cgg aca aga agt gtt ctt  
633

Leu Arg Ala Glu Met Val Thr Ile Gly Gly Arg Thr Arg Ser Val Leu  
185 190 195

gtc gta gct gct gac aaa gag atg cac ggc gtc gag tct gtg cat ttt  
681

Val Val Ala Ala Asp Lys Glu Met His Gly Val Glu Ser Val His Phe  
200 205 210

ttg caa aat gct ctc aag tcg ctg ctt gag cgg tca agc aag tcg ttg  
729

Leu Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Leu  
215 220 225

atg gaa cgt agt tct ggt ggt gga gga gga gaa cgg tca aag cgg cgt  
777

Met Glu Arg Ser Ser Gly Gly Gly Gly Gly Glu Arg Ser Lys Arg Arg  
230 235 240

cgt gcg ctg gat cac atc ata atg gtg tga aatgatgaga attgagcaca  
827

Arg Ala Leu Asp His Ile Ile Met Val  
245 250

ctaaaaagtc tataattgat taatatatat agggatatgat cataattaac ttgggtataa  
887

ttacccaaaac cttttttatt cctctttaat aatatatatg ttatatggtt ttagttacta  
947

agtcttgga gtgtaagcaa atgttgtaag taggtttggt gtgttctttt tcttttcttt  
1007

tttttttctt tttcaaaaaa aaaaaaaaaa  
1037

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184

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1 5 10 15

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20 25 30

Thr Met Gln Ser Leu Cys Gly Ser Ser Ser Ser Thr Ser Ser Tyr Tyr  
35 40 45

Pro Leu Ala Ile Ser Gly Ile Gly Glu Thr Met Ala Gln Asp Arg Ala  
50 55 60



Leu Ala Ala Leu Arg Asn His Lys Glu Ala Glu Arg Arg Arg Arg Glu  
65 70 75 80

Arg Ile Asn Ser His Leu Asn Lys Leu Arg Asn Val Leu Ser Cys Asn  
85 90 95

Ser Lys Thr Asp Lys Ala Thr Leu Leu Ala Lys Val Val Gln Arg Val  
100 105 110

Arg Glu Leu Lys Gln Gln Thr Leu Glu Thr Ser Asp Ser Asp Gln Thr  
115 120 125

Leu Leu Pro Ser Glu Thr Asp Glu Ile Ser Val Leu His Phe Gly Asp  
130 135 140

Tyr Ser Asn Asp Gly His Ile Ile Phe Lys Ala Ser Leu Cys Cys Glu  
145 150 155 160

Asp Arg Ser Asp Leu Leu Pro Asp Leu Met Glu Ile Leu Lys Ser Leu  
165 170 175

Asn Met Lys Thr Leu Arg Ala Glu Met Val Thr Ile Gly Gly Arg Thr  
180 185 190

Arg Ser Val Leu Val Val Ala Ala Asp Lys Glu Met His Gly Val Glu  
195 200 205

Ser Val His Phe Leu Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser  
210 215 220

Ser Lys Ser Leu Met Glu Arg Ser Ser Gly Gly Gly Gly Glu Arg  
225 230 235 240

Ser Lys Arg Arg Arg Ala Leu Asp His Ile Ile Met Val  
245 250

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58

Met  
1

gga aac tat cgg tgg ccg tca aag cta tca aag tta tca ctc aga gca  
106

Gly Asn Tyr Arg Trp Pro Ser Lys Leu Ser Lys Leu Ser Leu Arg Ala



	5		10		15
aaa caa acg aat ctg tac cgc gtc att cta atc gcg atc ctc tgc gtc					
154					
Lys Gln Thr Asn Leu Tyr Arg Val Ile Leu Ile Ala Ile Leu Cys Val					
	20		25		30
acc ttt tac ttc gtc gga gta tgg caa cac tcc ggc aga gga atc tca					
202					
Thr Phe Tyr Phe Val Gly Val Trp Gln His Ser Gly Arg Gly Ile Ser					
	35		40		45
cgc tct tcc att tct aac cac gag ctc acg tcc gtg ccc tgc acg ttt					
250					
Arg Ser Ser Ile Ser Asn His Glu Leu Thr Ser Val Pro Cys Thr Phe					
	50		55		60
cct cac caa acc aca ccg att ctc aac ttc gcc tcc cgt cac aca gcc					
298					
Pro His Gln Thr Thr Pro Ile Leu Asn Phe Ala Ser Arg His Thr Ala					
		70		75	80
cct gac ctt cct ccg acg ata acg gac gcg cgt gtt gtt caa atc ccg					
346					
Pro Asp Leu Pro Pro Thr Ile Thr Asp Ala Arg Val Val Gln Ile Pro					
	85		90		95
tcg tgc ggc gtt gaa ttc tcg gag tac acg ccc tgc gag ttc gtg aat					
394					
Ser Cys Gly Val Glu Phe Ser Glu Tyr Thr Pro Cys Glu Phe Val Asn					
	100		105		110
cgg tct ttg aat ttc cca aga gag agg ctt ata tac aga gag aga cac					
442					
Arg Ser Leu Asn Phe Pro Arg Glu Arg Leu Ile Tyr Arg Glu Arg His					
	115		120		125
tgt ccg gaa aaa cac gag ata gtc agg tgt cgg att cca gcg ccg tac					
490					
Cys Pro Glu Lys His Glu Ile Val Arg Cys Arg Ile Pro Ala Pro Tyr					
	130		135		140
ggt tac agt tta cct ttt cgg tgg ccg gag agc cgt gac gtg gcg tgg					
538					
Gly Tyr Ser Leu Pro Phe Arg Trp Pro Glu Ser Arg Asp Val Ala Trp					
	150		155		160
ttt gct aac gtg ccg cat acg gaa cta acg gtg gag aag aag aat cag					
586					
Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn Gln					
	165		170		175
aac tgg gta agg tat gag aag gat agg ttt tta ttt cct ggt ggt ggt					
634					
Asn Trp Val Arg Tyr Glu Lys Asp Arg Phe Leu Phe Pro Gly Gly Gly					
	180		185		190
acg atg ttt cca cgt gga gct gat gct tac atc gac gag atc gga ccg					
682					
Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Glu Ile Gly Arg					
	195		200		205



ttg ata aat ctc aaa gat gga tca att cgg aca gcc att gat act gga  
 730  
 Leu Ile Asn Leu Lys Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr Gly  
 210 215 220 225  
 tgt ggg gta gcg agc ttt ggg gcg tat cta atg tcg agg aac ata gta  
 778  
 Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Met Ser Arg Asn Ile Val  
 230 235 240  
 acg atg tcg ttt gca cca aga gac aca cac gaa gct cag gtt cag ttc  
 826  
 Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln Phe  
 245 250 255  
 gca ctt gag aga gga gtc cct gcc atc ata gga gtg tta gcc tct att  
 874  
 Ala Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Val Leu Ala Ser Ile  
 260 265 270  
 agg ctc cca ttt ccg gcc aga gcc ttc gac att gct cat tgc tct cga  
 922  
 Arg Leu Pro Phe Pro Ala Arg Ala Phe Asp Ile Ala His Cys Ser Arg  
 275 280 285  
 tgt ctc att cct tgg ggc caa tac aac ggg acg tat ctc ata gaa gtg  
 970  
 Cys Leu Ile Pro Trp Gly Gln Tyr Asn Gly Thr Tyr Leu Ile Glu Val  
 290 295 300 305  
 gat agg gta ctg aga ccg ggg ggg tat tgg att ttg tcg gga ccg ccg  
 1018  
 Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro Pro  
 310 315 320  
 att aac tgg cag aga cac tgg aag ggt tgg gaa aga act aga gac gat  
 1066  
 Ile Asn Trp Gln Arg His Trp Lys Gly Trp Glu Arg Thr Arg Asp Asp  
 325 330 335  
 ctc aac tcg gag cag tct cag atc gag agg gtg gct agg agc ttg tgt  
 1114  
 Leu Asn Ser Glu Gln Ser Gln Ile Glu Arg Val Ala Arg Ser Leu Cys  
 340 345 350  
 tgg agg aaa ttg gtg cag aga gag gat ctt gcg gtt tgg cag aaa cct  
 1162  
 Trp Arg Lys Leu Val Gln Arg Glu Asp Leu Ala Val Trp Gln Lys Pro  
 355 360 365  
 acc aac cat gtt cac tgt aag cgc aat cgg ata gct tta gga cgc cct  
 1210  
 Thr Asn His Val His Cys Lys Arg Asn Arg Ile Ala Leu Gly Arg Pro  
 370 375 380 385  
 ccg ttc tgc cac ccg aca cta ccc aac cag ggc tgg tac act aag ctt  
 1258  
 Pro Phe Cys His Arg Thr Leu Pro Asn Gln Gly Trp Tyr Thr Lys Leu  
 390 395 400



gaa acc tgt ttg acg ccg ttg ccg gaa gta aca gga tct gag atc aaa  
 1306  
 Glu Thr Cys Leu Thr Pro Leu Pro Glu Val Thr Gly Ser Glu Ile Lys  
 405 410 415

gaa gta gcg ggt gga cag ttg gcg aga tgg cct gag aga ttg aat gct  
 1354  
 Glu Val Ala Gly Gly Gln Leu Ala Arg Trp Pro Glu Arg Leu Asn Ala  
 420 425 430

ctt cct ccg agg atc aaa agt gga agc ttg gaa ggg atc act gag gat  
 1402  
 Leu Pro Pro Arg Ile Lys Ser Gly Ser Leu Glu Gly Ile Thr Glu Asp  
 435 440 445

gaa ttt gtc agc aac aca gag aaa tgg cag aga aga gtg tct tac tac  
 1450  
 Glu Phe Val Ser Asn Thr Glu Lys Trp Gln Arg Arg Val Ser Tyr Tyr  
 450 455 460 465

aag aaa tat gac caa cag cta gcg gag acg gga aga tac aga aac ttt  
 1498  
 Lys Lys Tyr Asp Gln Gln Leu Ala Glu Thr Gly Arg Tyr Arg Asn Phe  
 470 475 480

ctc gac atg aac gct cat ctt gga ggt ttc gcc tca gcc tta gtc gat  
 1546  
 Leu Asp Met Asn Ala His Leu Gly Gly Phe Ala Ser Ala Leu Val Asp  
 485 490 495

gat cct gta tgg gtc atg aat gtt gtc ccc gtg gag gcc agt gtt aac  
 1594  
 Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala Ser Val Asn  
 500 505 510

acc ctt gga gtt atc tat gag cga gga ttg att gga acg tat caa aac  
 1642  
 Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr Tyr Gln Asn  
 515 520 525

tgg tgt gaa gca atg tca act tac cca agg aca tac gat ttc atc cat  
 1690  
 Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His  
 530 535 540 545

gcc gat tcg gtg ttc agt ctg tac aaa gac aga tgt gac atg gaa gat  
 1738  
 Ala Asp Ser Val Phe Ser Leu Tyr Lys Asp Arg Cys Asp Met Glu Asp  
 550 555 560

atc ttg cta gaa atg gac agg att cta aga cca aag gga agc gtg atc  
 1786  
 Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Lys Gly Ser Val Ile  
 565 570 575

atc aga gac gac att gat gtg cta acc aaa gtg aag aag att aca gat  
 1834  
 Ile Arg Asp Asp Ile Asp Val Leu Thr Lys Val Lys Lys Ile Thr Asp  
 580 585 590



gcg atg caa tgg gaa ggg agg ata gga gat cat gaa aac gga cct ctt  
1882

Ala Met Gln Trp Glu Gly Arg Ile Gly Asp His Glu Asn Gly Pro Leu  
595 600 605

gaa aga gag aag att ttg ttt ctt gtg aag gag tac tgg acc gca cct  
1930

Glu Arg Glu Lys Ile Leu Phe Leu Val Lys Glu Tyr Trp Thr Ala Pro  
610 615 620 625

gcg cct gat cag tca tca gat cct tga tcaagcttgg aataattcat  
1977

Ala Pro Asp Gln Ser Ser Asp Pro  
630

aaaatttgta gctccattct tttttcttca aatgttttgt acacactaat cgactttggg  
2037

ggaagaaga aacaaacacc cgctaaattg tttcaaaccg gagattcatt gcgactttgt  
2097

gagaaaatga actagagagt ttactacaaa  
2127

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186

Met Gly Asn Tyr Arg Trp Pro Ser Lys Leu Ser Lys Leu Ser Leu Arg  
1 5 10 15

Ala Lys Gln Thr Asn Leu Tyr Arg Val Ile Leu Ile Ala Ile Leu Cys  
20 25 30

Val Thr Phe Tyr Phe Val Gly Val Trp Gln His Ser Gly Arg Gly Ile  
35 40 45

Ser Arg Ser Ser Ile Ser Asn His Glu Leu Thr Ser Val Pro Cys Thr  
50 55 60

Phe Pro His Gln Thr Thr Pro Ile Leu Asn Phe Ala Ser Arg His Thr  
65 70 75 80

Ala Pro Asp Leu Pro Pro Thr Ile Thr Asp Ala Arg Val Val Gln Ile  
85 90 95

Pro Ser Cys Gly Val Glu Phe Ser Glu Tyr Thr Pro Cys Glu Phe Val  
100 105 110

Asn Arg Ser Leu Asn Phe Pro Arg Glu Arg Leu Ile Tyr Arg Glu Arg  
115 120 125

His Cys Pro Glu Lys His Glu Ile Val Arg Cys Arg Ile Pro Ala Pro



130                      135                      140  
 Tyr Gly Tyr Ser Leu Pro Phe Arg Trp Pro Glu Ser Arg Asp Val Ala  
 145                      150                      155                      160  
 Trp Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn  
 165                      170                      175  
 Gln Asn Trp Val Arg Tyr Glu Lys Asp Arg Phe Leu Phe Pro Gly Gly  
 180                      185                      190  
 Gly Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Glu Ile Gly  
 195                      200                      205  
 Arg Leu Ile Asn Leu Lys Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr  
 210                      215                      220  
 Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Met Ser Arg Asn Ile  
 225                      230                      235                      240  
 Val Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln  
 245                      250                      255  
 Phe Ala Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Val Leu Ala Ser  
 260                      265                      270  
 Ile Arg Leu Pro Phe Pro Ala Arg Ala Phe Asp Ile Ala His Cys Ser  
 275                      280                      285  
 Arg Cys Leu Ile Pro Trp Gly Gln Tyr Asn Gly Thr Tyr Leu Ile Glu  
 290                      295                      300  
 Val Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro  
 305                      310                      315                      320  
 Pro Ile Asn Trp Gln Arg His Trp Lys Gly Trp Glu Arg Thr Arg Asp  
 325                      330                      335  
 Asp Leu Asn Ser Glu Gln Ser Gln Ile Glu Arg Val Ala Arg Ser Leu  
 340                      345                      350  
 Cys Trp Arg Lys Leu Val Gln Arg Glu Asp Leu Ala Val Trp Gln Lys  
 355                      360                      365  
 Pro Thr Asn His Val His Cys Lys Arg Asn Arg Ile Ala Leu Gly Arg  
 370                      375                      380



Pro Pro Phe Cys His Arg Thr Leu Pro Asn Gln Gly Trp Tyr Thr Lys  
385 390 395 400

Leu Glu Thr Cys Leu Thr Pro Leu Pro Glu Val Thr Gly Ser Glu Ile  
405 410 415

Lys Glu Val Ala Gly Gly Gln Leu Ala Arg Trp Pro Glu Arg Leu Asn  
420 425 430

Ala Leu Pro Pro Arg Ile Lys Ser Gly Ser Leu Glu Gly Ile Thr Glu  
435 440 445

Asp Glu Phe Val Ser Asn Thr Glu Lys Trp Gln Arg Arg Val Ser Tyr  
450 455 460

Tyr Lys Lys Tyr Asp Gln Gln Leu Ala Glu Thr Gly Arg Tyr Arg Asn  
465 470 475 480

Phe Leu Asp Met Asn Ala His Leu Gly Gly Phe Ala Ser Ala Leu Val  
485 490 495

Asp Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala Ser Val  
500 505 510

Asn Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr Tyr Gln  
515 520 525

Asn Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile  
530 535 540

His Ala Asp Ser Val Phe Ser Leu Tyr Lys Asp Arg Cys Asp Met Glu  
545 550 555 560

Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Lys Gly Ser Val  
565 570 575

Ile Ile Arg Asp Asp Ile Asp Val Leu Thr Lys Val Lys Lys Ile Thr  
580 585 590

Asp Ala Met Gln Trp Glu Gly Arg Ile Gly Asp His Glu Asn Gly Pro  
595 600 605

Leu Glu Arg Glu Lys Ile Leu Phe Leu Val Lys Glu Tyr Trp Thr Ala  
610 615 620



Pro Ala Pro Asp Gln Ser Ser Asp Pro  
625 630

<210> 187 <211> 1604 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (123)..(1217) <223> G1229

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caaccataag acaaaacaac gaacgaggaa gagagagaga gaaggatata tctctaata  
120

cg atg cag gag ata ata ccg gat ttt ctt gaa gag tgt gaa ttt gtc  
167

Met	Gln	Glu	Ile	Ile	Pro	Asp	Phe	Leu	Glu	Glu	Cys	Glu	Phe	Val
1			5					10					15	

gac act tca cta gcc gga gat gat cta ttt gcc atc tta gag agt ctt  
215

Asp	Thr	Ser	Leu	Ala	Gly	Asp	Asp	Leu	Phe	Ala	Ile	Leu	Glu	Ser	Leu
			20					25						30	

gaa ggt gcc gga gag ata tct ccg aca gct gca tct aca cct aaa gat  
263

Glu	Gly	Ala	Gly	Glu	Ile	Ser	Pro	Thr	Ala	Ala	Ser	Thr	Pro	Lys	Asp
			35					40						45	

gga acc aca agt tcc aag gag tta gtt aag gat caa gat tat gaa aac  
311

Gly	Thr	Thr	Ser	Ser	Lys	Glu	Leu	Val	Lys	Asp	Gln	Asp	Tyr	Glu	Asn
			50				55					60			

tca tct cct aag agg aaa aag caa aga cta gaa acc agg aaa gaa gag  
359

Ser	Ser	Pro	Lys	Arg	Lys	Lys	Gln	Arg	Leu	Glu	Thr	Arg	Lys	Glu	Glu
			65				70					75			

gac gaa gaa gaa gaa gac gga gac gga gaa gca gaa gaa gat aat aag  
407

Asp	Glu	Glu	Glu	Glu	Asp	Gly	Asp	Gly	Glu	Ala	Glu	Glu	Asp	Asn	Lys
						85				90				95	

caa gat ggg caa caa aag atg tct cat gta acc gtg gaa cgt aac cgg  
455

Gln	Asp	Gly	Gln	Gln	Lys	Met	Ser	His	Val	Thr	Val	Glu	Arg	Asn	Arg
						100				105				110	

aga aag caa atg aac gag cac tta acc gtt ttg cgt tct ctt atg cct  
503

Arg	Lys	Gln	Met	Asn	Glu	His	Leu	Thr	Val	Leu	Arg	Ser	Leu	Met	Pro
			115					120					125		

tgt ttc tac gtc aaa cgg ggg gac caa gca tcg atc ata gga gga gtt  
551

Cys	Phe	Tyr	Val	Lys	Arg	Gly	Asp	Gln	Ala	Ser	Ile	Ile	Gly	Gly	Val
			130				135					140			



gtg gag tac ata agc gag tta caa caa gtt ctc caa tct ttg gaa gcc  
 599  
 Val Glu Tyr Ile Ser Glu Leu Gln Gln Val Leu Gln Ser Leu Glu Ala  
 145 150 155

aag aaa caa cgt aaa acc tac gcc gaa gtc cta agc ccg aga gtt gtc  
 647  
 Lys Lys Gln Arg Lys Thr Tyr Ala Glu Val Leu Ser Pro Arg Val Val  
 160 165 170 175

ccg agc cct cgt cct tca ccg cct gtt cta agc cca aga aaa ccg cct  
 695  
 Pro Ser Pro Arg Pro Ser Pro Pro Val Leu Ser Pro Arg Lys Pro Pro  
 180 185 190

ctt agc ccg cgc atc aac cac cac cag att cac cac cac cta ctt ctc  
 743  
 Leu Ser Pro Arg Ile Asn His His Gln Ile His His His Leu Leu Leu  
 195 200 205

cct ccc ata agt cct cga aca cct cag cca aca agc cca tac cgg gcc  
 791  
 Pro Pro Ile Ser Pro Arg Thr Pro Gln Pro Thr Ser Pro Tyr Arg Ala  
 210 215 220

att cca ccg caa cta cca ctc atc cca cag cct ccg ctt cgc tct tac  
 839  
 Ile Pro Pro Gln Leu Pro Leu Ile Pro Gln Pro Pro Leu Arg Ser Tyr  
 225 230 235

agc tca ttg gcc agt tgc agc agc tta gga gat cca cct cca tac tct  
 887  
 Ser Ser Leu Ala Ser Cys Ser Ser Leu Gly Asp Pro Pro Pro Tyr Ser  
 240 245 250 255

cct gct tca tct tct tca tct cct tca gtt agt agt aac cat gag agt  
 935  
 Pro Ala Ser Ser Ser Ser Ser Pro Ser Val Ser Ser Asn His Glu Ser  
 260 265 270

agt gtg atc aat gag ctt gtt gct aac tca aaa tcg gct ttg gct gat  
 983  
 Ser Val Ile Asn Glu Leu Val Ala Asn Ser Lys Ser Ala Leu Ala Asp  
 275 280 285

gtg gaa gtg aag ttt tca gga gct aac gtg ctg ctc aaa acg gtg tcg  
 1031  
 Val Glu Val Lys Phe Ser Gly Ala Asn Val Leu Leu Lys Thr Val Ser  
 290 295 300

cat aag atc ccg gga caa gtt atg aag ata att gct gct ctt gaa gat  
 1079  
 His Lys Ile Pro Gly Gln Val Met Lys Ile Ile Ala Ala Leu Glu Asp  
 305 310 315

ttg gct ctt gag att ctt cag gtt aat att aac acc gtc gac gaa acc  
 1127  
 Leu Ala Leu Glu Ile Leu Gln Val Asn Ile Asn Thr Val Asp Glu Thr  
 320 325 330 335



atg ctt aat tct ttc acc atc aag att gga att gag tgc caa cta agt  
1175

Met Leu Asn Ser Phe Thr Ile Lys Ile Gly Ile Glu Cys Gln Leu Ser  
340 345 350

gca gaa gaa ctg gct caa caa att cag caa aca ttc tgc tag  
1217

Ala Glu Glu Leu Ala Gln Gln Ile Gln Gln Thr Phe Cys  
355 360

taaagaagga tttaatatag ctctgtataa accttaacga gagagcagta cgtactcact  
1277

ttctctcctt agtatccctt taattatctt ttcagttttc tgcaaagata tggagtttaa  
1337

aaaaataaaa ttgttatcta aagttttaat caaatattga ttaattataa ctaatatagg  
1397

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1457

taaatttttag aatttagacg tactcctacc atgtaatttt atttctgtca ttacatcaag  
1517

cattgtagct gtaattgcat atgaatgaac aatagtgtat gagtgatctc atgaataata  
1577

ttctttctgc aacaçaaaaa aaaaaaa  
1604

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Thr Ser Leu Ala Gly Asp Asp Leu Phe Ala Ile Leu Glu Ser Leu Glu  
20 25 30

Gly Ala Gly Glu Ile Ser Pro Thr Ala Ala Ser Thr Pro Lys Asp Gly  
35 40 45

Thr Thr Ser Ser Lys Glu Leu Val Lys Asp Gln Asp Tyr Glu Asn Ser  
50 55 60

Ser Pro Lys Arg Lys Lys Gln Arg Leu Glu Thr Arg Lys Glu Glu Asp  
65 70 75 80

Glu Glu Glu Glu Asp Gly Asp Gly Glu Ala Glu Glu Asp Asn Lys Gln  
85 90 95

Asp Gly Gln Gln Lys Met Ser His Val Thr Val Glu Arg Asn Arg Arg  
100 105 110



Lys Gln Met Asn Glu His Leu Thr Val Leu Arg Ser Leu Met Pro Cys  
 115 120 125

Phe Tyr Val Lys Arg Gly Asp Gln Ala Ser Ile Ile Gly Gly Val Val  
 130 135 140

Glu Tyr Ile Ser Glu Leu Gln Gln Val Leu Gln Ser Leu Glu Ala Lys  
 145 150 155 160

Lys Gln Arg Lys Thr Tyr Ala Glu Val Leu Ser Pro Arg Val Val Pro  
 165 170 175

Ser Pro Arg Pro Ser Pro Pro Val Leu Ser Pro Arg Lys Pro Pro Leu  
 180 185 190

Ser Pro Arg Ile Asn His His Gln Ile His His His Leu Leu Leu Pro  
 195 200 205

Pro Ile Ser Pro Arg Thr Pro Gln Pro Thr Ser Pro Tyr Arg Ala Ile  
 210 215 220

Pro Pro Gln Leu Pro Leu Ile Pro Gln Pro Pro Leu Arg Ser Tyr Ser  
 225 230 235 240

Ser Leu Ala Ser Cys Ser Ser Leu Gly Asp Pro Pro Pro Tyr Ser Pro  
 245 250 255

Ala Ser Ser Ser Ser Ser Pro Ser Val Ser Ser Asn His Glu Ser Ser  
 260 265 270

Val Ile Asn Glu Leu Val Ala Asn Ser Lys Ser Ala Leu Ala Asp Val  
 275 280 285

Glu Val Lys Phe Ser Gly Ala Asn Val Leu Leu Lys Thr Val Ser His  
 290 295 300

Lys Ile Pro Gly Gln Val Met Lys Ile Ile Ala Ala Leu Glu Asp Leu  
 305 310 315 320

Ala Leu Glu Ile Leu Gln Val Asn Ile Asn Thr Val Asp Glu Thr Met  
 325 330 335

Leu Asn Ser Phe Thr Ile Lys Ile Gly Ile Glu Cys Gln Leu Ser Ala  
 340 345 350



Glu Glu Leu Ala Gln Gln Ile Gln Gln Thr Phe Cys  
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 120

gaaacttttg acgagtgggt tcaaatttct ggtgaaaacg accagcaaga agttgttcaa  
 180

caacttcaca aggttctgcg accatttctt cttcggaggt taaaatcaga ttagagaaaa  
 240

ggcttacctc caaaaaagga gacaatactc aaagttggc atg tct caa atg caa  
 294

Met Ser Gln Met Gln  
 1 5

aaa cag tac tac aag gct tta ctg cag aag gat ctt gaa gtg gtt aat  
 342

Lys Gln Tyr Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Val Val Asn  
 10 15 20

ggt ggt gga gaa cgc aaa cgt ctg ttg aac ata gca atg caa ttg cgg  
 390

Gly Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg  
 25 30 35

aaa tgc tgc aat cac cct tat ctc ttc cag ggt gcg gag cct ggt ccc  
 438

Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro  
 40 45 50

cca tat act aca gga gat cac ctt gta aca aac gca ggt aag atg gtt  
 486

Pro Tyr Thr Thr Gly Asp His Leu Val Thr Asn Ala Gly Lys Met Val  
 55 60 65

ctc tta gat aaa ttg cta cct aag ttg aag gat cga gat tca agg gtt  
 534

Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Asp Arg Asp Ser Arg Val  
 70 75 80 85

ctg ata ttt tct cag atg aca agg ctt ttg gat att ctc gag gat tac  
 582

Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr  
 90 95 100

cta atg tat cgt ggt tac cag tac tgc cgt att gat gga aat act ggt  
 630

Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile Asp Gly Asn Thr Gly  
 105 110 115



ggt gac gaa cga gat gct tcc ata gaa gcc tat aac aag cca gga agt  
 678  
 Gly Asp Glu Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser  
 120 125 130

gag aaa ttc gtt ttc ttg tta tcc act aga gct gga gga ctt ggt atc  
 726  
 Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile  
 135 140 145

aat ctt gct act gca gat gtt gtg atc ctc tat gat agt gac tgg aac  
 774  
 Asn Leu Ala Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn  
 150 155 160 165

cct caa gtt gac ttg caa gct cag gat cgt gca cat agg att ggt caa  
 822  
 Pro Gln Val Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln  
 170 175 180

aaa aaa gaa gtt caa gtg ttc cgg ttc tgc acc gag aat gct att gag  
 870  
 Lys Lys Glu Val Gln Val Phe Arg Phe Cys Thr Glu Asn Ala Ile Glu  
 185 190 195

gct aaa gtc att gag aga gct tac aag aag ttg gca ctt gat gct ctg  
 918  
 Ala Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu  
 200 205 210

gtt att cag caa ggg aga ttg gca gaa cag aaa act gtt aat aag gat  
 966  
 Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr Val Asn Lys Asp  
 215 220 225

gag ttg ctt caa atg gtg aga tat ggt gct gaa atg gtg ttt agt tct  
 1014  
 Glu Leu Leu Gln Met Val Arg Tyr Gly Ala Glu Met Val Phe Ser Ser  
 230 235 240 245

aaa gat agc aca att acg gat gag gat att gac aga atc att gcc aaa  
 1062  
 Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg Ile Ile Ala Lys  
 250 255 260

gga gaa gag gca acg gct gaa ctt gat gcc aag atg aag aaa ttt act  
 1110  
 Gly Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr  
 265 270 275

gaa gat gca ata cag ttt aaa atg gat gac agt gct gac ttt tat gat  
 1158  
 Glu Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp  
 280 285 290

ttt gac gat gac aac aag gat gag agc aag gtg gat ttt aaa aag att  
 1206  
 Phe Asp Asp Asp Asn Lys Asp Glu Ser Lys Val Asp Phe Lys Lys Ile  
 295 300 305



gtg agt gaa aat tgg aat gat cca cca aaa aga gag aga aag cgc aac  
 1254  
 Val Ser Glu Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn  
 310 315 320 325

tac tct gaa gtt gaa tac ttc aag caa acg ttg cga caa ggt gct cca  
 1302  
 Tyr Ser Glu Val Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro  
 330 335 340

gct aaa cct aaa gag cct aga att cca cgc atg ccc caa ttg cat gat  
 1350  
 Ala Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp  
 345 350 355

ttt cag ttc ttt aac att cag agg ctg act gag ctg tat gaa aaa gaa  
 1398  
 Phe Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu  
 360 365 370

gtg cga tac ctt atg caa gca cat cag aaa act caa atg aaa gac aca  
 1446  
 Val Arg Tyr Leu Met Gln Ala His Gln Lys Thr Gln Met Lys Asp Thr  
 375 380 385

att gag gtt gat gaa cct gaa gaa gtt gga gat ccc tta act gct gaa  
 1494  
 Ile Glu Val Asp Glu Pro Glu Glu Val Gly Asp Pro Leu Thr Ala Glu  
 390 395 400 405

gaa gtg gaa gaa aag gag cta ttg ctg gaa gag ggt ttc tca aca tgg  
 1542  
 Glu Val Glu Glu Lys Glu Leu Leu Leu Glu Glu Gly Phe Ser Thr Trp  
 410 415 420

agc aga aga gac ttc aat gcc ttc att agg gct tgt gag aag tat ggc  
 1590  
 Ser Arg Arg Asp Phe Asn Ala Phe Ile Arg Ala Cys Glu Lys Tyr Gly  
 425 430 435

cgg aac gac ata aag agt att gcc tct gag atg gaa ggg aaa act gag  
 1638  
 Arg Asn Asp Ile Lys Ser Ile Ala Ser Glu Met Glu Gly Lys Thr Glu  
 440 445 450

gaa gag gtt gaa cga tat gct caa gtt ttc caa gtg cga tat aaa gag  
 1686  
 Glu Glu Val Glu Arg Tyr Ala Gln Val Phe Gln Val Arg Tyr Lys Glu  
 455 460 465

ctg aat gat tac gac aga atc atc aag aat att gag aga ggg gaa gca  
 1734  
 Leu Asn Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala  
 470 475 480 485

aga atc tct agg aaa gat gaa atc atg aaa gct att ggg aag aaa ctg  
 1782  
 Arg Ile Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu  
 490 495 500



gat cgc tac aga aac ccg tgg ctg gaa ctg aag att caa tat ggt cag  
 1830  
 Asp Arg Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln  
 505 510 515

aac aaa ggg aag ctg tac aat gaa gag tgc gac cgt ttc atg ata tgc  
 1878  
 Asn Lys Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys  
 520 525 530

atg gtc cat aaa ctt ggg tat gga aac tgg gat gag cta aag gca gcg  
 1926  
 Met Val His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala  
 535 540 545

ttt cgg aca tcc ccc ttg ttt agg ttt gac tgg ttt gta aaa tcc cgc  
 1974  
 Phe Arg Thr Ser Pro Leu Phe Arg Phe Asp Trp Phe Val Lys Ser Arg  
 550 555 560 565

aca act cag gaa ctt gca agg aga tgt gac aca cta atc agg ttg att  
 2022  
 Thr Thr Gln Glu Leu Ala Arg Arg Cys Asp Thr Leu Ile Arg Leu Ile  
 570 575 580

gag aaa gag aat caa gaa ttt gat gag aga gag agg caa gcc cga aaa  
 2070  
 Glu Lys Glu Asn Gln Glu Phe Asp Glu Arg Glu Arg Gln Ala Arg Lys  
 585 590 595

gag aag aag ctt tca aag agt gca acg cca tca aaa cga cct tcg ggt  
 2118  
 Glu Lys Lys Leu Ser Lys Ser Ala Thr Pro Ser Lys Arg Pro Ser Gly  
 600 605 610

agg caa gca aat gag agc cct tca tct ctt ctg aag aaa cga aag cag  
 2166  
 Arg Gln Ala Asn Glu Ser Pro Ser Ser Leu Leu Lys Lys Arg Lys Gln  
 615 620 625

ctg tca atg gat gat tat gga aag cgt agg aaa taa gaaggcttgt  
 2212  
 Leu Ser Met Asp Asp Tyr Gly Lys Arg Arg Lys  
 630 635 640

gttgaatcca tcactaagta atcagaaaga tttatgatca cttctagggtt tgattccgaa  
 2272

tcggagaatt agttagaaga agctccttag agacaaggat ctaatatattt gtaccgcaa  
 2332

gcatcactgc attgtctcgc acttctctta tttcttcaac gtgtatttta ctctattttg  
 2392

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 2452

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 2481



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Met Ser Gln Met Gln Lys Gln Tyr Tyr Lys Ala Leu Leu Gln Lys Asp  
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Leu Glu Val Val Asn Gly Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile  
20 25 30

Ala Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly  
35 40 45

Ala Glu Pro Gly Pro Pro Tyr Thr Thr Gly Asp His Leu Val Thr Asn  
50 55 60

Ala Gly Lys Met Val Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Asp  
65 70 75 80

Arg Asp Ser Arg Val Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp  
85 90 95

Ile Leu Glu Asp Tyr Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile  
100 105 110

Asp Gly Asn Thr Gly Gly Asp Glu Arg Asp Ala Ser Ile Glu Ala Tyr  
115 120 125

Asn Lys Pro Gly Ser Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala  
130 135 140

Gly Gly Leu Gly Ile Asn Leu Ala Thr Ala Asp Val Val Ile Leu Tyr  
145 150 155 160

Asp Ser Asp Trp Asn Pro Gln Val Asp Leu Gln Ala Gln Asp Arg Ala  
165 170 175

His Arg Ile Gly Gln Lys Lys Glu Val Gln Val Phe Arg Phe Cys Thr  
180 185 190

Glu Asn Ala Ile Glu Ala Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu  
195 200 205

Ala Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys  
210 215 220

Thr Val Asn Lys Asp Glu Leu Leu Gln Met Val Arg Tyr Gly Ala Glu  
225 230 235 240



Met Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp  
 245 250 255

Arg Ile Ile Ala Lys Gly Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys  
 260 265 270

Met Lys Lys Phe Thr Glu Asp Ala Ile Gln Phe Lys Met Asp Asp Ser  
 275 280 285

Ala Asp Phe Tyr Asp Phe Asp Asp Asp Asn Lys Asp Glu Ser Lys Val  
 290 295 300

Asp Phe Lys Lys Ile Val Ser Glu Asn Trp Asn Asp Pro Pro Lys Arg  
 305 310 315 320

Glu Arg Lys Arg Asn Tyr Ser Glu Val Glu Tyr Phe Lys Gln Thr Leu  
 325 330 335

Arg Gln Gly Ala Pro Ala Lys Pro Lys Glu Pro Arg Ile Pro Arg Met  
 340 345 350

Pro Gln Leu His Asp Phe Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu  
 355 360 365

Leu Tyr Glu Lys Glu Val Arg Tyr Leu Met Gln Ala His Gln Lys Thr  
 370 375 380

Gln Met Lys Asp Thr Ile Glu Val Asp Glu Pro Glu Glu Val Gly Asp  
 385 390 395 400

Pro Leu Thr Ala Glu Glu Val Glu Glu Lys Glu Leu Leu Leu Glu Glu  
 405 410 415

Gly Phe Ser Thr Trp Ser Arg Arg Asp Phe Asn Ala Phe Ile Arg Ala  
 420 425 430

Cys Glu Lys Tyr Gly Arg Asn Asp Ile Lys Ser Ile Ala Ser Glu Met  
 435 440 445

Glu Gly Lys Thr Glu Glu Glu Val Glu Arg Tyr Ala Gln Val Phe Gln  
 450 455 460

Val Arg Tyr Lys Glu Leu Asn Asp Tyr Asp Arg Ile Ile Lys Asn Ile  
 465 470 475 480



Glu Arg Gly Glu Ala Arg Ile Ser Arg Lys Asp Glu Ile Met Lys Ala  
485 490 495

Ile Gly Lys Lys Leu Asp Arg Tyr Arg Asn Pro Trp Leu Glu Leu Lys  
500 505 510

Ile Gln Tyr Gly Gln Asn Lys Gly Lys Leu Tyr Asn Glu Glu Cys Asp  
515 520 525

Arg Phe Met Ile Cys Met Val His Lys Leu Gly Tyr Gly Asn Trp Asp  
530 535 540

Glu Leu Lys Ala Ala Phe Arg Thr Ser Pro Leu Phe Arg Phe Asp Trp  
545 550 555 560

Phe Val Lys Ser Arg Thr Thr Gln Glu Leu Ala Arg Arg Cys Asp Thr  
565 570 575

Leu Ile Arg Leu Ile Glu Lys Glu Asn Gln Glu Phe Asp Glu Arg Glu  
580 585 590

Arg Gln Ala Arg Lys Glu Lys Lys Leu Ser Lys Ser Ala Thr Pro Ser  
595 600 605

Lys Arg Pro Ser Gly Arg Gln Ala Asn Glu Ser Pro Ser Ser Leu Leu  
610 615 620

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625 630 635 640

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109

Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu  
1 5 10 15

tat tct atc gga tct tct cca gat tct ttc tca tcc tct tct tct aac  
157

Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn  
20 25 30

aat tac tct ctt ccc ttc aac gag aac gac tca gag gaa atg ttt ctc  
205

Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu



35	40	45
tac ggt cta atc gag cag tcc acg caa caa acc tat att gac tcg gat		
253		
Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp		
50	55	60
agt caa gac ctt ccg atc aaa tcc gta agc tca aga aag tca gag aag		
301		
Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys		
65	70	80
tct tac aga ggc gta aga cga cgg cca tgg ggg aaa ttc gcg gcg gag		
349		
Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu		
	85	90
ata aga gat tcg act aga aac ggt att agg gtt tgg ctc ggg acg ttc		
397		
Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe		
	100	105
gaa agc gcg gaa gag gcg gct tta gcc tac gat caa gct gct ttc tcg		
445		
Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser		
	115	120
atg aga ggg tcc tcg gcg att ctc aat ttt tcg gcg gag aga gtt caa		
493		
Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln		
	130	135
gag tcg ctt tcg gag att aaa tat acc tac gag gat ggt tgt tct ccg		
541		
Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro		
145	150	155
gtt gtg gcg ttg aag agg aaa cac tcg atg aga cgg aga atg acc aat		
589		
Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn		
	165	170
aag aag acg aaa gat agt gac ttt gat cac cgc tcc gtg aag tta gat		
637		
Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp		
	180	185
aat gta gtt gtc ttt gag gat ttg gga gaa cag tac ctt gag gag ctt		
685		
Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu		
	195	200
ttg ggg tct tct gaa aat agt ggg act tgg tga aagattagga tttgtattag		
738		
Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp		
	210	215
ggaccttaag tttgaagtgg ttgattaatt ttaaccctaa tatgtttttt gtttgcttaa		
798		



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858

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859

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20 25 30

Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu  
35 40 45

Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp  
50 55 60

Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys  
65 70 75 80

Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu  
85 90 95

Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe  
100 105 110

Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser  
115 120 125

Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln  
130 135 140

Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro  
145 150 155 160

Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn  
165 170 175

Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp  
180 185 190

Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu  
195 200 205



Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp  
 210 215

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 120

ttccggcgaa atcggacggt cgagatcaat c atg cat cgt aga gca gca att  
 172

Met His Arg Arg Ala Ala Ile  
 1 5

caa gaa tcg gat gac gaa gaa gat gag act tac aac gac gtc gtt cct  
 220

Gln Glu Ser Asp Asp Glu Glu Asp Glu Thr Tyr Asn Asp Val Val Pro  
 10 15 20

gaa tct cct tct tct tgt gaa gac tca aag atc tca aaa cca act cca  
 268

Glu Ser Pro Ser Ser Cys Glu Asp Ser Lys Ile Ser Lys Pro Thr Pro  
 25 30 35

aag aaa agg agg aac gta gag aag aga gtt gtc tca gtt ccg ata gct  
 316

Lys Lys Arg Arg Asn Val Glu Lys Arg Val Val Ser Val Pro Ile Ala  
 40 45 50 55

gac gtg gaa gga tct aag agc aga ggc gaa gta tat cca ccg tcc gat  
 364

Asp Val Glu Gly Ser Lys Ser Arg Gly Glu Val Tyr Pro Pro Ser Asp  
 60 65 70

tca tgg gcc tgg aga aag tac gga caa aaa ccg atc aaa ggc tcg cct  
 412

Ser Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro  
 75 80 85

tat ccc agg gga tat tac aga tgt agt agc tca aaa gga tgt ccg gcg  
 460

Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Pro Ala  
 90 95 100

agg aag cag gtg gag aga agc cgt gtg gac cct tct aag ctt atg att  
 508

Arg Lys Gln Val Glu Arg Ser Arg Val Asp Pro Ser Lys Leu Met Ile  
 105 110 115

act tac gcc tgc gac cac aat cac cct ttc cct tcc tcc tcc gct aac  
 556

Thr Tyr Ala Cys Asp His Asn His Pro Phe Pro Ser Ser Ser Ala Asn  
 120 125 130 135



acc aaa tcc cac cac cgc tcc tcc gtc gtc ctc aaa acc gca aag aaa  
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 Thr Lys Ser His His Arg Ser Ser Val Val Leu Lys Thr Ala Lys Lys  
 140 145 150  
 gag gaa gaa tac gaa gag gag gaa gaa gaa cta acc gtc acc gcc gca  
 652  
 Glu Glu Glu Tyr Glu Glu Glu Glu Glu Glu Leu Thr Val Thr Ala Ala  
 155 160 165  
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 700  
 Glu Glu Pro Pro Ala Gly Leu Asp Leu Ser His Val Asp Ser Pro Leu  
 170 175 180  
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 748  
 Leu Leu Gly Gly Cys Tyr Ser Glu Ile Gly Glu Phe Gly Trp Phe Tyr  
 185 190 195  
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 796  
 Asp Ala Ser Ile Ser Ser Ser Ser Gly Ser Ser Asn Phe Leu Asp Val  
 200 205 210 215  
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 844  
 Thr Leu Glu Arg Gly Phe Ser Val Gly Gln Glu Glu Asp Glu Ser Leu  
 220 225 230  
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 892  
 Phe Gly Asp Leu Gly Asp Leu Pro Asp Cys Ala Ser Val Phe Arg Arg  
 235 240 245  
 ggg act gtt gcg acg gag gag caa cat cga aga tgt gat ttt ggc gcc  
 940  
 Gly Thr Val Ala Thr Glu Glu Gln His Arg Arg Cys Asp Phe Gly Ala  
 250 255 260  
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 987  
 Ile Pro Phe Cys Asp Ser Ser Arg  
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 20 25 30



Lys Ile Ser Lys Pro Thr Pro Lys Lys Arg Arg Asn Val Glu Lys Arg  
 35 40 45

Val Val Ser Val Pro Ile Ala Asp Val Glu Gly Ser Lys Ser Arg Gly  
 50 55 60

Glu Val Tyr Pro Pro Ser Asp Ser Trp Ala Trp Arg Lys Tyr Gly Gln  
 65 70 75 80

Lys Pro Ile Lys Gly Ser Pro Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser  
 85 90 95

Ser Ser Lys Gly Cys Pro Ala Arg Lys Gln Val Glu Arg Ser Arg Val  
 100 105 110

Asp Pro Ser Lys Leu Met Ile Thr Tyr Ala Cys Asp His Asn His Pro  
 115 120 125

Phe Pro Ser Ser Ser Ala Asn Thr Lys Ser His His Arg Ser Ser Val  
 130 135 140

Val Leu Lys Thr Ala Lys Lys Glu Glu Glu Tyr Glu Glu Glu Glu Glu  
 145 150 155 160

Glu Leu Thr Val Thr Ala Ala Glu Glu Pro Pro Ala Gly Leu Asp Leu  
 165 170 175

Ser His Val Asp Ser Pro Leu Leu Leu Gly Gly Cys Tyr Ser Glu Ile  
 180 185 190

Gly Glu Phe Gly Trp Phe Tyr Asp Ala Ser Ile Ser Ser Ser Ser Gly  
 195 200 205

Ser Ser Asn Phe Leu Asp Val Thr Leu Glu Arg Gly Phe Ser Val Gly  
 210 215 220

Gln Glu Glu Asp Glu Ser Leu Phe Gly Asp Leu Gly Asp Leu Pro Asp  
 225 230 235 240

Cys Ala Ser Val Phe Arg Arg Gly Thr Val Ala Thr Glu Glu Gln His  
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Arg Arg Cys Asp Phe Gly Ala Ile Pro Phe Cys Asp Ser Ser Arg  
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 105

Met Asn Asp Ala Asp Thr Asn Leu Gly Ser Ser Phe Ser Asp Asp Thr  
 1 5 10 15

cac tct gtg ttc gag ttt ccg gag cta gac ttg tca gat gaa tgg atg  
 153

His Ser Val Phe Glu Phe Pro Glu Leu Asp Leu Ser Asp Glu Trp Met  
 20 25 30

gat gat gat ctt gtg tct gcg gtt tcc ggg atg aat cag tct tat ggt  
 201

Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly  
 35 40 45

tat cag act agt gat gtt gct ggt gct tta ttc tca ggt tct tct agc  
 249

Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser  
 50 55 60

tgt ttc agt cat cct gaa tct cca agt acc aaa act tat gtt gct gct  
 297

Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala  
 65 70 75 80

aca gcc act gct tct gcc gac aac caa aac aag aaa gaa aag aaa aaa  
 345

Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys  
 85 90 95

att aaa ggg aga gtt gcg ttc aag aca cgg tcc gag gtg gaa gtg ctt  
 393

Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu  
 100 105 110

gac gac ggg ttc aag tgg aga aag tat ggg aag aag atg gtg aag aac  
 441

Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn  
 115 120 125

agc cca cat cca aga aac tac tac aaa tgt tca gtt gat ggc tgt ccc  
 489

Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro  
 130 135 140

gtg aag aaa agg gtt gaa cga gac aga gat gat ccg agc ttt gtg ata  
 537

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile  
 145 150 155 160

aca act tac gag ggt tcc cac aat cac tca agc atg aac taa  
 579

Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn



165

170

gactcgaact aaggetcaag gcgacatgc tatattcagc acatcttatt ttctatggtt  
639

acgaacgata cttaaaactg cttctagtgc ttatatcca ttgtaaactg gttgcaggtt  
699

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748

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Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly  
35 40 45

Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser  
50 55 60

Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala  
65 70 75 80

Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys  
85 90 95

Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu  
100 105 110

Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn  
115 120 125

Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro  
130 135 140

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile  
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 103  
 Glu Glu Thr Leu Arg Arg Gly Pro Trp Leu Glu Glu Glu Asp Glu Arg  
 10 15 20  
 cta gtg aag gtc att agt ctt ttg gga gaa cgt cgt tgg gat tct tta  
 151  
 Leu Val Lys Val Ile Ser Leu Leu Gly Glu Arg Arg Trp Asp Ser Leu  
 25 30 35  
 gca ata gtt tcc ggt ttg aag agg agt ggt aag agt tgc agg cta agg  
 199  
 Ala Ile Val Ser Gly Leu Lys Arg Ser Gly Lys Ser Cys Arg Leu Arg  
 40 45 50  
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 247  
 Trp Met Asn Tyr Leu Asn Pro Thr Leu Lys Arg Gly Pro Met Ser Gln  
 55 60 65  
 gaa gaa gag aga atc atc ttt cag ctc cat gct cta tgg ggt aac aag  
 295  
 Glu Glu Glu Arg Ile Ile Phe Gln Leu His Ala Leu Trp Gly Asn Lys  
 70 75 80 85  
 tgg tgc aag att gcg aga aga tta ccc ggt agg act gat aac gag ata  
 343  
 Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile  
 90 95 100  
 aag aac tat tgg aga act cat tat aga aag aaa cag gaa gct caa aac  
 391  
 Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala Gln Asn  
 105 110 115  
 tat gga aag ctc ttt gag tgg aga gga aat aca gga gaa gaa ttg ttg  
 439  
 Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu Leu Leu  
 120 125 130  
 cac aag tat aag gaa aca gag atc act agg aca aag acg acg tct caa  
 487  
 His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr Ser Gln  
 135 140 145  
 gaa cat ggt ttt gtt gaa gtt gtg agc atg gaa agt ggt aaa gaa gcc  
 535  
 Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys Glu Ala  
 150 155 160 165  
 aac ggt ggt gtt ggt gga aga gaa agc ttc ggt gtt atg aaa tca ccg  
 583  
 Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys Ser Pro  
 170 175 180



tat gaa aat cgg att tcg gat tgg ata tca gag att tct act gac cag  
631

Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr Asp Gln  
185 190 195

agt gaa gca aat ctt tca gaa gat cac agc agc aat agc tgc agt gag  
679

Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys Ser Glu  
200 205 210

aac aat att aac att ggt act tgg tgg ttt caa gag act agg gac ttt  
727

Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln Glu Thr Arg Asp Phe  
215 220 225

gag gag ttt tca tgt tct cta tgg tca taa ttctaaagtt gggtttattta  
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Glu Glu Phe Ser Cys Ser Leu Trp Ser  
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20 25 30

Arg Trp Asp Ser Leu Ala Ile Val Ser Gly Leu Lys Arg Ser Gly Lys  
35 40 45

Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Asn Pro Thr Leu Lys Arg  
50 55 60

Gly Pro Met Ser Gln Glu Glu Glu Arg Ile Ile Phe Gln Leu His Ala  
65 70 75 80

Leu Trp Gly Asn Lys Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg  
85 90 95

Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys  
100 105 110

Gln Glu Ala Gln Asn Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr  
115 120 125

Gly Glu Glu Leu Leu His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr



130                      135                      140  
 Lys Thr Thr Ser Gln Glu His Gly Phe Val Glu Val Val Ser Met Glu  
 145                      150                      155                      160  
 Ser Gly Lys Glu Ala Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly  
 165                      170                      175  
 Val Met Lys Ser Pro Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu  
 180                      185                      190  
 Ile Ser Thr Asp Gln Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser  
 195                      200                      205  
 Asn Ser Cys Ser Glu Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln  
 210                      215                      220  
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 gta aag aag atg aag aag gga ctt tgg tct cct gag gaa gac tca aag  
 96  
 Val Lys Lys Met Lys Lys Gly Leu Trp Ser Pro Glu Glu Asp Ser Lys  
 15                      20                      25                      30  
 ctg atg caa tac atg tta agc aat gga caa gga tgt tgg agt gat gtt  
 144  
 Leu Met Gln Tyr Met Leu Ser Asn Gly Gln Gly Cys Trp Ser Asp Val  
 35                      40                      45  
 gcg aaa aac gca gga ctt caa aga tgt ggc aaa agc tgc cgt ctt cgt  
 192  
 Ala Lys Asn Ala Gly Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg  
 50                      55                      60  
 tgg atc aac tat ctt cgt cct gac ctc aag cgt ggc gct ttc tct cct  
 240  
 Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe Ser Pro  
 65                      70                      75  
 caa gaa gag gat ctc atc att cgc ttt cat tcc atc ctc ggc aac agg  
 288  
 Gln Glu Glu Asp Leu Ile Ile Arg Phe His Ser Ile Leu Gly Asn Arg  
 80                      85                      90



tgg tct cag att gca gca cga ttg cct ggt cgg acc gat aac gag atc  
 336  
 Trp Ser Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile  
 95 100 105 110  
 aag aat ttc tgg aac tca aca ata aag aaa agg cta aag aag atg tcc  
 384  
 Lys Asn Phe Trp Asn Ser Thr Ile Lys Lys Arg Leu Lys Lys Met Ser  
 115 120 125  
 gat acc tcc aac tta atc aac aac tca tcc tca tca ccc aac aca gca  
 432  
 Asp Thr Ser Asn Leu Ile Asn Asn Ser Ser Ser Ser Pro Asn Thr Ala  
 130 135 140  
 agc gat tcc tct tct aat tcc gca tct tct ttg gat att aaa gac att  
 480  
 Ser Asp Ser Ser Ser Asn Ser Ala Ser Ser Leu Asp Ile Lys Asp Ile  
 145 150 155  
 ata gga agc ttc atg tcc tta caa gaa caa ggc ttc gtc aac cct tcc  
 528  
 Ile Gly Ser Phe Met Ser Leu Gln Glu Gln Gly Phe Val Asn Pro Ser  
 160 165 170  
 ttg acc cac ata caa acc aac aat cca ttt cca acg gga aac atg atc  
 576  
 Leu Thr His Ile Gln Thr Asn Asn Pro Phe Pro Thr Gly Asn Met Ile  
 175 180 185 190  
 agc cac ccg tgc aat gac gat ttt acc cct tat gta gat ggt atc tat  
 624  
 Ser His Pro Cys Asn Asp Asp Phe Thr Pro Tyr Val Asp Gly Ile Tyr  
 195 200 205  
 gga gta aac gca ggg gta caa ggg gaa ctc tac ttc cca cct ttg gaa  
 672  
 Gly Val Asn Ala Gly Val Gln Gly Glu Leu Tyr Phe Pro Pro Leu Glu  
 210 215 220  
 tgt gaa gaa ggt gat tgg tac aat gca aat ata aac aac cac tta gac  
 720  
 Cys Glu Glu Gly Asp Trp Tyr Asn Ala Asn Ile Asn Asn His Leu Asp  
 225 230 235  
 gag ttg aac act aat gga tcc gga aac gca cct gag ggt atg aga cca  
 768  
 Glu Leu Asn Thr Asn Gly Ser Gly Asn Ala Pro Glu Gly Met Arg Pro  
 240 245 250  
 gtg gaa gaa ttt tgg gac ctt gac cag ttg atg aac act gag gtt cct  
 816  
 Val Glu Glu Phe Trp Asp Leu Asp Gln Leu Met Asn Thr Glu Val Pro  
 255 260 265 270  
 tcg ttt tac ttc aac ttc aaa caa agc ata tga atatttttac gtcatttat  
 869  
 Ser Phe Tyr Phe Asn Phe Lys Gln Ser Ile  
 275 280



tcttttttct attgcgggtt atactcaaga ttcttagcca cacacacata aatgcaaata  
929

tatatacatt gttagagagt attttgtatt tcgtataatc ttttcgtact agggcttgag  
989

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1049

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Lys Met Lys Lys Gly Leu Trp Ser Pro Glu Glu Asp Ser Lys Leu Met  
20 25 30

Gln Tyr Met Leu Ser Asn Gly Gln Gly Cys Trp Ser Asp Val Ala Lys  
35 40 45

Asn Ala Gly Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile  
50 55 60

Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe Ser Pro Gln Glu  
65 70 75 80

Glu Asp Leu Ile Ile Arg Phe His Ser Ile Leu Gly Asn Arg Trp Ser  
85 90 95

Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn  
100 105 110

Phe Trp Asn Ser Thr Ile Lys Lys Arg Leu Lys Lys Met Ser Asp Thr  
115 120 125

Ser Asn Leu Ile Asn Asn Ser Ser Ser Ser Pro Asn Thr Ala Ser Asp  
130 135 140

Ser Ser Ser Asn Ser Ala Ser Ser Leu Asp Ile Lys Asp Ile Ile Gly  
145 150 155 160

Ser Phe Met Ser Leu Gln Glu Gln Gly Phe Val Asn Pro Ser Leu Thr  
165 170 175

His Ile Gln Thr Asn Asn Pro Phe Pro Thr Gly Asn Met Ile Ser His



180 185 190

Pro Cys Asn Asp Asp Phe Thr Pro Tyr Val Asp Gly Ile Tyr Gly Val  
195 200 205

Asn Ala Gly Val Gln Gly Glu Leu Tyr Phe Pro Pro Leu Glu Cys Glu  
210 215 220

Glu Gly Asp Trp Tyr Asn Ala Asn Ile Asn Asn His Leu Asp Glu Leu  
225 230 235 240

Asn Thr Asn Gly Ser Gly Asn Ala Pro Glu Gly Met Arg Pro Val Glu  
245 250 255

Glu Phe Trp Asp Leu Asp Gln Leu Met Asn Thr Glu Val Pro Ser Phe  
260 265 270

Tyr Phe Asn Phe Lys Gln Ser Ile -  
275 280

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110

Met Ile Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu  
1 5 10

gac gag aag ctc aag gat ctt gtc gaa caa tac ggt cct cac aat tgg  
158

Asp Glu Lys Leu Lys Asp Leu Val Glu Gln Tyr Gly Pro His Asn Trp  
15 20 25

aac gcc att gct ctc aag ctt cct ggt cgc tct ggt aag agt tgt aga  
206

Asn Ala Ile Ala Leu Lys Leu Pro Gly Arg Ser Gly Lys Ser Cys Arg  
30 35 40 45

ttg aga tgg ttt aat caa ttg gat cca agg atc aac cga aac cct ttc  
254

Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe  
50 55 60

acg gaa gaa gaa gaa gaa aga ctt tta gcg gct cat cgg atc cat ggg  
302

Thr Glu Glu Glu Glu Glu Arg Leu Leu Ala Ala His Arg Ile His Gly  
65 70 75

aac aga tgg tcc atc atc gca agg ctt ttc cct gga aga act gat aac  
350



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Asn Arg Trp Ser Ile Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn
   80                               85                               90

gcc gtc aag aac cat tgg cac gtc atc atg gct cgt cgc aca cgc caa
398
Ala Val Lys Asn His Trp His Val Ile Met Ala Arg Arg Thr Arg Gln
   95                               100                               105

acc tct aag cct cgt ctt ctt ccc tcg acg act tcg tct tct tct tta
446
Thr Ser Lys Pro Arg Leu Leu Pro Ser Thr Thr Ser Ser Ser Ser Leu
110                               115                               120                               125

atg gcg agt gaa caa atc atg atg agt tct ggt ggt tat aat cat aat
494
Met Ala Ser Glu Gln Ile Met Met Ser Ser Gly Gly Tyr Asn His Asn
   130                               135                               140

tat agt tcc gat gat cgg aag aaa ata ttt cca gca gac ttt ata aat
542
Tyr Ser Ser Asp Asp Arg Lys Lys Ile Phe Pro Ala Asp Phe Ile Asn
   145                               150                               155

ttc cct tac aaa ttc tct cat atc aat cat ctt cac ttc cta aag gag
590
Phe Pro Tyr Lys Phe Ser His Ile Asn His Leu His Phe Leu Lys Glu
   160                               165                               170

ttt ttc ccc gga aag atc gct tta agt cac aaa gca aat cag agt aag
638
Phe Phe Pro Gly Lys Ile Ala Leu Ser His Lys Ala Asn Gln Ser Lys
   175                               180                               185

aag cct atg gag ttc tac aat ttt cta caa gta aac aca gat tca aac
686
Lys Pro Met Glu Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Asn
190                               195                               200                               205

aag agc gag att ata gat caa gat tca ggt caa agc aaa cgc agt gac
734
Lys Ser Glu Ile Ile Asp Gln Asp Ser Gly Gln Ser Lys Arg Ser Asp
   210                               215                               220

tcg gac acc aaa cat gaa agt cat gtt cca ttc ttc gac ttt tta tcc
782
Ser Asp Thr Lys His Glu Ser His Val Pro Phe Phe Asp Phe Leu Ser
   225                               230                               235

gtt gga aac tct gcc tcc tag gattagtttt ttgcagtaa ctctaaatt
833
Val Gly Asn Ser Ala Ser
   240

tctagattaa ctatttagtc cgtatacgta cgagattatc taggtcgta gcatgtatgc
893

ttgatgtgta taatcactaa ctagttagct attacctgcg aaaattgtaa gaaaaatata
953

taatgttgat gtatcacaca ttctcaatgt ctgtaaaatt tccatcgagt tgtaactat
1013

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1041

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Ala Leu Lys Leu Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp  
35 40 45

Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu  
50 55 60

Glu Glu Glu Arg Leu Leu Ala Ala His Arg Ile His Gly Asn Arg Trp  
65 70 75 80

Ser Ile Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn Ala Val Lys  
85 90 95

Asn His Trp His Val Ile Met Ala Arg Arg Thr Arg Gln Thr Ser Lys  
100 105 110

Pro Arg Leu Leu Pro Ser Thr Thr Ser Ser Ser Ser Leu Met Ala Ser  
115 120 125

Glu Gln Ile Met Met Ser Ser Gly Gly Tyr Asn His Asn Tyr Ser Ser  
130 135 140

Asp Asp Arg Lys Lys Ile Phe Pro Ala Asp Phe Ile Asn Phe Pro Tyr  
145 150 155 160

Lys Phe Ser His Ile Asn His Leu His Phe Leu Lys Glu Phe Phe Pro  
165 170 175

Gly Lys Ile Ala Leu Ser His Lys Ala Asn Gln Ser Lys Lys Pro Met  
180 185 190

Glu Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Asn Lys Ser Glu  
195 200 205

Ile Ile Asp Gln Asp Ser Gly Gln Ser Lys Arg Ser Asp Ser Asp Thr



210

215

220

Lys His Glu Ser His Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn  
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Ser Ala Ser

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 57

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gga aga gca cca tgt tgt gac aaa acc aaa gtg aag aga gga cca tgg  
 105

Gly Arg Ala Pro Cys Cys Asp Lys Thr Lys Val Lys Arg Gly Pro Trp  
 5 10 15

agc cat gat gaa gac ttg aaa ctc atc tct ttc att cac aag aat ggt  
 153

Ser His Asp Glu Asp Leu Lys Leu Ile Ser Phe Ile His Lys Asn Gly  
 20 25 30 35

cat gag aat tgg aga tct ctc cca aag caa gct gga ttg ttg agg tgt  
 201

His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys  
 40 45 50

ggc aag agt tgt cgt ctg cga tgg att aat tac ctc aga cct gat gtg  
 249

Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Val  
 55 60 65

aaa cgt ggc aat ttc agt gca gag gaa gaa gac acc atc atc aaa ctt  
 297

Lys Arg Gly Asn Phe Ser Ala Glu Glu Glu Asp Thr Ile Ile Lys Leu  
 70 75 80

cac cag agc ttt ggt aac aag tgg tcg aag att gct tct aag ctg cct  
 345

His Gln Ser Phe Gly Asn Lys Trp Ser Lys Ile Ala Ser Lys Leu Pro  
 85 90 95

gga aga aca gac aat gag atc aag aat gtg tgg cat aca cat ctc aag  
 393

Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu Lys  
 100 105 110 115

aaa aga ttg agc tcg gaa act aac ctt aat gcc gat gaa gcg ggt tca  
 441

Lys Arg Leu Ser Ser Glu Thr Asn Leu Asn Ala Asp Glu Ala Gly Ser  
 120 125 130



aaa ggt tct ttg aat gaa gaa gag aac tct caa gag tca tct cca aat  
 489  
 Lys Gly Ser Leu Asn Glu Glu Glu Asn Ser Gln Glu Ser Ser Pro Asn  
 135 140 145  
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 Ala Ser Met Ser Phe Ala Gly Ser Asn Ile Ser Ser Lys Asp Asp Asp  
 150 155 160  
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 585  
 Ala Gln Ile Ser Gln Met Phe Glu His Ile Leu Thr Tyr Ser Glu Phe  
 165 170 175  
 acg ggg atg tta caa gag gta gac aaa cca gag ctg ctg gag atg cct  
 633  
 Thr Gly Met Leu Gln Glu Val Asp Lys Pro Glu Leu Leu Glu Met Pro  
 180 185 190 195  
 ttt gat tta gat cct gac att tgg agt ttc ata gat ggt tca gac tca  
 681  
 Phe Asp Leu Asp Pro Asp Ile Trp Ser Phe Ile Asp Gly Ser Asp Ser  
 200 205 210  
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 729  
 Phe Gln Gln Pro Glu Asn Arg Ala Leu Gln Glu Ser Glu Glu Asp Glu  
 215 220 225  
 gtt gat aaa tgg ttt aag cac ctg gaa agc gaa ctc ggg tta gaa gaa  
 777  
 Val Asp Lys Trp Phe Lys His Leu Glu Ser Glu Leu Gly Leu Glu Glu  
 230 235 240  
 aac gat aac caa caa caa caa cag cat aaa cag gga aca gaa gat gaa  
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 His Ser Ser Ser Leu Leu Glu Ser Tyr Glu Leu Leu Ile His  
 260 265 270  
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Lys Asn Gly His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ala Gly Leu  
35 40 45

Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg  
50 55 60

Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Glu Glu Glu Asp Thr Ile  
65 70 75 80

Ile Lys Leu His Gln Ser Phe Gly Asn Lys Trp Ser Lys Ile Ala Ser  
85 90 95

Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr  
100 105 110

His Leu Lys Lys Arg Leu Ser Ser Glu Thr Asn Leu Asn Ala Asp Glu  
115 120 125

Ala Gly Ser Lys Gly Ser Leu Asn Glu Glu Glu Asn Ser Gln Glu Ser  
130 135 140

Ser Pro Asn Ala Ser Met Ser Phe Ala Gly Ser Asn Ile Ser Ser Lys  
145 150 155 160

Asp Asp Asp Ala Gln Ile Ser Gln Met Phe Glu His Ile Leu Thr Tyr  
165 170 175

Ser Glu Phe Thr Gly Met Leu Gln Glu Val Asp Lys Pro Glu Leu Leu  
180 185 190

Glu Met Pro Phe Asp Leu Asp Pro Asp Ile Trp Ser Phe Ile Asp Gly  
195 200 205

Ser Asp Ser Phe Gln Gln Pro Glu Asn Arg Ala Leu Gln Glu Ser Glu  
210 215 220

Glu Asp Glu Val Asp Lys Trp Phe Lys His Leu Glu Ser Glu Leu Gly  
225 230 235 240

Leu Glu Glu Asn Asp Asn Gln Gln Gln Gln His Lys Gln Gly Thr



245 250 255  
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 Asn Ser Phe Asp Asn Lys Lys Pro Ser Cys Gln Arg Gly His Trp Arg  
 10 15 20

cct gtt gaa gat gac aat ctc cgg caa ctc gtt gaa caa tac ggt ccc  
 148  
 Pro Val Glu Asp Asp Asn Leu Arg Gln Leu Val Glu Gln Tyr Gly Pro  
 25 30 35

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 196  
 Lys Asn Trp Asn Phe Ile Ala Gln His Leu Tyr Gly Arg Ser Gly Lys  
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 Ser Cys Arg Leu Arg Trp Tyr Asn Gln Leu Asp Pro Asn Ile Thr Lys  
 60 65 70

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 Lys Pro Phe Thr Glu Glu Glu Glu Glu Arg Leu Leu Lys Ala His Arg  
 75 80 85

atc caa ggg aat cgt tgg gcc tcc ata gcc cga ctg ttc ccc ggg agg  
 340  
 Ile Gln Gly Asn Arg Trp Ala Ser Ile Ala Arg Leu Phe Pro Gly Arg  
 90 95 100

acc gac aac gct gtc aaa aac cat ttt cat gtc atc atg gct aga cgc  
 388  
 Thr Asp Asn Ala Val Lys Asn His Phe His Val Ile Met Ala Arg Arg  
 105 110 115

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 436  
 Lys Arg Glu Asn Phe Ser Ser Thr Ala Thr Ser Thr Phe Asn Gln Thr  
 120 125 130 135



tgg cat act gtt ttg agc cct agt tct agt ctt aca agg cta aat aga  
484  
Trp His Thr Val Leu Ser Pro Ser Ser Ser Leu Thr Arg Leu Asn Arg  
140 145 150

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Ser His Phe Gly Leu Trp Arg Tyr Arg Lys Asp Lys Ser Cys Gly Leu  
155 160 165

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580  
Trp Pro Tyr Ser Phe Val Ser Pro Pro Thr Asn Gly Gln Phe Gly Ser  
170 175 180

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628  
Ser Ser Val Ser Asn Val His His Glu Ile Tyr Leu Glu Arg Arg Lys  
185 190 195

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676  
Ser Lys Glu Leu Val Asp Pro Gln Asn Tyr Thr Phe His Ala Ala Thr  
200 205 210 215

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724  
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220 225 230

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772  
Asp Gly Glu Lys Asn Asp Val Thr Phe Ile Asp Phe Leu Gly Val Gly  
235 240 245

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Leu Val Glu Gln Tyr Gly Pro Lys Asn Trp Asn Phe Ile Ala Gln His  
35 40 45

Leu Tyr Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Tyr Asn Gln  
50 55 60



Leu Asp Pro Asn Ile Thr Lys Lys Pro Phe Thr Glu Glu Glu Glu Glu  
65 70 75 80

Arg Leu Leu Lys Ala His Arg Ile Gln Gly Asn Arg Trp Ala Ser Ile  
85 90 95

Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Phe  
100 105 110

His Val Ile Met Ala Arg Arg Lys Arg Glu Asn Phe Ser Ser Thr Ala  
115 120 125

Thr Ser Thr Phe Asn Gln Thr Trp His Thr Val Leu Ser Pro Ser Ser  
130 135 140

Ser Leu Thr Arg Leu Asn Arg Ser His Phe Gly Leu Trp Arg Tyr Arg  
145 150 155 160

Lys Asp Lys Ser Cys Gly Leu Trp Pro Tyr Ser Phe Val Ser Pro Pro  
165 170 175

Thr Asn Gly Gln Phe Gly Ser Ser Ser Val Ser Asn Val His His Glu  
180 185 190

Ile Tyr Leu Glu Arg Arg Lys Ser Lys Glu Leu Val Asp Pro Gln Asn  
195 200 205

Tyr Thr Phe His Ala Ala Thr Pro Asp His Lys Met Thr Ser Asn Glu  
210 215 220

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101



Ser Leu Lys Ile Asn Lys Asn Met Glu Glu Phe Thr Lys Val Glu Glu  
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 Glu Met Asp Val Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Glu  
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 197  
 Leu Ile Asn Tyr Ile Ala Ser His Gly Glu Gly Arg Trp Asn Ser Leu  
 40 45 50  
 gct cgt tgc gcc gaa ctc aaa agg acc gga aaa agc tgc aga ctt cgg  
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 Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg  
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 293  
 Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu  
 75 80 85  
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 341  
 Glu Glu Gln Leu Leu Ile Leu Glu Leu His Thr Arg Trp Gly Asn Arg  
 90 95 100  
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 389  
 Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile  
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 437  
 Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys  
 120 125 130  
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 485  
 Cys Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp  
 135 140 145 150  
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 Met Pro Arg Leu Val Glu Arg Ile Gln Ala Ala Ser Ile Gly Ser Val  
 155 160 165  
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 170 175 180  
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 Asn Asn Asn Thr Asn Asn Val Asp Asn Leu Ala Leu Met Ser Asn Pro  
 185 190 195  
 aat ggt tac atc acg ccg gat aat tcc agc gtg gca gta tct cct gta  
 677  
 Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser Val Ala Val Ser Pro Val  
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 Ser Asp Leu Thr Glu Cys Gln Val Ser Ser Glu Val Trp Lys Ile Gly  
 215                      220                      225                      230  
 cag gat gag aat ttg gtg gat cca aaa atg aca tcg ccg aat tat atg  
 773  
 Gln Asp Glu Asn Leu Val Asp Pro Lys Met Thr Ser Pro Asn Tyr Met  
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 821  
 Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp Phe Thr Lys Met Gln Asp  
                                  250                      255                      260  
 caa agt gac ctt aat tgg ttt gaa aat att aat ggg atg gta cca aat  
 869  
 Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile Asn Gly Met Val Pro Asn  
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 Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn Asp Glu Asp Phe Trp Leu  
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 tta caa caa cat caa caa gtc cac gac aat gga agc ttc tga  
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 Val Glu Glu Asp Leu Glu Leu Ile Asn Tyr Ile Ala Ser His Gly Glu  
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 Gly Arg Trp Asn Ser Leu Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly  
                                  50                      55                      60  
 Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg  
 65                      70                      75                      80  
 Arg Gly Asn Ile Thr Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His  
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Thr Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly  
100 105 110

Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys  
115 120 125

His Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Gln Gln Phe Lys Asp  
130 135 140

Thr Met Lys Tyr Leu Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala  
145 150 155 160

Ala Ser Ile Gly Ser Val Ser Met Ser Ser Cys Val Thr Thr Ser Ser  
165 170 175

Asp Gln Phe Val Ile Asn Asn Asn Asn Thr Asn Asn Val Asp Asn Leu  
180 185 190

Ala Leu Met Ser Asn Pro Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser  
195 200 205

Val Ala Val Ser Pro Val Ser Asp Leu Thr Glu Cys Gln Val Ser Ser  
210 215 220

Glu Val Trp Lys Ile Gly Gln Asp Glu Asn Leu Val Asp Pro Lys Met  
225 230 235 240

Thr Ser Pro Asn Tyr Met Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp  
245 250 255

Phe Thr Lys Met Gln Asp Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile  
260 265 270

Asn Gly Met Val Pro Asn Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn  
275 280 285

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Gly Ser Phe  
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120

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169

Met Asp Pro Ser Leu Ser Ala Thr Asn Asp Pro His His Pro  
1 5 10

cct cct cct cag ttc aca tct ttc cct cct ttc acc aac acc aac ccc  
217

Pro Pro Pro Gln Phe Thr Ser Phe Pro Pro Phe Thr Asn Thr Asn Pro  
15 20 25 30

ttc gcc tct cca aac cac ccc ttc ttc acc gga ccc acc gcc gtc ggc  
265

Phe Ala Ser Pro Asn His Pro Phe Phe Thr Gly Pro Thr Ala Val Ala  
35 40 45

ccg cca aac aac atc cat ctc tat caa gca gct cct ccg cag cag cca  
313

Pro Pro Asn Asn Ile His Leu Tyr Gln Ala Ala Pro Pro Gln Gln Pro  
50 55 60

caa aca tct cca gtt cct cct cat cca tct att tcc cac cct cct tac  
361

Gln Thr Ser Pro Val Pro Pro His Pro Ser Ile Ser His Pro Pro Tyr  
65 70 75

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409

Ser Asp Met Ile Cys Thr Ala Ile Ala Ala Leu Asn Glu Pro Asp Gly  
80 85 90

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457

Ser Ser Lys Gln Ala Ile Ser Arg Tyr Ile Glu Arg Ile Tyr Thr Gly  
95 100 105 110

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505

Ile Pro Thr Ala His Gly Ala Leu Leu Thr His His Leu Lys Thr Leu  
115 120 125

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553

Lys Thr Ser Gly Ile Leu Val Met Val Lys Lys Ser Tyr Lys Leu Ala  
130 135 140

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601

Ser Thr Pro Pro Pro Pro Pro Pro Thr Ser Val Ala Pro Ser Leu Glu  
145 150 155

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649

Pro Pro Arg Ser Asp Phe Ile Val Asn Glu Asn Gln Pro Leu Pro Asp  
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 210 215 220

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 305 310 315

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 Ala Ser Ser Val Ala Pro Pro Pro Pro Pro Pro Thr Asn Val Glu Ser  
 320 325 330

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 335 340 345 350

aag att gga ggt gtt atc agg aag cct atg aag ccg atg aga agc ttt  
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Ala Arg Thr Gly Lys Pro Val Gly Arg Pro Arg Lys Asn Ala Val Ser  
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1321

Val Gly Ala Ser Gly Arg Gln Asp Gly Asp Tyr Gly Glu Leu Lys Lys  
385 390 395

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1369

Lys Phe Glu Leu Phe Gln Ala Arg Ala Lys Asp Ile Val Ile Val Leu  
400 405 410

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1417

Lys Ser Glu Ile Gly Gly Ser Gly Asn Gln Ala Val Val Gln Ala Ile  
415 420 425 430

cag gac ctg gaa ggg ata gca gag aca aca aac gag cca aag cac atg  
1465

Gln Asp Leu Glu Gly Ile Ala Glu Thr Thr Asn Glu Pro Lys His Met  
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1513

Glu Glu Val Gln Leu Pro Asp Glu Glu His Leu Glu Thr Glu Pro Glu  
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Ala Glu Gly Gln Gly Gln Thr Glu Ala Glu Ala Met Gln Glu Ala Leu  
465 470 475

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Phe

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1677

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1797

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1857

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1917

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 Asn Asn Ile His Leu Tyr Gln Ala Ala Pro Pro Gln Gln Pro Gln Thr  
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 Ser Pro Val Pro Pro His Pro Ser Ile Ser His Pro Pro Tyr Ser Asp  
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 Lys Gln Ala Ile Ser Arg Tyr Ile Glu Arg Ile Tyr Thr Gly Ile Pro  
 100 105 110  
 Thr Ala His Gly Ala Leu Leu Thr His His Leu Lys Thr Leu Lys Thr  
 115 120 125  
 Ser Gly Ile Leu Val Met Val Lys Lys Ser Tyr Lys Leu Ala Ser Thr  
 130 135 140  
 Pro Pro Pro Pro Pro Pro Thr Ser Val Ala Pro Ser Leu Glu Pro Pro  
 145 150 155 160  
 Arg Ser Asp Phe Ile Val Asn Glu Asn Gln Pro Leu Pro Asp Pro Val  
 165 170 175  
 Leu Ala Ser Ser Thr Pro Gln Thr Ile Lys Arg Gly Arg Gly Arg Pro  
 180 185 190  
 Pro Lys Ala Lys Pro Asp Val Val Gln Pro Gln Pro Leu Thr Asn Gly  
 195 200 205  
 Lys Leu Thr Trp Glu Gln Ser Glu Leu Pro Val Ser Arg Pro Glu Glu  
 210 215 220  
 Ile Gln Ile Gln Pro Pro Gln Leu Pro Leu Gln Pro Gln Gln Pro Val  
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376



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ctttagctta gcttagcttc tactgatctg tttttgctac aaaatcccat ctttttcttt  
 120

aaaactcttt atctctgaat cttgagtttc ttgtagaaga agaagcaatt ttgaatcttt  
 180

cgtaatcata aagattcgtg gaggatctct actgatttgt cggaatctct cactacagaa  
 240

tcacttgatc ttatgtccgg atg gag gag aga gaa gga acc aac atc aac aac  
 293

Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn  
 1 5 10

aac atc act agc agt ttc ggc ttg aag cag caa cat gaa gct gct gct  
 341

Asn Ile Thr Ser Ser Phe Gly Leu Lys Gln Gln His Glu Ala Ala Ala  
 15 20 25

tct gat ggt ggt tac tca atg gac cca cca cca aga ccc gaa aac cct  
 389

Ser Asp Gly Gly Tyr Ser Met Asp Pro Pro Pro Arg Pro Glu Asn Pro  
 30 35 40

aac ccg ttt tta gtc cca ccc act act gtc ccc gcg gcc gcc acc gta  
 437

Asn Pro Phe Leu Val Pro Pro Thr Thr Val Pro Ala Ala Ala Thr Val  
 45 50 55

gca gca gct gtt act gag aat gcg gct act ccg ttt agc tta aca atg  
 485

Ala Ala Ala Val Thr Glu Asn Ala Ala Thr Pro Phe Ser Leu Thr Met  
 60 65 70 75

ccg acg gag aac act tca gct gag cag ctg aaa aag aag aga ggt agg  
 533

Pro Thr Glu Asn Thr Ser Ala Glu Gln Leu Lys Lys Lys Arg Gly Arg  
 80 85 90

ccg aga aag tat aat ccc gat ggg act ctt gtc gtg act tta tcg ccg  
 581

Pro Arg Lys Tyr Asn Pro Asp Gly Thr Leu Val Val Thr Leu Ser Pro  
 95 100 105

atg cca atc tcg tcc tct gtt ccg ttg acg tcg gag ttt cct cca agg  
 629

Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe Pro Pro Arg  
 110 115 120

aaa cga gga aga gga cgt ggc aag tct aat cga tgg ctc aag aag tct  
 677

Lys Arg Gly Arg Gly Arg Gly Lys Ser Asn Arg Trp Leu Lys Lys Ser  
 125 130 135



caa atg ttc caa ttc gat aga agt cct gtt gat acc aat ttg gca ggt  
 725  
 Gln Met Phe Gln Phe Asp Arg Ser Pro Val Asp Thr Asn Leu Ala Gly  
 140 145 150 155  
  
 gta gga act gct gat ttt gtt ggt gcc aac ttt aca cct cat gta ctg  
 773  
 Val Gly Thr Ala Asp Phe Val Gly Ala Asn Phe Thr Pro His Val Leu  
 160 165 170  
  
 atc gtc aac gcc gga gag gat gtg acg atg aag ata atg aca ttc tct  
 821  
 Ile Val Asn Ala Gly Glu Asp Val Thr Met Lys Ile Met Thr Phe Ser  
 175 180 185  
  
 caa caa gga tct cgt gct atc tgc atc ctt tca gct aat ggt ccc atc  
 869  
 Gln Gln Gly Ser Arg Ala Ile Cys Ile Leu Ser Ala Asn Gly Pro Ile  
 190 195 200  
  
 tcc aat gtt acg ctt cgt caa tct atg aca tcc ggt ggt act cta act  
 917  
 Ser Asn Val Thr Leu Arg Gln Ser Met Thr Ser Gly Gly Thr Leu Thr  
 205 210 215  
  
 tat gag ggt cgt ttt gag att ctc tct ttg acg ggt tcg ttt atg caa  
 965  
 Tyr Glu Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ser Phe Met Gln  
 220 225 230 235  
  
 aat gac tct gga gga act cga agt aga gct ggt ggt atg agt gtt tgc  
 1013  
 Asn Asp Ser Gly Gly Thr Arg Ser Arg Ala Gly Gly Met Ser Val Cys  
 240 245 250  
  
 ctt gca gga cca gat ggt cgt gtc ttt ggt gga gga ctc gct ggt ctc  
 1061  
 Leu Ala Gly Pro Asp Gly Arg Val Phe Gly Gly Gly Leu Ala Gly Leu  
 255 260 265  
  
 ttt ctt gct gct ggt cct gtc cag gta atg gta ggg act ttt ata gct  
 1109  
 Phe Leu Ala Ala Gly Pro Val Gln Val Met Val Gly Thr Phe Ile Ala  
 270 275 280  
  
 ggt caa gag cag tca cag ctg gag cta gca aaa gaa aga cgg cta aga  
 1157  
 Gly Gln Glu Gln Ser Gln Leu Glu Leu Ala Lys Glu Arg Arg Leu Arg  
 285 290 295  
  
 ttt ggg gct caa cca tct tct atc tcc ttt aac ata tcc gca gaa gaa  
 1205  
 Phe Gly Ala Gln Pro Ser Ser Ile Ser Phe Asn Ile Ser Ala Glu Glu  
 300 305 310 315  
  
 cgg aag gcg aga ttc gag agg ctt aac aag tct gtt gct att cct gca  
 1253  
 Arg Lys Ala Arg Phe Glu Arg Leu Asn Lys Ser Val Ala Ile Pro Ala  
 320 325 330



cca acc act tca tac acg cat gta aac aca aca aat gcg gtt cac agt  
1301

Pro Thr Thr Ser Tyr Thr His Val Asn Thr Thr Asn Ala Val His Ser  
335 340 345

tac tat aca aac tcg gtt aac cat gtc aag gat ccc ttc tcg tct atc  
1349

Tyr Tyr Thr Asn Ser Val Asn His Val Lys Asp Pro Phe Ser Ser Ile  
350 355 360

cca gta gga gga gga gga ggt gga gag gta gga gaa gaa gag ggt gaa  
1397

Pro Val Gly Gly Gly Gly Gly Gly Glu Val Gly Glu Glu Glu Gly Glu  
365 370 375

gaa gat gat gat gaa tta gaa ggt gaa gac gaa gaa ttc gga ggc gat  
1445

Glu Asp Asp Asp Glu Leu Glu Gly Glu Asp Glu Glu Phe Gly Gly Asp  
380 385 390 395

agc caa tct gac aac gag att ccg agc tga tgatgatcat acggtttctt  
1495

Ser Gln Ser Asp Asn Glu Ile Pro Ser  
400

ttcgcggtt tgtaggttt gatggatttc agattttggt tgattgtttt tattaacaca  
1555

gaatgttttag aagctgctat ctttaggttc ccatcctctt gtgattgttg agtatccttg  
1615

ttagaaacaa acttactgtt gcaaaactct cttaaaaaa gtttcacttt gctttccca  
1674

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212

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1 5 10 15

Phe Gly Leu Lys Gln Gln His Glu Ala Ala Ala Ser Asp Gly Gly Tyr  
20 25 30

Ser Met Asp Pro Pro Pro Arg Pro Glu Asn Pro Asn Pro Phe Leu Val  
35 40 45

Pro Pro Thr Thr Val Pro Ala Ala Ala Thr Val Ala Ala Ala Val Thr  
50 55 60

Glu Asn Ala Ala Thr Pro Phe Ser Leu Thr Met Pro Thr Glu Asn Thr  
65 70 75 80

Ser Ala Glu Gln Leu Lys Lys Lys Arg Gly Arg Pro Arg Lys Tyr Asn  
85 90 95



Pro Asp Gly Thr Leu Val Val Thr Leu Ser Pro Met Pro Ile Ser Ser  
100 105 110

Ser Val Pro Leu Thr Ser Glu Phe Pro Pro Arg Lys Arg Gly Arg Gly  
115 120 125

Arg Gly Lys Ser Asn Arg Trp Leu Lys Lys Ser Gln Met Phe Gln Phe  
130 135 140

Asp Arg Ser Pro Val Asp Thr Asn Leu Ala Gly Val Gly Thr Ala Asp  
145 150 155 160

Phe Val Gly Ala Asn Phe Thr Pro His Val Leu Ile Val Asn Ala Gly  
165 170 175

Glu Asp Val Thr Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg  
180 185 190

Ala Ile Cys Ile Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu  
195 200 205

Arg Gln Ser Met Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly Arg Phe  
210 215 220

Glu Ile Leu Ser Leu Thr Gly Ser Phe Met Gln Asn Asp Ser Gly Gly  
225 230 235 240

Thr Arg Ser Arg Ala Gly Gly Met Ser Val Cys Leu Ala Gly Pro Asp  
245 250 255

Gly Arg Val Phe Gly Gly Gly Leu Ala Gly Leu Phe Leu Ala Ala Gly  
260 265 270

Pro Val Gln Val Met Val Gly Thr Phe Ile Ala Gly Gln Glu Gln Ser  
275 280 285

Gln Leu Glu Leu Ala Lys Glu Arg Arg Leu Arg Phe Gly Ala Gln Pro  
290 295 300

Ser Ser Ile Ser Phe Asn Ile Ser Ala Glu Glu Arg Lys Ala Arg Phe  
305 310 315 320

Glu Arg Leu Asn Lys Ser Val Ala Ile Pro Ala Pro Thr Thr Ser Tyr  
325 330 335



Thr His Val Asn Thr Thr Asn Ala Val His Ser Tyr Tyr Thr Asn Ser  
340 345 350

Val Asn His Val Lys Asp Pro Phe Ser Ser Ile Pro Val Gly Gly Gly  
355 360 365

Gly Gly Gly Glu Val Gly Glu Glu Glu Gly Glu Glu Asp Asp Asp Glu  
370 375 380

Leu Glu Gly Glu Asp Glu Glu Phe Gly Gly Asp Ser Gln Ser Asp Asn  
385 390 395 400

Glu Ile Pro Ser

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gaagaaaaagg ctatattttaa aagaaaaatca agcaaaaagta gatcctcgg atg tat ggg  
118

Met Tyr Gly  
1

aag agg cct ttt gga ggt gat gaa tct gaa gaa agg gaa gaa gat gag  
166  
Lys Arg Pro Phe Gly Gly Asp Glu Ser Glu Glu Arg Glu Glu Asp Glu  
5 10 15

aac ttg ttc ccg gtc ttc tcg gcc cga tct caa cac gac atg cgt gtt  
214  
Asn Leu Phe Pro Val Phe Ser Ala Arg Ser Gln His Asp Met Arg Val  
20 25 30 35

atg gtc tcg gcc ttg act caa gta atc gga aac caa caa agc aaa tct  
262  
Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Gln Ser Lys Ser  
40 45 50

cat gat aac atc agc tct att gat gat aac tat cct tct gtg tat aat  
310  
His Asp Asn Ile Ser Ser Ile Asp Asp Asn Tyr Pro Ser Val Tyr Asn  
55 60 65

cca caa gac cct aat caa caa gtt gcg cct act cat caa gac caa ggg  
358  
Pro Gln Asp Pro Asn Gln Gln Val Ala Pro Thr His Gln Asp Gln Gly  
70 75 80

gac ttg agg agg aga cat tat aga ggt gta agg caa agg cca tgg gga  
406  
Asp Leu Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly  
85 90 95



aag tgg gca gct gaa atc cga gac cca aaa aag gcg gca cgt gtg tgg  
454  
Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp  
100 105 110 115  
ctc ggg aca ttt gaa acc gct gaa tct gcg gcc tta gct tat gat gaa  
502  
Leu Gly Thr Phe Glu Thr Ala Glu Ser Ala Ala Leu Ala Tyr Asp Glu  
120 125 130  
gca gcc cta aag ttc aaa gga agc aaa gca aaa ctc aat ttc ccg gag  
550  
Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu  
135 140 145  
agg gtt cag ctt gga agt aac tct aca tat tac tcc tcc aac caa att  
598  
Arg Val Gln Leu Gly Ser Asn Ser Thr Tyr Tyr Ser Ser Asn Gln Ile  
150 155 160  
cca caa atg gaa cca caa agt ata ccg aac tat aat caa tac tat cat  
646  
Pro Gln Met Glu Pro Gln Ser Ile Pro Asn Tyr Asn Gln Tyr Tyr His  
165 170 175  
gat gcg agt agt ggt gat atg cta agt ttt aat ttg ggc ggt ggg tat  
694  
Asp Ala Ser Ser Gly Asp Met Leu Ser Phe Asn Leu Gly Gly Gly Tyr  
180 185 190 195  
ggg agt ggt acc gga tat tca atg tct cat gat aat agt act acg act  
742  
Gly Ser Gly Thr Gly Tyr Ser Met Ser His Asp Asn Ser Thr Thr Thr  
200 205 210  
gct gct aca act tct tcg tct tct ggt ggc tct tct agg caa caa gaa  
790  
Ala Ala Thr Thr Ser Ser Ser Ser Gly Gly Ser Ser Arg Gln Gln Glu  
215 220 225  
gag caa gat tat gcc aga ttc tgg cgc ttt ggg gat tct tct tcc tct  
838  
Glu Gln Asp Tyr Ala Arg Phe Trp Arg Phe Gly Asp Ser Ser Ser Ser  
230 235 240  
cct cat tcg gga tat taa ttaggagatt tgatcagtta cttgtgatga  
886  
Pro His Ser Gly Tyr  
245  
agtaatgata catttcccg caaaattgag atgatcatat gcttctgaa tgtttttgag  
946  
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1006  
aaaaaaaaa aaaaaaaaaa aaaaaaaaa  
1034



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214

Met Tyr Gly Lys Arg Pro Phe Gly Gly Asp Glu Ser Glu Glu Arg Glu  
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Glu Asp Glu Asn Leu Phe Pro Val Phe Ser Ala Arg Ser Gln His Asp  
20 25 30

Met Arg Val Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Gln  
35 40 45

Ser Lys Ser His Asp Asn Ile Ser Ser Ile Asp Asp Asn Tyr Pro Ser  
50 55 60

Val Tyr Asn Pro Gln Asp Pro Asn Gln Gln Val Ala Pro Thr His Gln  
65 70 75 80

Asp Gln Gly Asp Leu Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg  
85 90 95

Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala  
100 105 110

Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ser Ala Ala Leu Ala  
115 120 125

Tyr Asp Glu Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys Leu Asn  
130 135 140

Phe Pro Glu Arg Val Gln Leu Gly Ser Asn Ser Thr Tyr Tyr Ser Ser  
145 150 155 160

Asn Gln Ile Pro Gln Met Glu Pro Gln Ser Ile Pro Asn Tyr Asn Gln  
165 170 175

Tyr Tyr His Asp Ala Ser Ser Gly Asp Met Leu Ser Phe Asn Leu Gly  
180 185 190

Gly Gly Tyr Gly Ser Gly Thr Gly Tyr Ser Met Ser His Asp Asn Ser  
195 200 205

Thr Thr Thr Ala Ala Thr Thr Ser Ser Ser Ser Gly Gly Ser Ser Arg  
210 215 220

Gln Gln Glu Glu Gln Asp Tyr Ala Arg Phe Trp Arg Phe Gly Asp Ser  
225 230 235 240



Ser Ser Ser Pro His Ser Gly Tyr  
245

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53

Met Ala Ser Ser His Gln Gln Gln Gln  
1 5

gaa caa gac cag tca gct tta gat ctc ata acc caa cac ctt ctt act  
101  
Glu Gln Asp Gln Ser Ala Leu Asp Leu Ile Thr Gln His Leu Leu Thr  
10 15 20 25

gat ttc cct tcc tta gac acc ttt gcc tcc acc atc cac cac tgc acc  
149  
Asp Phe Pro Ser Leu Asp Thr Phe Ala Ser Thr Ile His His Cys Thr  
30 35 40

acc tca act cta agc caa cgc aaa cca cct ctt gcc act ata gca gtt  
197  
Thr Ser Thr Leu Ser Gln Arg Lys Pro Pro Leu Ala Thr Ile Ala Val  
45 50 55

cct act act gca ccg gtg gtt caa gag aat gat caa agg cat tac aga  
245  
Pro Thr Thr Ala Pro Val Val Gln Glu Asn Asp Gln Arg His Tyr Arg  
60 65 70

ggc gtc agg aga aga cca tgg ggt aag tat gcg gct gag atc aga gac  
293  
Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp  
75 80 85

cca aac aag aaa ggt gtt cgt gtc tgg tta ggc act ttt gac aca gcc  
341  
Pro Asn Lys Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asp Thr Ala  
90 95 100 105

atg gaa gct gca aga ggt tat gac aag gca gct ttt aaa cta cga gga  
389  
Met Glu Ala Ala Arg Gly Tyr Asp Lys Ala Ala Phe Lys Leu Arg Gly  
110 115 120

agc aaa gct att ctt aac ttc cca ctt gaa gca gga aag cat gag gac  
437  
Ser Lys Ala Ile Leu Asn Phe Pro Leu Glu Ala Gly Lys His Glu Asp  
125 130 135

ttg gga gac aac aag aag act att tct tta aaa gca aag agg aag aga  
485  
Leu Gly Asp Asn Lys Lys Thr Ile Ser Leu Lys Ala Lys Arg Lys Arg  
140 145 150



cag gtg acg gag gat gaa agc cag ctg atc agc cgt aaa gct gtt aag  
533

Gln Val Thr Glu Asp Glu Ser Gln Leu Ile Ser Arg Lys Ala Val Lys  
155 160 165

agg gaa gaa gct cag gtt cag gct gat gct tgt cca tta acg cca tca  
581

Arg Glu Glu Ala Gln Val Gln Ala Asp Ala Cys Pro Leu Thr Pro Ser  
170 175 180 185

agt tgg aag ggg ttt tgg gac gga gca gac agt aaa gac atg gga ata  
629

Ser Trp Lys Gly Phe Trp Asp Gly Ala Asp Ser Lys Asp Met Gly Ile  
190 195 200

ttt tcc gtg cct ctg tta tct cct tgt cca tct ctt gga cac tct caa  
677

Phe Ser Val Pro Leu Leu Ser Pro Cys Pro Ser Leu Gly His Ser Gln  
205 210 215

ctc gta gtt act taa gcttcagagg gtcaaactgg aaaaaatcaa cattggattg  
732

Leu Val Val Thr  
220

ttttcaaagc ttctagatta gctgattgta aaaaaatggt ttactatatt cattcattct  
792

tcttaaagtc aattctttct acccttcc  
820

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Asp Leu Ile Thr Gln His Leu Leu Thr Asp Phe Pro Ser Leu Asp Thr  
20 25 30

Phe Ala Ser Thr Ile His His Cys Thr Thr Ser Thr Leu Ser Gln Arg  
35 40 45

Lys Pro Pro Leu Ala Thr Ile Ala Val Pro Thr Thr Ala Pro Val Val  
50 55 60

Gln Glu Asn Asp Gln Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp  
65 70 75 80

Gly Lys Tyr Ala Ala Glu Ile Arg Asp Pro Asn Lys Lys Gly Val Arg  
85 90 95

Val Trp Leu Gly Thr Phe Asp Thr Ala Met Glu Ala Ala Arg Gly Tyr  
100 105 110

385



Asp Lys Ala Ala Phe Lys Leu Arg Gly Ser Lys Ala Ile Leu Asn Phe  
 115 120 125

Pro Leu Glu Ala Gly Lys His Glu Asp Leu Gly Asp Asn Lys Lys Thr  
 130 135 140

Ile Ser Leu Lys Ala Lys Arg Lys Arg Gln Val Thr Glu Asp Glu Ser  
 145 150 155 160

Gln Leu Ile Ser Arg Lys Ala Val Lys Arg Glu Glu Ala Gln Val Gln  
 165 170 175

Ala Asp Ala Cys Pro Leu Thr Pro Ser Ser Trp Lys Gly Phe Trp Asp  
 180 185 190

Gly Ala Asp Ser Lys Asp Met Gly Ile Phe Ser Val Pro Leu Leu Ser  
 195 200 205

Pro Cys Pro Ser Leu Gly His Ser Gln Leu Val Val Thr  
 210 215 220

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ctcttgattc cataagcata tattaataaaa gctctctgct ttcttcaact ttcccgaggaa  
 120

aatcttcttg ttacaaagca tcaatctctt gttttaccaa ttttctctct ttattccttt  
 180

tttgcccttt acttttccta acttttgtct ttatatataa acacacgaca caaagaagaa  
 240

cacacataag ttaaaactat tacaacagtt ttaaagagag agatttaaaa a atg gag  
 297

Met Glu  
 1

aca gag aag aaa gtt tct ctc cca aga atc tta cga atc tot gtt act  
 345

Thr Glu Lys Lys Val Ser Leu Pro Arg Ile Leu Arg Ile Ser Val Thr  
 5 10 15

gat cct tac gca aca gat tcg tca agc gac gaa gaa gaa gaa gtt gat  
 393

Asp Pro Tyr Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Glu Val Asp  
 20 25 30



ttt gat gca tta tct aca aaa cga cgt cgt gtt aag aag tac gtg aag  
 441  
 Phe Asp Ala Leu Ser Thr Lys Arg Arg Arg Val Lys Lys Tyr Val Lys  
 35 40 45 50  
 gaa gtg gtg ctt gat tcg gtg gtt tct gat aaa gag aag ccg atg aag  
 489  
 Glu Val Val Leu Asp Ser Val Val Ser Asp Lys Glu Lys Pro Met Lys  
 55 60 65  
 aag aag aga aag aag cgc gtt gtt act gtt cca gtg gtt gtt acg acg  
 537  
 Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val Thr Thr  
 70 75 80  
 gcg acg agg aag ttt cgt gga gtg agg caa aga ccg tgg gga aaa tgg  
 585  
 Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp  
 85 90 95  
 gcg gcg gag att aga gat ccg agt aga cgt gtt agg gtt tgg tta ggt  
 633  
 Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp Leu Gly  
 100 105 110  
 act ttt gac acg gcg gag gaa gct gcc att gtt tac gat aac gca gct  
 681  
 Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn Ala Ala  
 115 120 125 130  
 att cag cta cgt ggt cct aac gca gag ctt aac ttc cct cct cct ccg  
 729  
 Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro Pro Pro  
 135 140 145  
 gtg acg gag aat gtt gaa gaa gct tcg acg gag gtg aaa gga gtt tcg  
 777  
 Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly Val Ser  
 150 155 160  
 gat ttt atc att ggc ggt gga gaa tgt ctt cgt tcg ccg gtt tct gtt  
 825  
 Asp Phe Ile Ile Gly Gly Gly Glu Cys Leu Arg Ser Pro Val Ser Val  
 165 170 175  
 ctc gaa tct ccg ttc tcc ggc gag tct act gcg gtt aaa gag gag ttt  
 873  
 Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Val Lys Glu Glu Phe  
 180 185 190  
 gtc ggt gta tcg acg gcg gag att gtg gtt aaa aag gag ccg tct ttt  
 921  
 Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro Ser Phe  
 195 200 205 210  
 aac ggt tca gat ttc tcg gcg ccg ttg ttc tcg gac gac gac gtt ttt  
 969  
 Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp Val Phe  
 215 220 225



ggt ttc tcg acg tcg atg agt gaa agt ttc ggc ggc gat tta ttt gga  
1017

Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu Phe Gly  
230 235 240

gat aat ctt ttt gcg gat atg agt ttt gga tcc ggg ttt gga ttc ggg  
1065

Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly Phe Gly  
245 250 255

tct ggg tct gga ttc tcc agc tgg cac gtt gag gac cat ttt caa gat  
1113

Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Phe Gln Asp  
260 265 270

att ggg gat tta ttc ggg tcg gat cct gtc tta act gtt taa  
1155

Ile Gly Asp Leu Phe Gly Ser Asp Pro Val Leu Thr Val  
275 280 285

gaaataactg gccgtttaac ggcgtttagt gaagttttgt taccggcgac ggcgaggatt  
1215

aaaaaaaaac ggcgatttat tttttgaatg aagatttggt aaata  
1260

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218

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Val Thr Asp Pro Tyr Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Glu  
20 25 30

Val Asp Phe Asp Ala Leu Ser Thr Lys Arg Arg Arg Val Lys Lys Tyr  
35 40 45

Val Lys Glu Val Val Leu Asp Ser Val Val Ser Asp Lys Glu Lys Pro  
50 55 60

Met Lys Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val  
65 70 75 80

Thr Thr Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly  
85 90 95

Lys Trp Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp  
100 105 110

Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn  
115 120 125



Ala Ala Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro  
 130 135 140

Pro Pro Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly  
 145 150 155 160

Val Ser Asp Phe Ile Ile Gly Gly Gly Glu Cys Leu Arg Ser Pro Val  
 165 170 175

Ser Val Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Val Lys Glu  
 180 185 190

Glu Phe Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro  
 195 200 205

Ser Phe Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp  
 210 215 220

Val Phe Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu  
 225 230 235 240

Phe Gly Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly  
 245 250 255

Phe Gly Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Phe  
 260 265 270

Gln Asp Ile Gly Asp Leu Phe Gly Ser Asp Pro Val Leu Thr Val  
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gga gaa gac gcc ggc ggc ggc gat gaa tat agg att ccg gaa tgg gaa  
 97

Gly Glu Asp Ala Gly Gly Gly Asp Glu Tyr Arg Ile Pro Glu Trp Glu  
 15 20 25 30

att ggt tta ccc aac gga gat gat ttg act ccg tta tct caa tat cta  
 145

Ile Gly Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu  
 35 40 45



gtc ccg tcg att ctc gcg tta gct ttc agc atg atc cca gaa cga agc  
 193  
 Val Pro Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser  
 50 55 60

cgt aca att cac gac gtc aat cgc gcg tcg caa atc acg ctc tct tcg  
 241  
 Arg Thr Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser  
 65 70 75

ttg aga agc agt acc aat gct tcg tct gtg atg gag gag gtc gtg gat  
 289  
 Leu Arg Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp  
 80 85 90

cga gtt gaa tcg agt gtt cca gga tca gat ccg aag aaa cag aag aaa  
 337  
 Arg Val Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys  
 95 100 105 110

tcg gat ggt ggt gaa gca gcg gcg gtg gag gat tcc acg gcg gag gaa  
 385  
 Ser Asp Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu  
 115 120 125

gga gac tcc ggg cct gaa gac gcg tct ggg aag aca tcg aaa cga ccg  
 433  
 Gly Asp Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro  
 130 135 140

cgt tta gtg tgg aca ccg cag cta cac aag aga ttt gtg gac gtt gtg  
 481  
 Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val  
 145 150 155

gct cat cta ggg att aaa aac gca gtg ccg aag acg att atg cag ctg  
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 Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu  
 160 165 170

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 577  
 Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln  
 175 180 185 190

aaa tat agg ctt tac ctt aaa cgg att caa gga ttg acg acg gaa gaa  
 625  
 Lys Tyr Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu  
 195 200 205

gat cct tat tcg tcg tcg gat cag ctc ttc tct tca acg ccg gtt cct  
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 Asp Pro Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro  
 210 215 220

cca cag agc ttt caa gac ggc gga gga agt aac gga aag ttg ggg gtt  
 721  
 Pro Gln Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val  
 225 230 235



ccg gtt ccg gtt ccg tcg atg gtg cct att cca ggc tat ggg aat caa  
769

Pro Val Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln  
240 245 250

atg ggt atg caa gga tat tat caa cag tat agt aac cat ggc aat gaa  
817

Met Gly Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu  
255 260 265 270

tca aac caa tat atg atg cag cag aat aag ttt gga aca atg gtg aca  
865

Ser Asn Gln Tyr Met Met Gln Gln Asn Lys Phe Gly Thr Met Val Thr  
275 280 285

tat cct tct gtt ggt ggt ggt gac gtg aat gac aag taa atggatctta  
914

Tyr Pro Ser Val Gly Gly Gly Asp Val Asn Asp Lys  
290 295

aaggctctata atttgctcta cagagagata ctgggttcttg gcttatgggtt tattttccca  
974

cttcattgagg ttgttgtgac ttttaattct ccatgttttc cacacaagtc tttattgcct  
1034

ttgtatagaa aatgatttcg agaaaatcac tgggaagcct ggtattgttg gaggatgaag  
1094

ccttctatga atgatttagt ttctactgt ctccattctt tatgaggtaa taaagccttc  
1154

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1274

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20 25 30

Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu Val Pro  
35 40 45

Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser Arg Thr  
50 55 60



Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser Leu Arg  
 65 70 75 80

Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp Arg Val  
 85 90 95

Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys Ser Asp  
 100 105 110

Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu Gly Asp  
 115 120 125

Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro Arg Leu  
 130 135 140

Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val Ala His  
 145 150 155 160

Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu Met Asn  
 165 170 175

Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln Lys Tyr  
 180 185 190

Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu Asp Pro  
 195 200 205

Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro Pro Gln  
 210 215 220

Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val Pro Val  
 225 230 235 240

Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln Met Gly  
 245 250 255

Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu Ser Asn  
 260 265 270

Gln Tyr Met Met Gln Gln Asn Lys Phe Gly Thr Met Val Thr Tyr Pro  
 275 280 285

Ser Val Gly Gly Gly Asp Val Asn Asp Lys  
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 116

Met Glu Val Ser  
 1

aac tct tgt tct tca ttt tct tca tcc tct gtc gac agt act aaa cct  
 164

Asn Ser Cys Ser Ser Phe Ser Ser Ser Ser Val Asp Ser Thr Lys Pro  
 5 10 15 20

tct cct tct gaa tct tct gtt aat ctc tcc ctt agt ctc aca ttt cct  
 212

Ser Pro Ser Glu Ser Ser Val Asn Leu Ser Leu Ser Leu Thr Phe Pro  
 25 30 35

tct act tct cca caa aga gaa gca aga caa gat tgg cca ccg ata aag  
 260

Ser Thr Ser Pro Gln Arg Glu Ala Arg Gln Asp Trp Pro Pro Ile Lys  
 40 45 50

tct aga tta aga gat aca cta aag ggt cgt cgt ctt ctt cgt cgt ggt  
 308

Ser Arg Leu Arg Asp Thr Leu Lys Gly Arg Arg Leu Leu Arg Arg Gly  
 55 60 65

gat gac act tct ctc ttt gtt aag gtt tat atg gaa ggt gtt ccc att  
 356

Asp Asp Thr Ser Leu Phe Val Lys Val Tyr Met Glu Gly Val Pro Ile  
 70 75 80

gga aga aaa ctc gac ctt tgc gta ttc tca ggc tac gag agt cta tta  
 404

Gly Arg Lys Leu Asp Leu Cys Val Phe Ser Gly Tyr Glu Ser Leu Leu  
 85 90 95 100

gaa aat ctc tct cac atg ttc gat act tca atc atc tgc ggt aat cga  
 452

Glu Asn Leu Ser His Met Phe Asp Thr Ser Ile Ile Cys Gly Asn Arg  
 105 110 115

gat cga aaa cat cat gtt ttg aca tat gaa gac aag gat gga gat tgg  
 500

Asp Arg Lys His His Val Leu Thr Tyr Glu Asp Lys Asp Gly Asp Trp  
 120 125 130

atg atg gtc gga gat att cca tgg gat atg ttt ctt gaa acc gtg aga  
 548

Met Met Val Gly Asp Ile Pro Trp Asp Met Phe Leu Glu Thr Val Arg  
 135 140 145

aga cta aag atc acg aga ccg gag agg tat taa aacttgatc ggtcaaggct  
 601

Arg Leu Lys Ile Thr Arg Pro Glu Arg Tyr  
 150 155



gtgattgcgc agttacgaga cgtgtaagat ttaggcattg atgaagagac ttgaggcggg  
661

acggagctat tgctgcatat tgcaacaaag gccttgaaga agttggagaa ttgattgatg  
721

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781

ccaagacttc tctttaaa  
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1 5 10 15

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20 25 30

Leu Thr Phe Pro Ser Thr Ser Pro Gln Arg Glu Ala Arg Gln Asp Trp  
35 40 45

Pro Pro Ile Lys Ser Arg Leu Arg Asp Thr Leu Lys Gly Arg Arg Leu  
50 55 60

Leu Arg Arg Gly Asp Asp Thr Ser Leu Phe Val Lys Val Tyr Met Glu  
65 70 75 80

Gly Val Pro Ile Gly Arg Lys Leu Asp Leu Cys Val Phe Ser Gly Tyr  
85 90 95

Glu Ser Leu Leu Glu Asn Leu Ser His Met Phe Asp Thr Ser Ile Ile  
100 105 110

Cys Gly Asn Arg Asp Arg Lys His His Val Leu Thr Tyr Glu Asp Lys  
115 120 125

Asp Gly Asp Trp Met Met Val Gly Asp Ile Pro Trp Asp Met Phe Leu  
130 135 140

Glu Thr Val Arg Arg Leu Lys Ile Thr Arg Pro Glu Arg Tyr  
145 150 155

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116

Met  
1

gaa cac caa ggt tgg agt ttt gag gag aat tat agt ttg tcc act aat  
164

Glu His Gln Gly Trp Ser Phe Glu Glu Asn Tyr Ser Leu Ser Thr Asn  
5 10 15

aga aga tct atc agg cca caa gat gaa cta gtg gag tta tta tgg cga  
212

Arg Arg Ser Ile Arg Pro Gln Asp Glu Leu Val Glu Leu Leu Trp Arg  
20 25 30

gat gga caa gtg gtt ctg cag agc caa act cat aga gaa caa acc caa  
260

Asp Gly Gln Val Val Leu Gln Ser Gln Thr His Arg Glu Gln Thr Gln  
35 40 45

acc cag aaa caa gat cat cat gaa gaa gcc cta aga tcc agc acc ttt  
308

Thr Gln Lys Gln Asp His His Glu Glu Ala Leu Arg Ser Ser Thr Phe  
50 55 60 65

ctt gaa gat caa gaa act gtc tct tgg atc caa tac cct cca gat gaa  
356

Leu Glu Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro Asp Glu  
70 75 80

gac cca ttc gaa ccc gac gac ttc tcc tcc cac ttc ttc tca acc atg  
404

Asp Pro Phe Glu Pro Asp Asp Phe Ser Ser His Phe Phe Ser Thr Met  
85 90 95

gat ccc ctc cag aga cca acc tca gag acg gtt aag cct aag tcc agt  
452

Asp Pro Leu Gln Arg Pro Thr Ser Glu Thr Val Lys Pro Lys Ser Ser  
100 105 110

cct gaa cct cct caa gtc atg gtt aag cct aag gcc tgt cct gac cct  
500

Pro Glu Pro Pro Gln Val Met Val Lys Pro Lys Ala Cys Pro Asp Pro  
115 120 125

cct cct caa gtc atg cct cct cca aaa ttt agg tta aca aat tca tca  
548

Pro Pro Gln Val Met Pro Pro Pro Lys Phe Arg Leu Thr Asn Ser Ser  
130 135 140 145

tcg ggg att agg gaa aca gaa atg gaa cag tac tcg gta acg acc gtt  
596

Ser Gly Ile Arg Glu Thr Glu Met Glu Gln Tyr Ser Val Thr Thr Val  
150 155 160

gga cct agc cat tgc gga agc aac cca tca cag aac gat ctc gat gtc  
644

Gly Pro Ser His Cys Gly Ser Asn Pro Ser Gln Asn Asp Leu Asp Val



165	170	175
tca atg agt cat gat cga agc aaa aac ata gaa gaa aag ctt aat ccg		
692		
Ser Met Ser His Asp Arg Ser Lys Asn Ile Glu Glu Lys Leu Asn Pro		
180	185	190
aac gca agt tcc tca tca ggt ggc tcc tct ggt tgc agc ttt ggc aaa		
740		
Asn Ala Ser Ser Ser Ser Gly Gly Ser Ser Gly Cys Ser Phe Gly Lys		
195	200	205
gat atc aaa gaa atg gct agt gga aga tgc atc aca acc gac cgt aag		
788		
Asp Ile Lys Glu Met Ala Ser Gly Arg Cys Ile Thr Thr Asp Arg Lys		
210	215	220 225
aga aaa cgt ata aat cac act gac gaa tct gta tct cta tca gat gca		
836		
Arg Lys Arg Ile Asn His Thr Asp Glu Ser Val Ser Leu Ser Asp Ala		
	230 235	240
atc ggt aac aag tcg aac caa cga tca gga tca aac cga agg agt cga		
884		
Ile Gly Asn Lys Ser Asn Gln Arg Ser Gly Ser Asn Arg Arg Ser Arg		
	245 250	255
gca gct gaa gtt cat aat ctc tcc gaa agg agg agg aga gat agg atc		
932		
Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile		
	260 265	270
aat gag aga atg aag gct ttg caa gaa cta ata cct cac tgc agt aaa		
980		
Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Lys		
	275 280	285
act gat aaa gct tcg att tta gac gaa gcc ata gat tat ttg aaa tca		
1028		
Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser		
290	295	300 305
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1076		
Leu Gln Leu Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala Ala		
	310 315	320
gcg gcg gct tcg gct ccg atg atg ttc ccc gga gtt caa cct cag cag		
1124		
Ala Ala Ala Ser Ala Pro Met Met Phe Pro Gly Val Gln Pro Gln Gln		
	325 330	335
ttc ata cgt cag ata cag agc ccg gta cag tta cct cga ttt ccg gtt		
1172		
Phe Ile Arg Gln Ile Gln Ser Pro Val Gln Leu Pro Arg Phe Pro Val		
	340 345	350
atg gat cag tct gca att cag aac aat ccc ggt tta gtt tgc caa aac		
1220		
Met Asp Gln Ser Ala Ile Gln Asn Asn Pro Gly Leu Val Cys Gln Asn		
	355 360	365



ccg gta caa aac cag atc atc tcc gac cgg ttt gct aga tac atc ggt  
1268

Pro Val Gln Asn Gln Ile Ile Ser Asp Arg Phe Ala Arg Tyr Ile Gly  
370 375 380 385

ggg ttc cca cac atg cag gcc gcg act cag atg cag ccg atg gag atg  
1316

Gly Phe Pro His Met Gln Ala Ala Thr Gln Met Gln Pro Met Glu Met  
390 395 400

ttg aga ttt agt tca ccg gcg gga cag caa agt caa caa ccg tcg tct  
1364

Leu Arg Phe Ser Ser Pro Ala Gly Gln Gln Ser Gln Gln Pro Ser Ser  
405 410 415

gtg ccg acg aag acc acc gac ggt tct cgt ttg gac cac tag  
1406

Val Pro Thr Lys Thr Thr Asp Gly Ser Arg Leu Asp His  
420 425 430

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1424

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20 25 30

Arg Asp Gly Gln Val Val Leu Gln Ser Gln Thr His Arg Glu Gln Thr  
35 40 45

Gln Thr Gln Lys Gln Asp His His Glu Glu Ala Leu Arg Ser Ser Thr  
50 55 60

Phe Leu Glu Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro Asp  
65 70 75 80

Glu Asp Pro Phe Glu Pro Asp Asp Phe Ser Ser His Phe Phe Ser Thr  
85 90 95

Met Asp Pro Leu Gln Arg Pro Thr Ser Glu Thr Val Lys Pro Lys Ser  
100 105 110

Ser Pro Glu Pro Pro Gln Val Met Val Lys Pro Lys Ala Cys Pro Asp  
115 120 125

Pro Pro Pro Gln Val Met Pro Pro Pro Lys Phe Arg Leu Thr Asn Ser



130                      135                      140  
 Ser Ser Gly Ile Arg Glu Thr Glu Met Glu Gln Tyr Ser Val Thr Thr  
 145                      150                      155                      160  
 Val Gly Pro Ser His Cys Gly Ser Asn Pro Ser Gln Asn Asp Leu Asp  
 165                      170                      175  
 Val Ser Met Ser His Asp Arg Ser Lys Asn Ile Glu Glu Lys Leu Asn  
 180                      185                      190  
 Pro Asn Ala Ser Ser Ser Ser Gly Gly Ser Ser Gly Cys Ser Phe Gly  
 195                      200                      205  
 Lys Asp Ile Lys Glu Met Ala Ser Gly Arg Cys Ile Thr Thr Asp Arg  
 210                      215                      220  
 Lys Arg Lys Arg Ile Asn His Thr Asp Glu Ser Val Ser Leu Ser Asp  
 225                      230                      235                      240  
 Ala Ile Gly Asn Lys Ser Asn Gln Arg Ser Gly Ser Asn Arg Arg Ser  
 245                      250                      255  
 Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Asp Arg  
 260                      265                      270  
 Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser  
 275                      280                      285  
 Lys Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys  
 290                      295                      300  
 Ser Leu Gln Leu Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala  
 305                      310                      315                      320  
 Ala Ala Ala Ala Ser Ala Pro Met Met Phe Pro Gly Val Gln Pro Gln  
 325                      330                      335  
 Gln Phe Ile Arg Gln Ile Gln Ser Pro Val Gln Leu Pro Arg Phe Pro  
 340                      345                      350  
 Val Met Asp Gln Ser Ala Ile Gln Asn Asn Pro Gly Leu Val Cys Gln  
 355                      360                      365  
 Asn Pro Val Gln Asn Gln Ile Ile Ser Asp Arg Phe Ala Arg Tyr Ile  
 370                      375                      380



Gly Gly Phe Pro His Met Gln Ala Ala Thr Gln Met Gln Pro Met Glu  
385 390 395 400

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405 410 415

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118

Met  
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166  
Leu Glu Gly Leu Val Ser Gln Glu Ser Leu Ser Leu Asn Ser Met Asp  
5 10 15

atg tct gta ctt gaa agg ctt aaa tgg gta caa cag caa caa cag caa  
214  
Met Ser Val Leu Glu Arg Leu Lys Trp Val Gln Gln Gln Gln Gln Gln  
20 25 30

ctg caa caa gtt gtg tcc cat agc agt aat aat tca cct gaa ctt ctt  
262  
Leu Gln Gln Val Val Ser His Ser Ser Asn Asn Ser Pro Glu Leu Leu  
35 40 45

cag ata ctt cag ttc cat gga agc aac aat gat gag ttg ttg gag agt  
310  
Gln Ile Leu Gln Phe His Gly Ser Asn Asn Asp Glu Leu Leu Glu Ser  
50 55 60 65

agt ttc agc caa ttt caa atg ctt gga tct ggt ttt gga cca aac tat  
358  
Ser Phe Ser Gln Phe Gln Met Leu Gly Ser Gly Phe Gly Pro Asn Tyr  
70 75 80

aac atg ggt ttt ggt cct cca cat gaa tcc att tca aga aca agt agc  
406  
Asn Met Gly Phe Gly Pro Pro His Glu Ser Ile Ser Arg Thr Ser Ser  
85 90 95

tgc cat atg gaa cct gtg gat aca atg gag gtt ttg ttg aag acc ggt  
454  
Cys His Met Glu Pro Val Asp Thr Met Glu Val Leu Leu Lys Thr Gly  
100 105 110



gaa gaa acc aga gcc gtt gcc ttg aag aac aag aga aaa cca gag gtt  
 502  
 Glu Glu Thr Arg Ala Val Ala Leu Lys Asn Lys Arg Lys Pro Glu Val  
 115 120 125  
 aag aca agg gaa gag caa aag aca gag aag aag atc aaa gta gag gct  
 550  
 Lys Thr Arg Glu Glu Gln Lys Thr Glu Lys Lys Ile Lys Val Glu Ala  
 130 135 140 145  
 gag aca gag tca agc atg aaa gga aaa tca aac atg gga aac act gaa  
 598  
 Glu Thr Glu Ser Ser Met Lys Gly Lys Ser Asn Met Gly Asn Thr Glu  
 150 155 160  
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 646  
 Ala Ser Ser Asp Thr Ser Lys Glu Thr Ser Lys Gly Ala Ser Glu Asn  
 165 170 175  
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 694  
 Gln Lys Leu Asp Tyr Ile His Val Arg Ala Arg Arg Gly Gln Ala Thr  
 180 185 190  
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 742  
 Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys  
 195 200 205  
 aaa atg aaa tat ctg caa gat att gtg cct gga tgc aat aag gtc aca  
 790  
 Lys Met Lys Tyr Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val Thr  
 210 215 220 225  
 gga aaa gct ggt atg ctt gat gag atc atc aat tat gtt caa tgt ctc  
 838  
 Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Cys Leu  
 230 235 240  
 caa aga caa gtc gag ttc ctg tcg atg aaa ctt gct gtc ttg aac ccg  
 886  
 Gln Arg Gln Val Glu Phe Leu Ser Met Lys Leu Ala Val Leu Asn Pro  
 245 250 255  
 gaa cta gag ctt gcc gtg gaa gat gta tcc gta aaa cag gct tac ttt  
 934  
 Glu Leu Glu Leu Ala Val Glu Asp Val Ser Val Lys Gln Ala Tyr Phe  
 260 265 270  
 aca aat gta gtt gct tca aag caa tca ata atg gtt gat gtg cca ttg  
 982  
 Thr Asn Val Val Ala Ser Lys Gln Ser Ile Met Val Asp Val Pro Leu  
 275 280 285  
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 1030  
 Phe Pro Leu Asp Gln Gln Gly Ser Leu Asp Leu Ser Ala Ile Asn Pro  
 290 295 300 305



aac caa acg aca tct atc gaa gct cca tct gga agc tgg gaa act caa  
1078

Asn Gln Thr Thr Ser Ile Glu Ala Pro Ser Gly Ser Trp Glu Thr Gln  
310 315 320

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1123

Ser Gln Ser Leu Tyr Asn Thr Ser Ser Leu Gly Phe His Tyr  
325 330 335

gcaagattca ttgaaacaac atggttgaca tcaatcaatc atcaaatca gaagcaaatt  
1183

ctattacatt tgctcatcaa agtagtaatt tcgaaatttg gttaatgcat tatectttga  
1243

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1303

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1306

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20 25 30

Gln Leu Gln Gln Val Val Ser His Ser Ser Asn Asn Ser Pro Glu Leu  
35 40 45

Leu Gln Ile Leu Gln Phe His Gly Ser Asn Asn Asp Glu Leu Leu Glu  
50 55 60

Ser Ser Phe Ser Gln Phe Gln Met Leu Gly Ser Gly Phe Gly Pro Asn  
65 70 75 80

Tyr Asn Met Gly Phe Gly Pro Pro His Glu Ser Ile Ser Arg Thr Ser  
85 90 95

Ser Cys His Met Glu Pro Val Asp Thr Met Glu Val Leu Leu Lys Thr  
100 105 110

Gly Glu Glu Thr Arg Ala Val Ala Leu Lys Asn Lys Arg Lys Pro Glu  
115 120 125

Val Lys Thr Arg Glu Glu Gln Lys Thr Glu Lys Lys Ile Lys Val Glu  
130 135 140



Ala Glu Thr Glu Ser Ser Met Lys Gly Lys Ser Asn Met Gly Asn Thr  
 145 150 155 160

Glu Ala Ser Ser Asp Thr Ser Lys Glu Thr Ser Lys Gly Ala Ser Glu  
 165 170 175

Asn Gln Lys Leu Asp Tyr Ile His Val Arg Ala Arg Arg Gly Gln Ala  
 180 185 190

Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser  
 195 200 205

Lys Lys Met Lys Tyr Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val  
 210 215 220

Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Cys  
 225 230 235 240

Leu Gln Arg Gln Val Glu Phe Leu Ser Met Lys Leu Ala Val Leu Asn  
 245 250 255

Pro Glu Leu Glu Leu Ala Val Glu Asp Val Ser Val Lys Gln Ala Tyr  
 260 265 270

Phe Thr Asn Val Val Ala Ser Lys Gln Ser Ile Met Val Asp Val Pro  
 275 280 285

Leu Phe Pro Leu Asp Gln Gln Gly Ser Leu Asp Leu Ser Ala Ile Asn  
 290 295 300

Pro Asn Gln Thr Thr Ser Ile Glu Ala Pro Ser Gly Ser Trp Glu Thr  
 305 310 315 320

Gln Ser Gln Ser Leu Tyr Asn Thr Ser Ser Leu Gly Phe His Tyr  
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cccttaatat atatatatgc tcacacacac acatatatat atacatatataa gcatcgctc  
 120

aagcattaaa atttttacga accaaacaaa caaaaatt atg aat aat tat aat atg  
 176



Met Asn Asn Tyr Asn Met  
1 5

aac cca tct ctc ttc caa aat tac act tgg aac aac atc atc aac agc  
224  
Asn Pro Ser Leu Phe Gln Asn Tyr Thr Trp Asn Asn Ile Ile Asn Ser  
10 15 20

agc aac aac aac aac aag aat gat gat cat cat cat caa cat aat aat  
272  
Ser Asn Asn Asn Asn Lys Asn Asp Asp His His His Gln His Asn Asn  
25 30 35

gat cca atc ggt atg gcc atg gac cag tac aca cag ctc cat atc ttc  
320  
Asp Pro Ile Gly Met Ala Met Asp Gln Tyr Thr Gln Leu His Ile Phe  
40 45 50

aat cct ttc tct tct tct cat ttc cct cct ctc tct tct tcc ctc aca  
368  
Asn Pro Phe Ser Ser Ser His Phe Pro Pro Leu Ser Ser Ser Leu Thr  
55 60 65 70

acc acc act ctt ctc tcc gga gat caa gaa gac gac gaa gac gaa gaa  
416  
Thr Thr Thr Leu Leu Ser Gly Asp Gln Glu Asp Asp Glu Asp Glu Glu  
75 80 85

gaa cct cta gag gaa ctc ggt gct atg aag gaa atg atg tac aag atc  
464  
Glu Pro Leu Glu Glu Leu Gly Ala Met Lys Glu Met Met Tyr Lys Ile  
90 95 100

gca gcc atg caa tcg gtt gac atc gac cca gca acc gtc aag aaa ccc  
512  
Ala Ala Met Gln Ser Val Asp Ile Asp Pro Ala Thr Val Lys Lys Pro  
105 110 115

aaa cgc cgt aac gtg agg atc tcc gac gac cct cag agt gtg gcg gct  
560  
Lys Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Ser Val Ala Ala  
120 125 130

aga cat cgc cgt gag aga atc agt gag agg atc aga att ctt cag aga  
608  
Arg His Arg Arg Glu Arg Ile Ser Glu Arg Ile Arg Ile Leu Gln Arg  
135 140 145 150

ctc gtg cca ggt ggc act aaa atg gat acg gct tca atg ctc gat gaa  
656  
Leu Val Pro Gly Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu  
155 160 165

gct ata cgc tat gtc aag ttc ttg aaa cgg cag atc cgg cta ctc aat  
704  
Ala Ile Arg Tyr Val Lys Phe Leu Lys Arg Gln Ile Arg Leu Leu Asn  
170 175 180

aat aat acc gga tat act cct ccg ccg ccg caa gat caa gct tct cag  
752  
Asn Asn Thr Gly Tyr Thr Pro Pro Pro Pro Gln Asp Gln Ala Ser Gln



185 190 195  
 gcg gtg acg acg tca tgg gtt tca ccg cca cca ccg cca agt ttc ggc  
 800  
 Ala Val Thr Thr Ser Trp Val Ser Pro Pro Pro Pro Pro Ser Phe Gly  
 200 205 210  
 cgt ggg gga aga gga gta gga gaa tta atc tag acaagatgac atttcatta  
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 Arg Gly Gly Arg Gly Val Gly Glu Leu Ile  
 215 220  
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 20 25 30

His His Gln His Asn Asn Asp Pro Ile Gly Met Ala Met Asp Gln Tyr  
 35 40 45

Thr Gln Leu His Ile Phe Asn Pro Phe Ser Ser Ser His Phe Pro Pro  
 50 55 60

Leu Ser Ser Ser Leu Thr Thr Thr Thr Leu Leu Ser Gly Asp Gln Glu  
 65 70 75 80

Asp Asp Glu Asp Glu Glu Glu Pro Leu Glu Glu Leu Gly Ala Met Lys  
 85 90 95

Glu Met Met Tyr Lys Ile Ala Ala Met Gln Ser Val Asp Ile Asp Pro  
 100 105 110

Ala Thr Val Lys Lys Pro Lys Arg Arg Asn Val Arg Ile Ser Asp Asp  
 115 120 125

Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile Ser Glu Arg  
 130 135 140

Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys Met Asp Thr  
 145 150 155 160

Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Val Lys Phe Leu Lys Arg  
 165 170 175



Gln Ile Arg Leu Leu Asn Asn Asn Thr Gly Tyr Thr Pro Pro Pro Pro  
 180 185 190

Gln Asp Gln Ala Ser Gln Ala Val Thr Thr Ser Trp Val Ser Pro Pro  
 195 200 205

Pro Pro Pro Ser Phe Gly Arg Gly Gly Arg Gly Val Gly Glu Leu Ile  
 210 215 220

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 96  
 Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu  
 20 25 30  
 ctt tac aag cca att gtg tta tct tgt ggt cat cta tca tgt ttt tgg  
 144  
 Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp  
 35 40 45  
 tgc gta cat aag tcc atg aat ggc ttt cgt gag tct cat tgt ccg ata  
 192  
 Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile  
 50 55 60  
 tgt aga gac ccg tat gtt cac ttt ccc tct gtg tgc cag aag ctt tat  
 240  
 Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr  
 65 70 75 80  
 ttt ctg tta aag aag atg tac cca ctt gct cat aag aag aga gaa gaa  
 288  
 Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu  
 85 90 95  
 caa gtt tta aag gaa gag caa gaa cga gaa tgt ttt tct cct cag att  
 336  
 Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile  
 100 105 110  
 gat ctt gtt ttg gat ttg tct gtg tgt agt gga gat tct ctc aat gtc  
 384  
 Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val  
 115 120 125  
 tct gat aaa cag aag gtg gaa gag tgt tcg aat gca gcg aac tta tta  
 432  
 Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu



130	135	140
tct agt tca tca agt aga ggt gac att cca tgt atc ccc aaa aat caa		
480		
Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln		
145	150	155 160
gaa ccc aca gat gca aaa gct ctt aat gtt cat gaa aat gaa tta ctt		
528		
Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu		
	165	170 175
aag gat aac aaa gtc agt aag cag att tcg aaa gat gat ttg ctc tgt		
576		
Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys		
	180	185 190
tca gca tgt aag gag ctg ctt gta cga ccc gta gtt ctc aat tgc gga		
624		
Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly		
	195	200 205
cat gtg tat tgt gaa gga tgt gta gta gat atg gct gaa gaa agc gaa		
672		
His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu		
	210	215 220
aag atc aaa tgt caa gag tgt aat gtt tgt gac cca aga gga ttt cca		
720		
Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro		
225	230	235 240
aaa gtt tgt ttg att ctt gaa cag ctt ttg gag gaa aac ttt cct gaa		
768		
Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu		
	245	250 255
gaa tac aat tca aga agc agt aag gtt cag aaa acg ctc gcc cat aat		
816		
Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn		
	260	265 270
agc aaa gga aat att caa agc tat ctc aaa gaa ggc ccg tcc tta tca		
864		
Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser		
	275	280 285
aac gac aat aac aat gat gat ccc tgg ttg gca aac cct gga tca aat		
912		
Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn		
	290	295 300
gtt cac ttt gga gct ggt tgt gat tct tgt ggg gtg tat cca atc ata		
960		
Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile		
305	310	315 320
ggg gat cga tac aga tgc aaa gac tgc aag gag gaa att ggg tat gac		
1008		
Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp		
	325	330 335



ctt tgc aaa gac tgt tac gag act cct tog aaa gtt cca ggg aga ttc  
1056

Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe  
340 345 350

aac cag caa cac act cct gac cac agg ctt gag ctt gca cgg tct cct  
1104

Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro  
355 360 365

cag gtt ctg atc aat ttc aat tct atc ggt atc ctt ctc gga ccc gtt  
1152

Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val  
370 375 380

atc tca aat gaa ggc atg gat aca gat gaa ggc gag gaa ggg cct cct  
1200

Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro  
385 390 395 400

ggt tct tct aat gag tca tca agc aca gaa tga  
1233

Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu  
405 410

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230

Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln  
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Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu  
20 25 30

Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp  
35 40 45

Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile  
50 55 60

Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr  
65 70 75 80

Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu  
85 90 95

Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile  
100 105 110

Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val  
115 120 125



Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu  
 130 135 140

Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln  
 145 150 155 160

Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu  
 165 170 175

Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys  
 180 185 190

Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly  
 195 200 205

His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu  
 210 215 220

Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro  
 225 230 235 240

Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu  
 245 250 255

Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn  
 260 265 270

Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser  
 275 280 285

Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn  
 290 295 300

Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile  
 305 310 315 320

Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp  
 325 330 335

Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe  
 340 345 350

Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro  
 355 360 365



Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val  
 370 375 380

Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro  
 385 390 395 400

Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu  
 405 410

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 agc ggg ttt cac ggc gga atc aga cga ttc ccg tta gca gct cag ccg  
 96  
 Ser Gly Phe His Gly Gly Ile Arg Arg Phe Pro Leu Ala Ala Gln Pro  
 20 25 30  
 gag att atg aga gct gct gag aaa gac gat caa tac gct tct ttc atc  
 144  
 Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile  
 35 40 45  
 cac gaa gct tgc cgc gat gcc ttc cga cac ctt ttc ggt aca aga atc  
 192  
 His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile  
 50 55 60  
 gct ctt gct tac cag aag gag atg aag cta ctt gga cag atg ctt tac  
 240  
 Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr  
 65 70 75 80  
 tat gtt ctt acg aca ggt tca ggg caa caa act tta gga gag gaa tat  
 288  
 Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr  
 85 90 95  
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 336  
 Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro  
 100 105 110  
 gct aga cgt gct ttg ttc ata ttg tac cag acc gca gtt cca tat atc  
 384  
 Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile  
 115 120 125  
 gca gag aga att agc act cga gct gct acg caa gca gtc acc ttt gat  
 432  
 Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp  
 130 135 140



gag tct gat gag ttt ttt ggt gat agt cat atc cac tca cca aga atg  
 480  
 Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met  
 145 150 155 160  
 ata gat ctt cca tct tca tct caa gtt gaa act tca act tct gta gta  
 528  
 Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val  
 165 170 175  
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 576  
 Ser Arg Leu Asn Asp Arg Leu Met Arg Ser Trp His Arg Ala Ile Gln  
 180 185 190  
 cga tgg cct gtg gtt ctt cct gtt gcc cgc gaa gtc tta caa ctg gtt  
 624  
 Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val  
 195 200 205  
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 672  
 Leu Arg Ala Asn Leu Met Leu Phe Tyr Phe Glu Gly Phe Tyr Tyr His  
 210 215 220  
 ata tcg aaa cgt gca tcc ggg gtt cgt tat gtt ttc ata gga aag caa  
 720  
 Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln  
 225 230 235 240  
 ctg aat cag aga cct aga tac caa att ctt ggg gtt ttc ctt cta atc  
 768  
 Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile  
 245 250 255  
 caa ttg tgc atc ctt gct gct gag ggc ttg cgt cgg agt aat ttg tca  
 816  
 Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser  
 260 265 270  
 tct atc act agc tcc att cag cag gct tct ata gga tct tat caa act  
 864  
 Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr  
 275 280 285  
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 912  
 Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile  
 290 295 300  
 act tcg gaa gct gaa aag gga aac tgg tct acc tcc gat tca act tca  
 960  
 Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser  
 305 310 315 320  
 acg gag gca gta ggg aaa tgc act ctc tgc tta agc acc cgt cag cac  
 1008  
 Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His  
 325 330 335



cca acg gcc act cct tgt ggt cat gtg ttt tgt tgg agc tgc att atg  
1056

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met  
340 345 350

gaa tgg tgc aac gag aag caa gaa tgc cct ctt tgt cga acg ccc aat  
1104

Glu Trp Cys Asn Glu Lys Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn  
355 360 365

acc cat tca agt ttg gtt tgt ttg tat cat tct gat ttt tag  
1146

Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe  
370 375 380

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20 25 30

Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile  
35 40 45

His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile  
50 55 60

Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr  
65 70 75 80

Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr  
85 90 95

Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro  
100 105 110

Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile  
115 120 125

Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp  
130 135 140

Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met  
145 150 155 160

Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val  
165 170 175



Ser Arg Leu Asn Asp Arg Leu Met Arg Ser Trp His Arg Ala Ile Gln  
 180 185 190

Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val  
 195 200 205

Leu Arg Ala Asn Leu Met Leu Phe Tyr Phe Glu Gly Phe Tyr Tyr His  
 210 215 220

Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln  
 225 230 235 240

Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile  
 245 250 255

Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser  
 260 265 270

Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr  
 275 280 285

Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile  
 290 295 300

Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser  
 305 310 315 320

Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His  
 325 330 335

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met  
 340 345 350

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Arg Ser Pro Glu Ser Ile Ala Lys Phe Ala Gly Arg Ala Ile Phe Pro 20 25 30			
gct tta cag ggg aaa tcg tgt ccg ata tgc ctc gaa aat cta acc gag 144			
Ala Leu Gln Gly Lys Ser Cys Pro Ile Cys Leu Glu Asn Leu Thr Glu 35 40 45			
cga aga tcc gcc gcc gtg atc acg gtg tgc aag cac gga tac tgc ctt 192			
Arg Arg Ser Ala Ala Val Ile Thr Val Cys Lys His Gly Tyr Cys Leu 50 55 60			
gct tgt att cgg aag tgg agc agc ttc aag agg aat tgt cct ctt tgt 240			
Ala Cys Ile Arg Lys Trp Ser Ser Phe Lys Arg Asn Cys Pro Leu Cys 65 70 75 80			
aac act cgt ttt gat tcc tgg ttt atc gtt agt gat ttt gct tct aga 288			
Asn Thr Arg Phe Asp Ser Trp Phe Ile Val Ser Asp Phe Ala Ser Arg 85 90 95			
aaa tac cat aag gag caa tta cca att ctt cgt gat cgt gag act tta 336			
Lys Tyr His Lys Glu Gln Leu Pro Ile Leu Arg Asp Arg Glu Thr Leu 100 105 110			
act tat cat cgg aat aat cct tcc gat cgc cgg agg ata att caa agg 384			
Thr Tyr His Arg Asn Asn Pro Ser Asp Arg Arg Arg Ile Ile Gln Arg 115 120 125			
tcg agg gat gtt ttg gaa aac tct agc tca aga tca agg cca ttg cca 432			
Ser Arg Asp Val Leu Glu Asn Ser Ser Ser Arg Ser Arg Pro Leu Pro 130 135 140			
tgg cgg aga tca ttt gga cga cca ggt tca gtt cct gat tct gtt atc 480			
Trp Arg Arg Ser Phe Gly Arg Pro Gly Ser Val Pro Asp Ser Val Ile 145 150 155 160			
ttc cag cga aag ctt cag tgg cga gct agc ata tac act aag caa tta 528			
Phe Gln Arg Lys Leu Gln Trp Arg Ala Ser Ile Tyr Thr Lys Gln Leu 165 170 175			
cga gct gtt cga tta cat tca agg cgc ttg gaa cta agt ttg gcg gtg 576			
Arg Ala Val Arg Leu His Ser Arg Arg Leu Glu Leu Ser Leu Ala Val 180 185 190			
aat gat tac acc aaa gca aag ata act gaa aga att gag cca tgg att 624			
Asn Asp Tyr Thr Lys Ala Lys Ile Thr Glu Arg Ile Glu Pro Trp Ile 195 200 205			



aga aga gag ctt cag gca gtc ctt gga gat cct gat ccc tca gtt att  
672

Arg Arg Glu Leu Gln Ala Val Leu Gly Asp Pro Asp Pro Ser Val Ile  
210 215 220

gtt cat ttt gcg tca gct ctt ttc atc aaa agg ctt gag aga gag aat  
720

Val His Phe Ala Ser Ala Leu Phe Ile Lys Arg Leu Glu Arg Glu Asn  
225 230 235 240

aat cga caa acc ggg cag acc ggg atg ttg gtg gaa gat gaa gtc tcc  
768

Asn Arg Gln Thr Gly Gln Thr Gly Met Leu Val Glu Asp Glu Val Ser  
245 250 255

tct ctt cga aaa ttc ttg tct gat aag gtg gat ata ttt tgg cat gaa  
816

Ser Leu Arg Lys Phe Leu Ser Asp Lys Val Asp Ile Phe Trp His Glu  
260 265 270

cta aga tgt ttt gcg gag agt ata ctc.acg atg gag act tat gat gca  
864

Leu Arg Cys Phe Ala Glu Ser Ile Leu Thr Met Glu Thr Tyr Asp Ala  
275 280 285

gtg gtt gaa tac aat gag gtg gag taa  
891

Val Val Glu Tyr Asn Glu Val Glu  
290 295

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234

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20 25 30

Ala Leu Gln Gly Lys Ser Cys Pro Ile Cys Leu Glu Asn Leu Thr Glu  
35 40 45

Arg Arg Ser Ala Ala Val Ile Thr Val Cys Lys His Gly Tyr Cys Leu  
50 55 60

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Lys Tyr His Lys Glu Gln Leu Pro Ile Leu Arg Asp Arg Glu Thr Leu  
100 105 110



Thr Tyr His Arg Asn Asn Pro Ser Asp Arg Arg Arg Ile Ile Gln Arg  
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Ser Arg Asp Val Leu Glu Asn Ser Ser Ser Arg Ser Arg Pro Leu Pro  
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Trp Arg Arg Ser Phe Gly Arg Pro Gly Ser Val Pro Asp Ser Val Ile  
 145 150 155 160

Phe Gln Arg Lys Leu Gln Trp Arg Ala Ser Ile Tyr Thr Lys Gln Leu  
 165 170 175

Arg Ala Val Arg Leu His Ser Arg Arg Leu Glu Leu Ser Leu Ala Val  
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Asn Asp Tyr Thr Lys Ala Lys Ile Thr Glu Arg Ile Glu Pro Trp Ile  
 195 200 205

Arg Arg Glu Leu Gln Ala Val Leu Gly Asp Pro Asp Pro Ser Val Ile  
 210 215 220

Val His Phe Ala Ser Ala Leu Phe Ile Lys Arg Leu Glu Arg Glu Asn  
 225 230 235 240

Asn Arg Gln Thr Gly Gln Thr Gly Met Leu Val Glu Asp Glu Val Ser  
 245 250 255

Ser Leu Arg Lys Phe Leu Ser Asp Lys Val Asp Ile Phe Trp His Glu  
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 96



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 85 90 95  
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 336  
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 115 120 125  
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Lys Thr Ala Ser Asn Thr Ala Glu Glu Ser Met Phe His Pro Leu Pro 245 250 255		
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Thr Pro Glu Asp Phe Tyr Ser Lys Lys Arg Pro Leu Ser Ser Lys Asp 275 280 285		
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gat gag gca gca aca atg ctt cac ccg tgt tgg gaa gca tac tgt tta 1152		
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Ala Asp Lys Arg Glu Leu Val Val Tyr Leu Asn Ser Phe Thr Gly Asp 385 390 395 400		
gct aca ata cac ttc cct agc aca ctt caa atg gca aga gga gga ata 1248		
Ala Thr Ile His Phe Pro Ser Thr Leu Gln Met Ala Arg Gly Gly Ile 405 410 415		



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 1392  
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 Gly Ile Tyr Ala Val Arg Trp Phe Arg Ile Val Leu Asp Glu Ala His  
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 1824  
 Val Ala Asp Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Gln Asn Asn  
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 645 650 655

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 675 680 685

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 770 775 780

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 785 790 795 800



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 2496  
 Cys Leu Leu Ala Ser Trp Arg Asn Ser Thr Ser Gly Leu Cys Pro Val  
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tgt agg aac act gta agc aaa caa gaa ctc atc aca gca cca acc gaa  
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atc act gct ctt ctg gaa gag ctt gaa ggt ctt cgt tct tca ggc tct  
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 Ile Thr Ala Leu Leu Glu Glu Leu Glu Gly Leu Arg Ser Ser Gly Ser  
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 Ile Pro Leu Ser Arg Asn Asn Phe Ser Phe Val Arg Leu Asp Gly Thr  
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cta agt cag cag caa cga gag aag gtc ctt aaa gaa ttt tcc gaa gat  
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ggc agt atc ctg gta ctg ttg atg tct cta aaa gct ggt ggc gtt ggg  
 2832  
 Gly Ser Ile Leu Val Leu Leu Met Ser Leu Lys Ala Gly Gly Val Gly  
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ata aat cta aca gct gcg tcc aat gct ttt gtc atg gat cca tgg tgg  
 2880  
 Ile Asn Leu Thr Ala Ala Ser Asn Ala Phe Val Met Asp Pro Trp Trp  
                     945                    950                    955                    960

aac cca gcg gta gag gaa caa gct gtt atg cgt att cat cgt ata ggg  
 2928  
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caa act aag gaa gtc aaa atc aga aga ttc atc gtt aag gga acg gtt  
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gaa gag aga atg gag gcg gtt cag gcg agg aag cag aga atg atc tct  
3024

Glu Glu Arg Met Glu Ala Val Gln Ala Arg Lys Gln Arg Met Ile Ser  
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3069

Gly Ala Leu Thr Asp Gln Glu Val Arg Ser Ala Arg Ile Glu Glu  
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35 40 45

Ser Phe Ala Lys Pro Asp Val Ala Thr Pro Thr Pro Ser Gly Ser Asn  
50 55 60

Gly Gly Lys Arg Val Asp Ser Gly Leu Lys Gly Cys Thr Phe Gly Asp  
65 70 75 80

Ser Gly Ser Val Gly Ala Asn His Arg Val Glu Glu Glu Asn Glu Ser  
85 90 95

Val Asn Gly Gly Gly Glu Glu Ser Val Ser Gly Asn Glu Trp Trp Phe  
100 105 110

Val Gly Cys Ser Glu Leu Ala Gly Leu Ser Thr Cys Lys Gly Arg Lys  
115 120 125

Leu Lys Ser Gly Asp Glu Leu Val Phe Thr Phe Pro His Ser Lys Gly  
130 135 140

Leu Lys Pro Glu Thr Thr Pro Gly Lys Arg Gly Phe Gly Arg Gly Arg  
145 150 155 160

Pro Ala Leu Arg Gly Ala Ser Asp Ile Val Arg Phe Ser Thr Lys Asp  
165 170 175



Ser Gly Glu Ile Gly Arg Ile Pro Asn Glu Trp Ala Arg Cys Leu Leu  
 180 185 190

Pro Leu Val Arg Asp Lys Lys Ile Arg Ile Glu Gly Ser Cys Lys Ser  
 195 200 205

Ala Pro Glu Ala Leu Ser Ile Met Asp Thr Ile Leu Leu Ser Val Ser  
 210 215 220

Val Tyr Ile Asn Ser Ser Met Phe Gln Lys His Ser Ala Thr Ser Phe  
 225 230 235 240

Lys Thr Ala Ser Asn Thr Ala Glu Glu Ser Met Phe His Pro Leu Pro  
 245 250 255

Asn Leu Phe Arg Leu Leu Gly Leu Ile Pro Phe Lys Lys Ala Glu Phe  
 260 265 270

Thr Pro Glu Asp Phe Tyr Ser Lys Lys Arg Pro Leu Ser Ser Lys Asp  
 275 280 285

Gly Ser Ala Ile Pro Thr Ser Leu Leu Gln Leu Asn Lys Val Lys Asn  
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Met Asn Gln Asp Ala Asn Gly Asp Glu Asn Glu Gln Cys Ile Ser Asp  
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Gly Asp Leu Asp Asn Ile Val Gly Val Gly Asp Ser Ser Gly Leu Lys  
 325 330 335

Glu Met Glu Thr Pro His Thr Leu Leu Cys Glu Leu Arg Pro Tyr Gln  
 340 345 350

Lys Gln Ala Leu His Trp Met Thr Gln Leu Glu Lys Gly Asn Cys Thr  
 355 360 365

Asp Glu Ala Ala Thr Met Leu His Pro Cys Trp Glu Ala Tyr Cys Leu  
 370 375 380

Ala Asp Lys Arg Glu Leu Val Val Tyr Leu Asn Ser Phe Thr Gly Asp  
 385 390 395 400

Ala Thr Ile His Phe Pro Ser Thr Leu Gln Met Ala Arg Gly Gly Ile  
 405 410 415



Leu Ala Asp Ala Met Gly Leu Gly Lys Thr Val Met Thr Ile Ser Leu  
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Leu Leu Ala His Ser Trp Lys Ala Ala Ser Thr Gly Phe Leu Cys Pro  
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Asn Tyr Glu Gly Asp Lys Val Ile Ser Ser Ser Val Asp Asp Leu Thr  
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Ser Pro Pro Val Lys Ala Thr Lys Phe Leu Gly Phe Asp Lys Arg Leu  
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Leu Glu Gln Lys Ser Val Leu Gln Asn Gly Gly Asn Leu Ile Val Cys  
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Lys Pro Gly Ser Leu Ser Val Tyr Val His Tyr Gly Gln Ser Arg Pro  
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Lys Asp Ala Lys Leu Leu Ser Gln Ser Asp Val Val Ile Thr Thr Tyr  
                   530                                  535                                  540

Gly Val Leu Thr Ser Glu Phe Ser Gln Glu Asn Ser Ala Asp His Glu  
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Gly Ile Tyr Ala Val Arg Trp Phe Arg Ile Val Leu Asp Glu Ala His  
                                   565                                  570                                  575

Thr Ile Lys Asn Ser Lys Ser Gln Ile Ser Leu Ala Ala Ala Ala Leu  
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Val Ala Asp Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Gln Asn Asn  
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Gly Thr Trp Ala Trp Trp Asn Lys Leu Val Gln Lys Pro Phe Glu Glu  
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Gly Asp Glu Arg Gly Leu Lys Leu Val Gln Ser Ile Leu Lys Pro Ile  
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Met Leu Arg Arg Thr Lys Ser Ser Thr Asp Arg Glu Gly Arg Pro Ile  
660 665 670

Leu Val Leu Pro Pro Ala Asp Ala Arg Val Ile Tyr Cys Glu Leu Ser  
675 680 685

Glu Ser Glu Arg Asp Phe Tyr Asp Ala Leu Phe Lys Arg Ser Lys Val  
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705 710 715 720

Ser Ile Leu Glu Leu Leu Leu Arg Leu Arg Gln Cys Cys Asp His Pro  
725 730 735

Phe Leu Val Met Ser Arg Gly Asp Thr Ala Glu Tyr Ser Asp Leu Asn  
740 745 750

Lys Leu Ser Lys Arg Phe Leu Ser Gly Lys Ser Ser Gly Leu Glu Arg  
755 760 765

Glu Gly Lys Asp Val Pro Ser Glu Ala Phe Val Gln Glu Val Val Glu  
770 775 780

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785 790 795 800

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805 810 815

Cys Leu Leu Ala Ser Trp Arg Asn Ser Thr Ser Gly Leu Cys Pro Val  
820 825 830

Cys Arg Asn Thr Val Ser Lys Gln Glu Leu Ile Thr Ala Pro Thr Glu  
835 840 845

Ser Arg Phe Gln Val Asp Val Glu Lys Asn Trp Val Glu Ser Ser Lys  
850 855 860

Ile Thr Ala Leu Leu Glu Glu Leu Glu Gly Leu Arg Ser Ser Gly Ser  
865 870 875 880

Lys Ser Ile Leu Phe Ser Gln Trp Thr Ala Phe Leu Asp Leu Leu Gln  
885 890 895

Ile Pro Leu Ser Arg Asn Asn Phe Ser Phe Val Arg Leu Asp Gly Thr



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 Glu Glu Arg Met Glu Ala Val Gln Ala Arg Lys Gln Arg Met Ile Ser  
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 Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly  
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 Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu  
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           50                      55                      60  
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 85 90 95  
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 336  
 Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala  
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 384  
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 115 120 125  
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 130 135 140  
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 528  
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 576  
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 180 185 190  
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 624  
 Ser Gly Arg Lys Thr Leu Pro Leu Phe Pro Leu Gln Pro Leu Asn Ala  
 195 200 205  
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 210 215 220  
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 720  
 Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe  
 225 230 235 240  
 att gat ttc ttt tct ggt ggt tct act tct act cgt ttc gat agt aat  
 768  
 Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn  
 245 250 255  
 ggt aat ggg ttg taa  
 783  
 Gly Asn Gly Leu



260

<210> 238 <211> 260 <212> PRT <213> Arabidopsis thaliana <400>  
238

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1 5 10 15

Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly  
20 25 30

Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu  
35 40 45

Arg Ala Tyr Gly His Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln  
50 55 60

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Arg Met Ala  
65 70 75 80

Tyr Phe Asn Arg Leu Leu His Lys Thr Ser Arg Phe Phe Tyr Pro Pro  
85 90 95

Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala  
100 105 110

Ser Asp His His Met Asn Gln His Gly Ser Val Tyr Thr Asn Asp Leu  
115 120 125

Leu His Arg Asn Asn Val Met Ile Pro Ser Gly Gly Tyr Glu Lys Arg  
130 135 140

Thr Val Thr Gln His Gln Lys Gln Leu Ser Asp Ile Arg Thr Thr Ala  
145 150 155 160

Ala Thr Arg Met Pro Ile Ser Pro Ser Ser Leu Arg Phe Asp Arg Phe  
165 170 175

Ala Leu Arg Asp Asn Cys Tyr Ala Gly Glu Asp Ile Asn Val Asn Ser  
180 185 190

Ser Gly Arg Lys Thr Leu Pro Leu Phe Pro Leu Gln Pro Leu Asn Ala  
195 200 205

Ser Asn Ala Asp Gly Met Gly Ser Ser Ser Phe Ala Leu Gly Ser Asp  
210 215 220



Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe  
 225 230 235 240

Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn  
 245 250 255

Gly Asn Gly Leu  
 260

<210> 239 <211> 828 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(828) <223> G1543

<400> 239  
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 48  
 Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu  
 1 5 10 15  
 tat gct cta tat cat atg gat tac gca tgc gtg tgt atg tat aaa tat  
 96  
 Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr  
 20 25 30  
 aaa ggc atc gtc acg ctt caa gtt tgt ctc ttt tat att aaa ctg aga  
 144  
 Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg  
 35 40 45  
 gtt ttc ctc tca aac ttt acc ttt tct tct tcg atc cta gct ctt aag  
 192  
 Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys  
 50 55 60  
 aac cct aat aat tca ttg atc aaa ata atg gcg att ttg ccg gaa aac  
 240  
 Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn  
 65 70 75 80  
 tct tca aac ttg gat ctt act atc tcc gtt cca ggc ttc tct tca tcc  
 288  
 Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser  
 85 90 95  
 cct ctc tcc gat gaa gga agt ggc gga gga aga gac cag cta agg cta  
 336  
 Pro Leu Ser Asp Glu Gly Ser Gly Gly Gly Arg Asp Gln Leu Arg Leu  
 100 105 110  
 gac atg aat cgg tta ccg tcg tct gaa gac gga gac gat gaa gaa ttc  
 384  
 Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe  
 115 120 125  
 agt cac gat gat ggc tct gct cct ccg cga aag aaa ctc cgt cta acc  
 432  
 Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr  
 130 135 140



aga gaa cag tca cgt ctt ctt gaa gat agt ttc aga cag aat cat acc  
 480  
 Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr  
 145 150 155 160  
  
 ctt aat ccc aaa caa aag gaa gta ctt gcc aag cat ttg atg cta cgg  
 528  
 Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg  
 165 170 175  
  
 cca aga caa att gaa gtt tgg ttt caa aac cgt aga gca agg agc aaa  
 576  
 Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys  
 180 185 190  
  
 ttg aag caa acc gag atg gaa tgc gag tat ctc aaa agg tgg ttt ggt  
 624  
 Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly  
 195 200 205  
  
 tca tta acg gaa gaa aac cac agg ctc cat aga gaa gta gaa gag ctt  
 672  
 Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu  
 210 215 220  
  
 aga gcc ata aag gtt ggc cca aca acg gtg aac tct gcc tcg agc ctt  
 720  
 Arg Ala Ile Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu  
 225 230 235 240  
  
 act atg tgt cct cgc tgc gag cga gtt acc cct gcc gcg agc cct tcg  
 768  
 Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser  
 245 250 255  
  
 agg gcg gtg gtg ccg gtt ccg gct aag aaa acg ttt ccg ccg caa gag  
 816  
 Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu  
 260 265 270  
  
 cgt gat cgt tga  
 828  
 Arg Asp Arg  
 275

<210> 240 <211> 275 <212> PRT <213> Arabidopsis thaliana <400>  
 240

Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu  
 1 5 10 15

Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr  
 20 25 30

Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg  
 35 40 45



Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys  
 50 55 60

Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn  
 65 70 75 80

Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser  
 85 90 95

Pro Leu Ser Asp Glu Gly Ser Gly Gly Gly Arg Asp Gln Leu Arg Leu  
 100 105 110

Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe  
 115 120 125

Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr  
 130 135 140

Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr  
 145 150 155 160

Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg  
 165 170 175

Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys  
 180 185 190

Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly  
 195 200 205

Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu  
 210 215 220

Arg Ala Ile Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu  
 225 230 235 240

Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser  
 245 250 255

Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu  
 260 265 270

Arg Asp Arg  
 275



<210> 241 <211> 1962 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(1962) <223> G1574

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 1 5 10 15  
 gaa gag aag acc act gtt aac gag agg gtc atc tat cag gct gca tta  
 96  
 Glu Glu Lys Thr Thr Val Asn Glu Arg Val Ile Tyr Gln Ala Ala Leu  
 20 25 30  
 caa gat ctg aag caa ccc aag acc gaa aag gat cta cct cct ggt gtt  
 144  
 Gln Asp Leu Lys Gln Pro Lys Thr Glu Lys Asp Leu Pro Pro Gly Val  
 35 40 45  
 ctt aca gtt cct ctt atg agg cat cag aaa att gca ttg aac tgg atg  
 192  
 Leu Thr Val Pro Leu Met Arg His Gln Lys Ile Ala Leu Asn Trp Met  
 50 55 60  
 cgt aag aaa gaa aaa aga agc agg cac tgt ttg gga ggg ata tta gca  
 240  
 Arg Lys Lys Glu Lys Arg Ser Arg His Cys Leu Gly Gly Ile Leu Ala  
 65 70 75 80  
 gat gat cag gga ctt ggt aaa acg atc tcg acg atc tct ctt atc ctg  
 288  
 Asp Asp Gln Gly Leu Gly Lys Thr Ile Ser Thr Ile Ser Leu Ile Leu  
 85 90 95  
 tta caa aag ttg aag tca caa tca aag cag aga aag cga aaa ggt caa  
 336  
 Leu Gln Lys Leu Lys Ser Gln Ser Lys Gln Arg Lys Arg Lys Gly Gln  
 100 105 110  
 aac tct ggt ggt aca ttg att gtt tgt cca gca agt gtt gta aaa caa  
 384  
 Asn Ser Gly Gly Thr Leu Ile Val Cys Pro Ala Ser Val Val Lys Gln  
 115 120 125  
 tgg gca aga gaa gtt aaa gag aag gtt tct gat gaa cac aaa ctc tct  
 432  
 Trp Ala Arg Glu Val Lys Glu Lys Val Ser Asp Glu His Lys Leu Ser  
 130 135 140  
 gtt tta gtc cac cat gga tct cac aga acc aaa gat cca aca gaa ata  
 480  
 Val Leu Val His His Gly Ser His Arg Thr Lys Asp Pro Thr Glu Ile  
 145 150 155 160  
 gca ata tat gat gtg gtc atg aca act tac gcc att gtt aca aat gaa  
 528  
 Ala Ile Tyr Asp Val Val Met Thr Thr Tyr Ala Ile Val Thr Asn Glu  
 165 170 175  
 gtt cca caa aac cct atg ctg aat cgt tat gat agt atg aga ggc aga  
 576



Val Pro Gln Asn Pro Met Leu Asn Arg Tyr Asp Ser Met Arg Gly Arg  
 180 185 190  
 gaa agc ctt gac gga tcg agt ttg att cag cct cac gtt ggt gca cta  
 624  
 Glu Ser Leu Asp Gly Ser Ser Leu Ile Gln Pro His Val Gly Ala Leu  
 195 200 205  
 gga aga gtt agg tgg ttg aga gta gta tta gat gaa gct cat aca att  
 672  
 Gly Arg Val Arg Trp Leu Arg Val Val Leu Asp Glu Ala His Thr Ile  
 210 215 220  
 aaa aac cat aga acc cta att gca aaa gct tgt ttt agc ctt aga gcc  
 720  
 Lys Asn His Arg Thr Leu Ile Ala Lys Ala Cys Phe Ser Leu Arg Ala  
 225 230 235 240  
 aaa agg aga tgg tgt ttg act gga acg ccg ata aag aac aaa gta gac  
 768  
 Lys Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Lys Asn Lys Val Asp  
 245 250 255  
 gat ctt tat agc tat ttc aga ttt ctt aga tat cat cca tat gcc atg  
 816  
 Asp Leu Tyr Ser Tyr Phe Arg Phe Leu Arg Tyr His Pro Tyr Ala Met  
 260 265 270  
 tgc aat tca ttt cac caa aga atc aaa gct cca att gat aaa aag cct  
 864  
 Cys Asn Ser Phe His Gln Arg Ile Lys Ala Pro Ile Asp Lys Lys Pro  
 275 280 285  
 ctt cat ggt tac aag aag ctt caa gct att cta agg ggt ata atg ttg  
 912  
 Leu His Gly Tyr Lys Lys Leu Gln Ala Ile Leu Arg Gly Ile Met Leu  
 290 295 300  
 cgc cgc acc aaa gaa tgg tct ttc tac agg aag ctt gaa ttg aat tca  
 960  
 Arg Arg Thr Lys Glu Trp Ser Phe Tyr Arg Lys Leu Glu Leu Asn Ser  
 305 310 315 320  
 cgt tgg aag ttt gag gaa tat gct gct gat ggg act ttg cat gaa cac  
 1008  
 Arg Trp Lys Phe Glu Glu Tyr Ala Ala Asp Gly Thr Leu His Glu His  
 325 330 335  
 atg gct tat ctt ttg gtg atg ctt ttg cga cta cgc caa gct tgt aac  
 1056  
 Met Ala Tyr Leu Leu Val Met Leu Leu Arg Leu Arg Gln Ala Cys Asn  
 340 345 350  
 cat cca caa ctt gtt aac gga tat agt cac tca gat act aca aga aaa  
 1104  
 His Pro Gln Leu Val Asn Gly Tyr Ser His Ser Asp Thr Thr Arg Lys  
 355 360 365  
 atg tca gat gga gtt cga gta gcc cct aga gag aat cta atc atg ttc  
 1152  
 Met Ser Asp Gly Val Arg Val Ala Pro Arg Glu Asn Leu Ile Met Phe



370                                      375                                      380  
 ctc gat ctc ttg aaa tta tcc tca acc acc tgc tct gtt tgt agt gat  
 1200  
 Leu Asp Leu Leu Lys Leu Ser Ser Thr Thr Cys Ser Val Cys Ser Asp  
 385                                      390                                      395                                      400  
 cca cca aaa gac cct gtt gtt act ttg tgt ggc cat gtg ttt tgt tat  
 1248  
 Pro Pro Lys Asp Pro Val Val Thr Leu Cys Gly His Val Phe Cys Tyr  
 405                                      410                                      415  
 gag tgt gtg tct gta aac att aac ggg gat aac aat acg tgc cct gca  
 1296  
 Glu Cys Val Ser Val Asn Ile Asn Gly Asp Asn Asn Thr Cys Pro Ala  
 420                                      425                                      430  
 ctt aat tgc cac agc cag ctt aaa cat gat gtt gtt ttc act gaa tct  
 1344  
 Leu Asn Cys His Ser Gln Leu Lys His Asp Val Val Phe Thr Glu Ser  
 435                                      440                                      445  
 gca gtt aga agt tgc atc aac gat tat gat gat cct gaa gat aaa aat  
 1392  
 Ala Val Arg Ser Cys Ile Asn Asp Tyr Asp Asp Pro Glu Asp Lys Asn  
 450                                      455                                      460  
 gct tta gtt gca tca agg cga gtt tat ttc atc gaa aat ccg agc tgt  
 1440  
 Ala Leu Val Ala Ser Arg Arg Val Tyr Phe Ile Glu Asn Pro Ser Cys  
 465                                      470                                      475                                      480  
 gat aga gat tct tca gtc gct tgc aga gca agg cag tcc aga cac tcc  
 1488  
 Asp Arg Asp Ser Ser Val Ala Cys Arg Ala Arg Gln Ser Arg His Ser  
 485                                      490                                      495  
 acc aat aaa gac aat agt atc agt gga ctg aat ctc att ttt acg ttt  
 1536  
 Thr Asn Lys Asp Asn Ser Ile Ser Gly Leu Asn Leu Ile Phe Thr Phe  
 500                                      505                                      510  
 ctc aaa gac aaa tgt aat gat tat gaa aca ggt gcg atg ttg atg tct  
 1584  
 Leu Lys Asp Lys Cys Asn Asp Tyr Glu Thr Gly Ala Met Leu Met Ser  
 515                                      520                                      525  
 ctt aaa gct gga aac ctt gga ttg aat atg gta gct gca agt cat gtc  
 1632  
 Leu Lys Ala Gly Asn Leu Gly Leu Asn Met Val Ala Ala Ser His Val  
 530                                      535                                      540  
 att cta ctg gac cta tgg tgg aat cca aca aca gag gat caa gct att  
 1680  
 Ile Leu Leu Asp Leu Trp Trp Asn Pro Thr Thr Glu Asp Gln Ala Ile  
 545                                      550                                      555                                      560  
 gat cga gct cat cgt atc gga caa act cga gct gtt acg gtc act cgt  
 1728  
 Asp Arg Ala His Arg Ile Gly Gln Thr Arg Ala Val Thr Val Thr Arg  
 565                                      570                                      575



att gcc atc aaa aat acc gtt gag gaa cga att ttg act ctt cat gaa  
1776

Ile Ala Ile Lys Asn Thr Val Glu Glu Arg Ile Leu Thr Leu His Glu  
580 585 590

cgt aaa agg aac att gtt gca tct gca ttg ggt gaa aaa aac tgg caa  
1824

Arg Lys Arg Asn Ile Val Ala Ser Ala Leu Gly Glu Lys Asn Trp Gln  
595 600 605

aag ttc tgc gat tca act aac act aga aga tct cga ata tct gtt ttt  
1872

Lys Phe Cys Asp Ser Thr Asn Thr Arg Arg Ser Arg Ile Ser Val Phe  
610 615 620

tgg tgt gta gaa tat ccc aga gtt ttt att gat aag agg aat aaa acc  
1920

Trp Cys Val Glu Tyr Pro Arg Val Phe Ile Asp Lys Arg Asn Lys Thr  
625 630 635 640

ttt agc tat tta ata agt cac aag tgt gaa tgt aat gaa taa  
1962

Phe Ser Tyr Leu Ile Ser His Lys Cys Glu Cys Asn Glu  
645 650

<210> 242 <211> 653 <212> PRT <213> Arabidopsis thaliana <400>  
242

Met Asp Asp Thr Met Asp Met Ser Ser Gly Ser Asp Glu Glu Val Gln  
1 5 10 15

Glu Glu Lys Thr Thr Val Asn Glu Arg Val Ile Tyr Gln Ala Ala Leu  
20 25 30

Gln Asp Leu Lys Gln Pro Lys Thr Glu Lys Asp Leu Pro Pro Gly Val  
35 40 45

Leu Thr Val Pro Leu Met Arg His Gln Lys Ile Ala Leu Asn Trp Met  
50 55 60

Arg Lys Lys Glu Lys Arg Ser Arg His Cys Leu Gly Gly Ile Leu Ala  
65 70 75 80

Asp Asp Gln Gly Leu Gly Lys Thr Ile Ser Thr Ile Ser Leu Ile Leu  
85 90 95

Leu Gln Lys Leu Lys Ser Gln Ser Lys Gln Arg Lys Arg Lys Gly Gln  
100 105 110

Asn Ser Gly Gly Thr Leu Ile Val Cys Pro Ala Ser Val Val Lys Gln  
115 120 125



Trp Ala Arg Glu Val Lys Glu Lys Val Ser Asp Glu His Lys Leu Ser  
 130 135 140  
 Val Leu Val His His Gly Ser His Arg Thr Lys Asp Pro Thr Glu Ile  
 145 150 155 160  
 Ala Ile Tyr Asp Val Val Met Thr Thr Tyr Ala Ile Val Thr Asn Glu  
 165 170 175  
 Val Pro Gln Asn Pro Met Leu Asn Arg Tyr Asp Ser Met Arg Gly Arg  
 180 185 190  
 Glu Ser Leu Asp Gly Ser Ser Leu Ile Gln Pro His Val Gly Ala Leu  
 195 200 205  
 Gly Arg Val Arg Trp Leu Arg Val Val Leu Asp Glu Ala His Thr Ile  
 210 215 220  
 Lys Asn His Arg Thr Leu Ile Ala Lys Ala Cys Phe Ser Leu Arg Ala  
 225 230 235 240  
 Lys Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Lys Asn Lys Val Asp  
 245 250 255  
 Asp Leu Tyr Ser Tyr Phe Arg Phe Leu Arg Tyr His Pro Tyr Ala Met  
 260 265 270  
 Cys Asn Ser Phe His Gln Arg Ile Lys Ala Pro Ile Asp Lys Lys Pro  
 275 280 285  
 Leu His Gly Tyr Lys Lys Leu Gln Ala Ile Leu Arg Gly Ile Met Leu  
 290 295 300  
 Arg Arg Thr Lys Glu Trp Ser Phe Tyr Arg Lys Leu Glu Leu Asn Ser  
 305 310 315 320  
 Arg Trp Lys Phe Glu Glu Tyr Ala Ala Asp Gly Thr Leu His Glu His  
 325 330 335  
 Met Ala Tyr Leu Leu Val Met Leu Leu Arg Leu Arg Gln Ala Cys Asn  
 340 345 350  
 His Pro Gln Leu Val Asn Gly Tyr Ser His Ser Asp Thr Thr Arg Lys  
 355 360 365



Met Ser Asp Gly Val Arg Val Ala Pro Arg Glu Asn Leu Ile Met Phe  
 370 375 380

Leu Asp Leu Leu Lys Leu Ser Ser Thr Thr Cys Ser Val Cys Ser Asp  
 385 390 395 400

Pro Pro Lys Asp Pro Val Val Thr Leu Cys Gly His Val Phe Cys Tyr  
 405 410 415

Glu Cys Val Ser Val Asn Ile Asn Gly Asp Asn Asn Thr Cys Pro Ala  
 420 425 430

Leu Asn Cys His Ser Gln Leu Lys His Asp Val Val Phe Thr Glu Ser  
 435 440 445

Ala Val Arg Ser Cys Ile Asn Asp Tyr Asp Asp Pro Glu Asp Lys Asn  
 450 455 460

Ala Leu Val Ala Ser Arg Arg Val Tyr Phe Ile Glu Asn Pro Ser Cys  
 465 470 475 480

Asp Arg Asp Ser Ser Val Ala Cys Arg Ala Arg Gln Ser Arg His Ser  
 485 490 495

Thr Asn Lys Asp Asn Ser Ile Ser Gly Leu Asn Leu Ile Phe Thr Phe  
 500 505 510

Leu Lys Asp Lys Cys Asn Asp Tyr Glu Thr Gly Ala Met Leu Met Ser  
 515 520 525

Leu Lys Ala Gly Asn Leu Gly Leu Asn Met Val Ala Ala Ser His Val  
 530 535 540

Ile Leu Leu Asp Leu Trp Trp Asn Pro Thr Thr Glu Asp Gln Ala Ile  
 545 550 555 560

Asp Arg Ala His Arg Ile Gly Gln Thr Arg Ala Val Thr Val Thr Arg  
 565 570 575

Ile Ala Ile Lys Asn Thr Val Glu Glu Arg Ile Leu Thr Leu His Glu  
 580 585 590

Arg Lys Arg Asn Ile Val Ala Ser Ala Leu Gly Glu Lys Asn Trp Gln  
 595 600 605

Lys Phe Cys Asp Ser Thr Asn Thr Arg Arg Ser Arg Ile Ser Val Phe



610

615

620

Trp Cys Val Glu Tyr Pro Arg Val Phe Ile Asp Lys Arg Asn Lys Thr  
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Phe Ser Tyr Leu Ile Ser His Lys Cys Glu Cys Asn Glu  
 645 650

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 <221> CDS <222> (1)..(807) <223> G1586

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 48  
 Met Asn Gln Glu Gly Ala Ser His Ser Pro Ser Ser Thr Ser Thr Glu  
 1 5 10 15  
 cca gtc cgg gca cgt tgg tca cct aaa ccg gag caa atc ttg ata ctc  
 96  
 Pro Val Arg Ala Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu  
 20 25 30  
 gaa tcc atc ttc aac agt ggt act gtt aac cca cca aaa gat gaa acg  
 144  
 Glu Ser Ile Phe Asn Ser Gly Thr Val Asn Pro Pro Lys Asp Glu Thr  
 35 40 45  
 gtg agg ata aga aag atg ctt gag aaa ttc ggt gct gtg gga gac gca  
 192  
 Val Arg Ile Arg Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala  
 50 55 60  
 aac gtc ttc tac tgg ttt caa aac cga cgg tca aga tct cgc cgg aga  
 240  
 Asn Val Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg  
 65 70 75 80  
 cac cgg cag ctt tta gca gcc acc acc gca gcc gcc acc tcc ata gga  
 288  
 His Arg Gln Leu Leu Ala Ala Thr Thr Ala Ala Ala Thr Ser Ile Gly  
 85 90 95  
 gct gaa gac cac cag cac atg acg gcc atg agc atg cat caa tat cct  
 336  
 Ala Glu Asp His Gln His Met Thr Ala Met Ser Met His Gln Tyr Pro  
 100 105 110  
 tgc agc aac aac gag att gat ttg ggg ttt gga agt tgt agc aac tta  
 384  
 Cys Ser Asn Asn Glu Ile Asp Leu Gly Phe Gly Ser Cys Ser Asn Leu  
 115 120 125  
 tca gct aat tac ttc ctt aat gga tcg tcg tca tct caa atc cct tcc  
 432  
 Ser Ala Asn Tyr Phe Leu Asn Gly Ser Ser Ser Ser Gln Ile Pro Ser  
 130 135 140



ttt ttc ctc ggc ctc tct tct tca agt ggt ggg tgt gag aac aac aat  
480

Phe Phe Leu Gly Leu Ser Ser Ser Ser Gly Gly Cys Glu Asn Asn Asn  
145 150 155 160

ggt atg gag aat ctc ttc aaa atg tat ggc cat gaa tct gat cat aat  
528

Gly Met Glu Asn Leu Phe Lys Met Tyr Gly His Glu Ser Asp His Asn  
165 170 175

cat cag cag cag cat cat agc tca aat gct gca tca gtt tta aac cca  
576

His Gln Gln Gln His His Ser Ser Asn Ala Ala Ser Val Leu Asn Pro  
180 185 190

tct gat caa aac tcc aac tcc caa tac gaa caa gaa ggg ttt atg acg  
624

Ser Asp Gln Asn Ser Asn Ser Gln Tyr Glu Gln Glu Gly Phe Met Thr  
195 200 205

gtg ttt ata aac gga gtt cct atg gaa gta aca aaa gga gca ata gac  
672

Val Phe Ile Asn Gly Val Pro Met Glu Val Thr Lys Gly Ala Ile Asp  
210 215 220

atg aaa aca atg ttc ggt gat gat tcg gtg tta ctt cat tcc tct ggt  
720

Met Lys Thr Met Phe Gly Asp Asp Ser Val Leu Leu His Ser Ser Gly  
225 230 235 240

ctt cct ctt ccc act gat gag ttt ggt ttc ttg atg cat tct tta caa  
768

Leu Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln  
245 250 255

cat gga caa act tat ttc ctg gta ccg aga cag aca tga  
807

His Gly Gln Thr Tyr Phe Leu Val Pro Arg Gln Thr  
260 265

<210> 244 <211> 268 <212> PRT <213> Arabidopsis thaliana <400>  
244

Met Asn Gln Glu Gly Ala Ser His Ser Pro Ser Ser Thr Ser Thr Glu  
1 5 10 15

Pro Val Arg Ala Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu  
20 25 30

Glu Ser Ile Phe Asn Ser Gly Thr Val Asn Pro Pro Lys Asp Glu Thr  
35 40 45

Val Arg Ile Arg Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala  
50 55 60

Asn Val Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg



[illegible]

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<221> CDS <222> (22)..(855) <223> G1634
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      Met Glu Thr Leu His Pro Leu Leu Ser His
      1          5          10

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gtg cca act tct gac cac cgg ttt gta gtt caa gag atg atg tgc ttg  
 99  
 Val Pro Thr Ser Asp His Arg Phe Val Val Gln Glu Met Met Cys Leu  
 15 20 25

caa agc tcg agc tgg act aaa gaa gag aac aag aag ttt gag cga gct  
 147  
 Gln Ser Ser Ser Trp Thr Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala  
 30 35 40

ctt gct gtc tac gct gat gac acg cct gat cgc tgg ttc aaa gtt gct  
 195  
 Leu Ala Val Tyr Ala Asp Asp Thr Pro Asp Arg Trp Phe Lys Val Ala  
 45 50 55

gct atg atc cct gga aag acc ata tca gat gtc atg agg caa tac tct  
 243  
 Ala Met Ile Pro Gly Lys Thr Ile Ser Asp Val Met Arg Gln Tyr Ser  
 60 65 70

aag ctt gaa gaa gac ctc ttc gat atc gaa gca gga ctt gtc ccg atc  
 291  
 Lys Leu Glu Glu Asp Leu Phe Asp Ile Glu Ala Gly Leu Val Pro Ile  
 75 80 85 90

ccg ggt tac cgt tca gtt act cct tgt gga ttt gat cag gtt gtg agt  
 339  
 Pro Gly Tyr Arg Ser Val Thr Pro Cys Gly Phe Asp Gln Val Val Ser  
 95 100 105

cca cgt gac ttt gat gcg tat cgt aaa ctt cct aat gga gcc aga gga  
 387  
 Pro Arg Asp Phe Asp Ala Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly  
 110 115 120

ttt gat caa gac cgt agg aaa gga gtt cca tgg acg gag gaa gaa cac  
 435  
 Phe Asp Gln Asp Arg Arg Lys Gly Val Pro Trp Thr Glu Glu Glu His  
 125 130 135

agg aga ttc ttg tta ggg ctt ctc aag tat ggg aaa gga gat tgg aga  
 483  
 Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg  
 140 145 150

aac ata tcg agg aac ttt gtg gga tca aaa aca cca act cag gtt gca  
 531  
 Asn Ile Ser Arg Asn Phe Val Gly Ser Lys Thr Pro Thr Gln Val Ala  
 155 160 165 170

agt cat gcc caa aag tac tac caa aga cag ctt tcc ggt gcg aaa gac  
 579  
 Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp  
 175 180 185

aaa cga cgg cct agc att cac gac atc acc acc gtc aat ctt ctc aat  
 627  
 Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Val Asn Leu Leu Asn  
 190 195 200



gcc aat ctt agc cgt cca tcg tct gat cac ggt tgc tta gtc tca aaa  
 675  
 Ala Asn Leu Ser Arg Pro Ser Ser Asp His Gly Cys Leu Val Ser Lys  
           205                                  210                                  215

cag gcc gag ccg aaa cta ggg ttc acc gac agg gat aat gca gag gag  
 723  
 Gln Ala Glu Pro Lys Leu Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu  
           220                                  225                                  230

gga gtt atg ttt ctt ggt cag aat cta tcc tcg gtc ttc tct tcc tac  
 771  
 Gly Val Met Phe Leu Gly Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr  
 235                                  240                                  245                                  250

gat cct gcc att aag ttt tcc gga gca aat gtt tac ggt gaa gga ggt  
 819  
 Asp Pro Ala Ile Lys Phe Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly  
                                   255                                  260                                  265

tac tgt atc tca caa gat ctt gaa acg aga aaa tga gaattttgaa  
 865  
 Tyr Cys Ile Ser Gln Asp Leu Glu Thr Arg Lys  
                                   270                                  275

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 896

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Arg Phe Val Val Gln Glu Met Met Cys Leu Gln Ser Ser Ser Trp Thr  
                                   20                                  25                                  30

Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala Leu Ala Val Tyr Ala Asp  
                                   35                                  40                                  45

Asp Thr Pro Asp Arg Trp Phe Lys Val Ala Ala Met Ile Pro Gly Lys  
                                   50                                  55                                  60

Thr Ile Ser Asp Val Met Arg Gln Tyr Ser Lys Leu Glu Glu Asp Leu  
 65                                  70                                  75                                  80

Phe Asp Ile Glu Ala Gly Leu Val Pro Ile Pro Gly Tyr Arg Ser Val  
                                   85                                  90                                  95

Thr Pro Cys Gly Phe Asp Gln Val Val Ser Pro Arg Asp Phe Asp Ala  
                                   100                                  105                                  110

Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly Phe Asp Gln Asp Arg Arg



115                      120                      125  
 Lys Gly Val Pro Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly  
     130                      135                      140  
 Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe  
     145                      150                      155                      160  
 Val Gly Ser Lys Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr  
                     165                      170                      175  
 Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile  
                     180                      185                      190  
 His Asp Ile Thr Thr Val Asn Leu Leu Asn Ala Asn Leu Ser Arg Pro  
                     195                      200                      205  
 Ser Ser Asp His Gly Cys Leu Val Ser Lys Gln Ala Glu Pro Lys Leu  
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 Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu Gly Val Met Phe Leu Gly  
     225                      230                      235                      240  
 Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr Asp Pro Ala Ile Lys Phe  
                     245                      250                      255  
 Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly Tyr Cys Ile Ser Gln Asp  
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 Leu Glu Thr Arg Lys  
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 1                      5                      10                      15  
 ttg agg aat aga gat gaa gaa act gca gac aag cag ata caa ttc aat  
 96  
 Leu Arg Asn Arg Asp Glu Glu Thr Ala Asp Lys Gln Ile Gln Phe Asn  
                     20                      25                      30  
 gac caa agt ttt ggg gga aat gac tat gca ccc aag gta cgg aag cca  
 144  
 Asp Gln Ser Phe Gly Gly Asn Asp Tyr Ala Pro Lys Val Arg Lys Pro  
                     35                      40                      45



tac acg ata aca aaa gag aga gag aga tgg aca gat gaa gag cac aag  
 192  
 Tyr Thr Ile Thr Lys Glu Arg Glu Arg Trp Thr Asp Glu Glu His Lys  
 50 55 60  
 aag ttt gtt gaa gcc ttg aaa tta tac ggg cga gct tgg aga cga ata  
 240  
 Lys Phe Val Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile  
 65 70 75 80  
 gaa gaa cat gtg ggc tca aag acc gca gtt cag att cga agc cat gct  
 288  
 Glu Glu His Val Gly Ser Lys Thr Ala Val Gln Ile Arg Ser His Ala  
 85 90 95  
 cag aag ttt ttc tct aag gtt gct cga gaa gca act gga ggt gat ggg  
 336  
 Gln Lys Phe Phe Ser Lys Val Ala Arg Glu Ala Thr Gly Gly Asp Gly  
 100 105 110  
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 384  
 Ser Ser Val Glu Pro Ile Val Ile Pro Pro Pro Arg Pro Lys Arg Lys  
 115 120 125  
 cca gcg cat ccg tac cct cgt aag ttt ggg aac gag gca gat caa aca  
 432  
 Pro Ala His Pro Tyr Pro Arg Lys Phe Gly Asn Glu Ala Asp Gln Thr  
 130 135 140  
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 480  
 Ser Arg Ser Val Ser Pro Ser Glu Arg Asp Thr Gln Ser Pro Thr Ser  
 145 150 155 160  
 gtg ttg tcc act gtt gga tca gaa gca ttg tgt tcc ctt gat tcg agt  
 528  
 Val Leu Ser Thr Val Gly Ser Glu Ala Leu Cys Ser Leu Asp Ser Ser  
 165 170 175  
 tca ccc aat cga agc ttg tcc cca gtt tct tct gca tca cca cca gct  
 576  
 Ser Pro Asn Arg Ser Leu Ser Pro Val Ser Ser Ala Ser Pro Pro Ala  
 180 185 190  
 gct ctt aca acc act gca aat gca cct gaa gag ctt gag act ctg aag  
 624  
 Ala Leu Thr Thr Thr Ala Asn Ala Pro Glu Glu Leu Glu Thr Leu Lys  
 195 200 205  
 ctg gag ttg ttt cct agt gag aga ctc tta aac agg gag agc tcg atc  
 672  
 Leu Glu Leu Phe Pro Ser Glu Arg Leu Leu Asn Arg Glu Ser Ser Ile  
 210 215 220  
 aag gaa cca acg aag caa agt ctt aaa ctc ttt ggg aag aca gtt ttg  
 720  
 Lys Glu Pro Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr Val Leu  
 225 230 235 240



gta tct gat tca ggc atg tcc tct tct cta aca act tca aca tat tgt  
768

Val Ser Asp Ser Gly Met Ser Ser Ser Leu Thr Thr Ser Thr Tyr Cys  
245 250 255

aaa tcc cca att cag cca tta cca cgg aaa ctc tca tca tcc aag aca  
816

Lys Ser Pro Ile Gln Pro Leu Pro Arg Lys Leu Ser Ser Ser Lys Thr  
260 265 270

cta ccc ata ata aga aac tca caa gaa gaa ctc ttg agc tgc tgg ata  
864

Leu Pro Ile Ile Arg Asn Ser Gln Glu Glu Leu Leu Ser Cys Trp Ile  
275 280 285

caa gtc cct ctt aag caa gaa gat gtg gaa aat aga tgt ttg gat tca  
912

Gln Val Pro Leu Lys Gln Glu Asp Val Glu Asn Arg Cys Leu Asp Ser  
290 295 300

gga aag gct gtc caa aac gaa gga tca tcg act gga tca aac act ggt  
960

Gly Lys Ala Val Gln Asn Glu Gly Ser Ser Thr Gly Ser Asn Thr Gly  
305 310 315 320

tcg gtg gat gat acg gga cac acg gaa aag acc aca gaa ccc gaa aca  
1008

Ser Val Asp Asp Thr Gly His Thr Glu Lys Thr Thr Glu Pro Glu Thr  
325 330 335

atg cta tgt caa tgg gag ttt aaa cca agt gag agg tct gca ttt tct  
1056

Met Leu Cys Gln Trp Glu Phe Lys Pro Ser Glu Arg Ser Ala Phe Ser  
340 345 350

gag ctc aga aga aca aac tcc gag tca aat tca aga gga ttt ggt cca  
1104

Glu Leu Arg Arg Thr Asn Ser Glu Ser Asn Ser Arg Gly Phe Gly Pro  
355 360 365

tac aag aag aga aag atg gta aca gaa gaa gaa gag cat gag att cat  
1152

Tyr Lys Lys Arg Lys Met Val Thr Glu Glu Glu Glu His Glu Ile His  
370 375 380

ctc cac tta taa

1164

Leu His Leu

385

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20 25 30



Asp Gln Ser Phe Gly Gly Asn Asp Tyr Ala Pro Lys Val Arg Lys Pro  
 35 40 45  
 Tyr Thr Ile Thr Lys Glu Arg Glu Arg Trp Thr Asp Glu Glu His Lys  
 50 55 60  
 Lys Phe Val Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile  
 65 70 75 80  
 Glu Glu His Val Gly Ser Lys Thr Ala Val Gln Ile Arg Ser His Ala  
 85 90 95  
 Gln Lys Phe Phe Ser Lys Val Ala Arg Glu Ala Thr Gly Gly Asp Gly  
 100 105 110  
 Ser Ser Val Glu Pro Ile Val Ile Pro Pro Pro Arg Pro Lys Arg Lys  
 115 120 125  
 Pro Ala His Pro Tyr Pro Arg Lys Phe Gly Asn Glu Ala Asp Gln Thr  
 130 135 140  
 Ser Arg Ser Val Ser Pro Ser Glu Arg Asp Thr Gln Ser Pro Thr Ser  
 145 150 155 160  
 Val Leu Ser Thr Val Gly Ser Glu Ala Leu Cys Ser Leu Asp Ser Ser  
 165 170 175  
 Ser Pro Asn Arg Ser Leu Ser Pro Val Ser Ser Ala Ser Pro Pro Ala  
 180 185 190  
 Ala Leu Thr Thr Thr Ala Asn Ala Pro Glu Glu Leu Glu Thr Leu Lys  
 195 200 205  
 Leu Glu Leu Phe Pro Ser Glu Arg Leu Leu Asn Arg Glu Ser Ser Ile  
 210 215 220  
 Lys Glu Pro Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr Val Leu  
 225 230 235 240  
 Val Ser Asp Ser Gly Met Ser Ser Ser Leu Thr Thr Ser Thr Tyr Cys  
 245 250 255  
 Lys Ser Pro Ile Gln Pro Leu Pro Arg Lys Leu Ser Ser Ser Lys Thr  
 260 265 270



Leu Pro Ile Ile Arg Asn Ser Gln Glu Glu Leu Leu Ser Cys Trp Ile  
 275 280 285

Gln Val Pro Leu Lys Gln Glu Asp Val Glu Asn Arg Cys Leu Asp Ser  
 290 295 300

Gly Lys Ala Val Gln Asn Glu Gly Ser Ser Thr Gly Ser Asn Thr Gly  
 305 310 315 320

Ser Val Asp Asp Thr Gly His Thr Glu Lys Thr Thr Glu Pro Glu Thr  
 325 330 335

Met Leu Cys Gln Trp Glu Phe Lys Pro Ser Glu Arg Ser Ala Phe Ser  
 340 345 350

Glu Leu Arg Arg Thr Asn Ser Glu Ser Asn Ser Arg Gly Phe Gly Pro  
 355 360 365

Tyr Lys Lys Arg Lys Met Val Thr Glu Glu Glu Glu His Glu Ile His  
 370 375 380

Leu His Leu  
 385

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 51

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 1 5 10

aag atg ttt gag caa gct ttg gtt ctt ttt cct gaa gga tct cct aat  
 99

Lys Met Phe Glu Gln Ala Leu Val Leu Phe Pro Glu Gly Ser Pro Asn  
 15 20 25

cgg tgg gag aga atc gct gat cag ctt cat aaa tct gct ggt gaa gtt  
 147

Arg Trp Glu Arg Ile Ala Asp Gln Leu His Lys Ser Ala Gly Glu Val  
 30 35 40

agg gag cat tac gag gtc ttg gtt cat gat gtt ttc gag att gat tct  
 195

Arg Glu His Tyr Glu Val Leu Val His Asp Val Phe Glu Ile Asp Ser  
 45 50 55

ggt cga gtt gat gtc cct gat tac atg gat gac tcg gcg gct gcg gcg  
 243

Gly Arg Val Asp Val Pro Asp Tyr Met Asp Asp Ser Ala Ala Ala Ala  
 60 65 70 75



gcg ggt tgg gat tcc gct ggt cag atc tct ttt ggg tct aaa cat ggc  
291

Ala Gly Trp Asp Ser Ala Gly Gln Ile Ser Phe Gly Ser Lys His Gly  
80 85 90

gag agt gaa cgc aaa aga gga act cct tgg aca gag aac gaa cac aaa  
339

Glu Ser Glu Arg Lys Arg Gly Thr Pro Trp Thr Glu Asn Glu His Lys  
95 100 105

ttg ttt ctg atc gga tta aag aga tat ggt aag gga gat tgg agg agt  
387

Leu Phe Leu Ile Gly Leu Lys Arg Tyr Gly Lys Gly Asp Trp Arg Ser  
110 115 120

atc tcg aga aac gtt gtg gtg acg agg aca ccg acg caa gtc gcg agt  
435

Ile Ser Arg Asn Val Val Val Thr Arg Thr Pro Thr Gln Val Ala Ser  
125 130 135

cac gct cag aag tat ttt ctg aga cag aac tcg gtg aag aag gag agg  
483

His Ala Gln Lys Tyr Phe Leu Arg Gln Asn Ser Val Lys Lys Glu Arg  
140 145 150 155

aaa agg tcg agc atc cat gat ata act acg gtt gat gct act ttg gct  
531

Lys Arg Ser Ser Ile His Asp Ile Thr Thr Val Asp Ala Thr Leu Ala  
160 165 170

atg cct ggg tct aac atg gac tgg act ggc caa cac ggg agt cct gtt  
579

Met Pro Gly Ser Asn Met Asp Trp Thr Gly Gln His Gly Ser Pro Val  
175 180 185

cag gcg ccg cag cag caa cag att atg tct gag ttc ggt cag caa ttg  
627

Gln Ala Pro Gln Gln Gln Gln Ile Met Ser Glu Phe Gly Gln Gln Leu  
190 195 200

aat cct ggt cat ttc gag gat ttt ggg ttt cgg atg tga tg  
668

Asn Pro Gly His Phe Glu Asp Phe Gly Phe Arg Met  
205 210 215

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250

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1 5 10 15

Ala Leu Val Leu Phe Pro Glu Gly Ser Pro Asn Arg Trp Glu Arg Ile  
20 25 30

Ala Asp Gln Leu His Lys Ser Ala Gly Glu Val Arg Glu His Tyr Glu  
35 40 45



Val Leu Val His Asp Val Phe Glu Ile Asp Ser Gly Arg Val Asp Val  
50 55 60

Pro Asp Tyr Met Asp Asp Ser Ala Ala Ala Ala Gly Trp Asp Ser  
65 70 75 80

Ala Gly Gln Ile Ser Phe Gly Ser Lys His Gly Glu Ser Glu Arg Lys  
85 90 95

Arg Gly Thr Pro Trp Thr Glu Asn Glu His Lys Leu Phe Leu Ile Gly  
100 105 110

Leu Lys Arg Tyr Gly Lys Gly Asp Trp Arg Ser Ile Ser Arg Asn Val  
115 120 125

Val Val Thr Arg Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr  
130 135 140

Phe Leu Arg Gln Asn Ser Val Lys Lys Glu Arg Lys Arg Ser Ser Ile  
145 150 155 160

His Asp Ile Thr Thr Val Asp Ala Thr Leu Ala Met Pro Gly Ser Asn  
165 170 175

Met Asp Trp Thr Gly Gln His Gly Ser Pro Val Gln Ala Pro Gln Gln  
180 185 190

Gln Gln Ile Met Ser Glu Phe Gly Gln Gln Leu Asn Pro Gly His Phe  
195 200 205

Glu Asp Phe Gly Phe Arg Met  
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120

ctttttcagt ttctotttct ctttttgaca gaagagaccg agaagca atg gga agg  
176

Met Gly Arg  
1

gct ccg tgt tgt gag aaa atc ggg ttg aag aga ggg aga tgg aca gcc  
224



Ala Pro Cys Cys Glu Lys Ile Gly Leu Lys Arg Gly Arg Trp Thr Ala  
 5 10 15  
 gag gaa gat gag atc ctc acc aag tat att cag acc aat ggt gaa ggt  
 272  
 Glu Glu Asp Glu Ile Leu Thr Lys Tyr Ile Gln Thr Asn Gly Glu Gly  
 20 25 30 35  
 tct tgg cga tct ttg cct aag aaa gct gga ttg ttg aga tgt gga aag  
 320  
 Ser Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Leu Arg Cys Gly Lys  
 40 45 50  
 agc tgt aga cta agg tgg ata aac tac tta aga aga gac tta aaa aga  
 368  
 Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Arg Asp Leu Lys Arg  
 55 60 65  
 gga aat att act tcc gac gaa gaa gaa ata atc gtc aag ttg cat tcc  
 416  
 Gly Asn Ile Thr Ser Asp Glu Glu Glu Ile Ile Val Lys Leu His Ser  
 70 75 80  
 ctt ctc ggc aac aga tgg tca ctt att gca aca cat cta cca gga aga  
 464  
 Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Thr His Leu Pro Gly Arg  
 85 90 95  
 aca gac aac gaa att aaa aac tat tgg aac tca cat ctc agc cgc aaa  
 512  
 Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys  
 100 105 110 115  
 atc tat gcc ttc act gcc gtt tcc gga gat gga cac aat cta ctc gtc  
 560  
 Ile Tyr Ala Phe Thr Ala Val Ser Gly Asp Gly His Asn Leu Leu Val  
 120 125 130  
 aac gat gta gtc ttg aag aaa tct tgt tca tgc tct tct gga gcc aag  
 608  
 Asn Asp Val Val Leu Lys Lys Ser Cys Ser Ser Ser Ser Gly Ala Lys  
 135 140 145  
 aac aat aac aag acc aag aag aag aag gga agg act agt agg tca  
 656  
 Asn Asn Asn Lys Thr Lys Lys Lys Lys Lys Gly Arg Thr Ser Arg Ser  
 150 155 160  
 tcc atg aag aaa cac aag caa atg gtg acg gcc tca caa tgt ttc tca  
 704  
 Ser Met Lys Lys His Lys Gln Met Val Thr Ala Ser Gln Cys Phe Ser  
 165 170 175  
 caa cct aag gag cta gag agt gat ttc agt gag gga ggg caa aat ggt  
 752  
 Gln Pro Lys Glu Leu Glu Ser Asp Phe Ser Glu Gly Gly Gln Asn Gly  
 180 185 190 195  
 aat ttt gaa gga gag tct ttg ggg cct tat gag tgg ttg gat ggt gag  
 800  
 Asn Phe Glu Gly Glu Ser Leu Gly Pro Tyr Glu Trp Leu Asp Gly Glu



	200	205	210
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848			
Leu Glu Arg Leu Leu Ser Ser Cys Val Trp Glu Cys Thr Ser Glu Glu			
215	220	225	
gct gtg att gga gta aat gat gaa aag gtg tgt gag agt ggg gac aat			
896			
Ala Val Ile Gly Val Asn Asp Glu Lys Val Cys Glu Ser Gly Asp Asn			
230	235	240	
agt agt tgt tgt gtt aat ttg ttt gaa gaa gaa caa gga agc gag aca			
944			
Ser Ser Cys Cys Val Asn Leu Phe Glu Glu Glu Gln Gly Ser Glu Thr			
245	250	255	
aag att ggt cac gta gga atc aca gag gtt gat cat gat atg acg gtg			
992			
Lys Ile Gly His Val Gly Ile Thr Glu Val Asp His Asp Met Thr Val			
260	265	270	275
gaa aga gaa aga gag gga agt ttt tta agt tcg aat tca aat gaa aat			
1040			
Glu Arg Glu Arg Glu Gly Ser Phe Leu Ser Ser Asn Ser Asn Glu Asn			
280	285	290	
aat gat aaa gat tgg tgg gtt ggt cta tgt aat tct tca gaa gtt ggg			
1088			
Asn Asp Lys Asp Trp Trp Val Gly Leu Cys Asn Ser Ser Glu Val Gly			
295	300	305	
ttt ggg gtt gat gag gag ttg ctt gat tgg gag ttt caa ggt aat gtc			
1136			
Phe Gly Val Asp Glu Glu Leu Leu Asp Trp Glu Phe Gln Gly Asn Val			
310	315	320	
act tgt caa agt gat gat cta tgg gat ctc tca gat att gga gag ata			
1184			
Thr Cys Gln Ser Asp Asp Leu Trp Asp Leu Ser Asp Ile Gly Glu Ile			
325	330	335	
aca ttg gag tga ttgtaccgag caagtggatt ggcggccgct ctagacaggc			
1236			
Thr Leu Glu			
340			
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aagt			
1300			
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20 25 30

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Leu Arg  
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Arg Asp  
50 55 60

Leu Lys Arg Gly Asn Ile Thr Ser Asp Glu Glu Glu Ile Ile Val Lys  
65 70 75 80

Leu His Ser Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Thr His Leu  
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu  
100 105 110

Ser Arg Lys Ile Tyr Ala Phe Thr Ala Val Ser Gly Asp Gly His Asn  
115 120 125

Leu Leu Val Asn Asp Val Val Leu Lys Lys Ser Cys Ser Ser Ser Ser  
130 135 140

Gly Ala Lys Asn Asn Asn Lys Thr Lys Lys Lys Lys Lys Gly Arg Thr  
145 150 155 160

Ser Arg Ser Ser Met Lys Lys His Lys Gln Met Val Thr Ala Ser Gln  
165 170 175

Cys Phe Ser Gln Pro Lys Glu Leu Glu Ser Asp Phe Ser Glu Gly Gly  
180 185 190

Gln Asn Gly Asn Phe Glu Gly Glu Ser Leu Gly Pro Tyr Glu Trp Leu  
195 200 205

Asp Gly Glu Leu Glu Arg Leu Leu Ser Ser Cys Val Trp Glu Cys Thr  
210 215 220

Ser Glu Glu Ala Val Ile Gly Val Asn Asp Glu Lys Val Cys Glu Ser  
225 230 235 240

Gly Asp Asn Ser Ser Cys Cys Val Asn Leu Phe Glu Glu Glu Gln Gly  
245 250 255

Ser Glu Thr Lys Ile Gly His Val Gly Ile Thr Glu Val Asp His Asp



260 265 270

Met Thr Val Glu Arg Glu Arg Glu Gly Ser Phe Leu Ser Ser Asn Ser  
275 280 285

Asn Glu Asn Asn Asp Lys Asp Trp Trp Val Gly Leu Cys Asn Ser Ser  
290 295 300

Glu Val Gly Phe Gly Val Asp Glu Glu Leu Leu Asp Trp Glu Phe Gln  
305 310 315 320

Gly Asn Val Thr Cys Gln Ser Asp Asp Leu Trp Asp Leu Ser Asp Ile  
325 330 335

Gly Glu Ile Thr Leu Glu  
340

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ctc atg gag gaa act aag agc ggc gtc gca gct tct ggt gaa ggt gcc  
96  
Leu Met Glu Glu Thr Lys Ser Gly Val Ala Ala Ser Gly Glu Gly Ala  
20 25 30  
acg tgg acg gcg gca gag aac aag gca ttc gag aat gct ttg gcg gtt  
144  
Thr Trp Thr Ala Ala Glu Asn Lys Ala Phe Glu Asn Ala Leu Ala Val  
35 40 45  
tac gac gac aac act cct gat cgg tgg cag aag gtg gct gcg gtg att  
192  
Tyr Asp Asp Asn Thr Pro Asp Arg Trp Gln Lys Val Ala Ala Val Ile  
50 55 60  
ccg ggg aag aca gtg agt gac gta att aga cag tat aac gat ttg gaa  
240  
Pro Gly Lys Thr Val Ser Asp Val Ile Arg Gln Tyr Asn Asp Leu Glu  
65 70 75 80  
gct gat gtc agc agc atc gag gcc ggt tta atc ccg gtc ccc ggt tac  
288  
Ala Asp Val Ser Ser Ile Glu Ala Gly Leu Ile Pro Val Pro Gly Tyr  
85 90 95  
atc acc tcg ccg cct ttc act cta gat tgg gcc ggc ggc ggt ggc gga  
336  
Ile Thr Ser Pro Pro Phe Thr Leu Asp Trp Ala Gly Gly Gly Gly Gly  
100 105 110



tgt aac ggg ttt aaa ccg ggt cat cag gtt tgt aat aaa cgg tcg cag  
 384  
 Cys Asn Gly Phe Lys Pro Gly His Gln Val Cys Asn Lys Arg Ser Gln  
 115 120 125  
 gcc ggt aga tcg ccg gag ctg gag cgg aag aaa ggc gtt cct tgg acg  
 432  
 Ala Gly Arg Ser Pro Glu Leu Glu Arg Lys Lys Gly Val Pro Trp Thr  
 130 135 140  
 gag gaa gaa cac aag cta ttt cta atg ggt ttg aag aaa tat ggg aaa  
 480  
 Glu Glu Glu His Lys Leu Phe Leu Met Gly Leu Lys Lys Tyr Gly Lys  
 145 150 155 160  
 gga gat tgg aga aac ata tct cgg aac ttt gtg ata acg cga acg cca  
 528  
 Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Ile Thr Arg Thr Pro  
 165 170 175  
 aca caa gta gct agc cac gcc caa aag tac ttc atc cgg caa ctt tcc  
 576  
 Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg Gln Leu Ser  
 180 185 190  
 ggc ggc aag gac aag aga cga gca agc att cac gac ata acc acc gta  
 624  
 Gly Gly Lys Asp Lys Arg Arg Ala Ser Ile His Asp Ile Thr Thr Val  
 195 200 205  
 aat ctc gaa gag gag gct tct ttg gag acc aat aag agc tcc att gtt  
 672  
 Asn Leu Glu Glu Glu Ala Ser Leu Glu Thr Asn Lys Ser Ser Ile Val  
 210 215 220  
 gtt gga gat cag cgt tca agg cta acc gcg ttt cct tgg aac caa acg  
 720  
 Val Gly Asp Gln Arg Ser Arg Leu Thr Ala Phe Pro Trp Asn Gln Thr  
 225 230 235 240  
 gac aac aat gga aca cag gca gac gct ttc aat ata acg att gga aac  
 768  
 Asp Asn Asn Gly Thr Gln Ala Asp Ala Phe Asn Ile Thr Ile Gly Asn  
 245 250 255  
 gct att agt ggc gtt cat tca tac ggc cag gtt atg att gga ggg tat  
 816  
 Ala Ile Ser Gly Val His Ser Tyr Gly Gln Val Met Ile Gly Gly Tyr  
 260 265 270  
 aac aat gca gat tct tgc tat gac gcc caa aac aca atg ttt caa cta  
 864  
 Asn Asn Ala Asp Ser Cys Tyr Asp Ala Gln Asn Thr Met Phe Gln Leu  
 275 280 285  
 tag  
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1 5 10 15

Leu Met Glu Glu Thr Lys Ser Gly Val Ala Ala Ser Gly Glu Gly Ala  
20 25 30

Thr Trp Thr Ala Ala Glu Asn Lys Ala Phe Glu Asn Ala Leu Ala Val  
35 40 45

Tyr Asp Asp Asn Thr Pro Asp Arg Trp Gln Lys Val Ala Ala Val Ile  
50 55 60

Pro Gly Lys Thr Val Ser Asp Val Ile Arg Gln Tyr Asn Asp Leu Glu  
65 70 75 80

Ala Asp Val Ser Ser Ile Glu Ala Gly Leu Ile Pro Val Pro Gly Tyr  
85 90 95

Ile Thr Ser Pro Pro Phe Thr Leu Asp Trp Ala Gly Gly Gly Gly Gly  
100 105 110

Cys Asn Gly Phe Lys Pro Gly His Gln Val Cys Asn Lys Arg Ser Gln  
115 120 125

Ala Gly Arg Ser Pro Glu Leu Glu Arg Lys Lys Gly Val Pro Trp Thr  
130 135 140

Glu Glu Glu His Lys Leu Phe Leu Met Gly Leu Lys Lys Tyr Gly Lys  
145 150 155 160

Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Ile Thr Arg Thr Pro  
165 170 175

Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg Gln Leu Ser  
180 185 190

Gly Gly Lys Asp Lys Arg Arg Ala Ser Ile His Asp Ile Thr Thr Val  
195 200 205

Asn Leu Glu Glu Glu Ala Ser Leu Glu Thr Asn Lys Ser Ser Ile Val  
210 215 220

Val Gly Asp Gln Arg Ser Arg Leu Thr Ala Phe Pro Trp Asn Gln Thr  
225 230 235 240



Asp Asn Asn Gly Thr Gln Ala Asp Ala Phe Asn Ile Thr Ile Gly Asn  
 245 250 255

Ala Ile Ser Gly Val His Ser Tyr Gly Gln Val Met Ile Gly Gly Tyr  
 260 265 270

Asn Asn Ala Asp Ser Cys Tyr Asp Ala Gln Asn Thr Met Phe Gln Leu  
 275 280 285

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Met Asp Asn Asn Asn Asn Asn  
 1 5

aac aac cag caa cca cca cca acc tcc gtc tat cca cct ggc tcc gcc  
 102

Asn Asn Gln Gln Pro Pro Pro Thr Ser Val Tyr Pro Pro Gly Ser Ala  
 10 15 20

gtc aca acc gta atc cct cct cca cca tct gga tct gca tca ata gtc  
 150

Val Thr Thr Val Ile Pro Pro Pro Pro Ser Gly Ser Ala Ser Ile Val  
 25 30 35

acc gga gga gga gcg aca tac cac cac ctc ctc cag caa caa cag caa  
 198

Thr Gly Gly Gly Ala Thr Tyr His His Leu Leu Gln Gln Gln Gln Gln  
 40 45 50 55

cag ctt caa atg ttc tgg aca tac cag aga caa gag atc gaa cag gta  
 246

Gln Leu Gln Met Phe Trp Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val  
 60 65 70

aac gat ttc aaa aac cat cag ctc cct cta gct cgt atc aaa aaa atc  
 294

Asn Asp Phe Lys Asn His Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile  
 75 80 85

atg aaa gct gat gaa gat gtg cgt atg atc tcc gcc gaa gca ccg att  
 342

Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Ile  
 90 95 100

ctc ttc gcg aaa gct tgt gag ctt ttc att ctc gaa ctt acg att aga  
 390

Leu Phe Ala Lys Ala Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg  
 105 110 115

tct tgg ctt cac gct gaa gag aac aaa cgt cgt acg ctt cag aaa aac  
 438

Ser Trp Leu His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn



456



Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His Gln Leu Pro  
65 70 75 80

Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met  
85 90 95

Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys Glu Leu Phe  
100 105 110

Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu Glu Asn Lys  
115 120 125

Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile Thr Arg Thr  
130 135 140

Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Glu Glu Ile Lys  
145 150 155 160

Glu Glu Glu Asp Ala Ala Ser Ala Leu Gly Gly Gly Gly Met Val Ala  
165 170 175

Pro Ala Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro  
180 185 190

Ala Val Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Ser  
195 200 205

Gly Val Tyr Ala Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln  
210 215 220

Asn Ser Ala Gly Gly Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser  
225 230 235 240

Ser Gly His Gly Asn Leu Asp Ser Gln Gly  
245 250

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caaaatctcc ttacttaaac tcacaaactc ctcacaaatt ttctgaatct ttcagttgaa  
120

catataacaa cattcataac a atg gct gga ggt aca gct cta act cca acc  
171



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Met Ala Gly Gly Thr Ala Leu Thr Pro Thr
1           5           10

tct gta gga tcc aag tct gtt cca atg agg aac cat gaa gca aca gag
219
Ser Val Gly Ser Lys Ser Val Pro Met Arg Asn His Glu Ala Thr Glu
15           20           25

aga ggc aac acc aac aac aac ctg aga gca tta ccc aaa gcc gtc caa
267
Arg Gly Asn Thr Asn Asn Asn Leu Arg Ala Leu Pro Lys Ala Val Gln
30           35           40

ccg gtt tca tca atc gaa gga gag atg gct aag agg cca cgt ggc aga
315
Pro Val Ser Ser Ile Glu Gly Glu Met Ala Lys Arg Pro Arg Gly Arg
45           50           55

ccc gct ggc tcc aag aac aaa ccc aaa cca cca atc att gtg act cac
363
Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Val Thr His
60           65           70

gac agt cca aat tcc ctc aga gct aac gcc gtt gag atc agc tca ggt
411
Asp Ser Pro Asn Ser Leu Arg Ala Asn Ala Val Glu Ile Ser Ser Gly
75           80           85           90

tgt gac atc tgt gag act tta tcg gat ttt gca aga agg aaa cag aga
459
Cys Asp Ile Cys Glu Thr Leu Ser Asp Phe Ala Arg Arg Lys Gln Arg
95           100           105

ggg ctc tgc att ctc agt gcc aat ggt tgt gtc acc aat gtg aca tta
507
Gly Leu Cys Ile Leu Ser Ala Asn Gly Cys Val Thr Asn Val Thr Leu
110           115           120

agg caa cca gct tca tca gga gca att gtc aca tta cac gga cgt tac
555
Arg Gln Pro Ala Ser Ser Gly Ala Ile Val Thr Leu His Gly Arg Tyr
125           130           135

gag atc ctc tca ttg ctt gga tca atc ttg cct cca cca gca cca ctt
603
Glu Ile Leu Ser Leu Leu Gly Ser Ile Leu Pro Pro Pro Ala Pro Leu
140           145           150

gga ata act ggt ctg acc att tac tta gcc gga cct caa gga cag gtt
651
Gly Ile Thr Gly Leu Thr Ile Tyr Leu Ala Gly Pro Gln Gly Gln Val
155           160           165           170

gtt ggt gga gga gtg gtt ggt ggg cta atc gca tct ggt cct gtt gtt
699
Val Gly Gly Gly Val Val Gly Gly Leu Ile Ala Ser Gly Pro Val Val
175           180           185

ctc atg gct gca tct ttc atg aat gct gtt ttt gat cgt ctt cct atg
747
Leu Met Ala Ala Ser Phe Met Asn Ala Val Phe Asp Arg Leu Pro Met

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190 195 200  
 gat gat gat gaa gct gcc tct atg cag aac cag cag tac tac cag aat  
 795  
 Asp Asp Asp Glu Ala Ala Ser Met Gln Asn Gln Gln Tyr Tyr Gln Asn  
 205 210 215  
 gga aga tcc cgt cct tta gat gac att cat gga ctg cct caa aat ctg  
 843  
 Gly Arg Ser Arg Pro Leu Asp Asp Ile His Gly Leu Pro Gln Asn Leu  
 220 225 230  
 ctc act aat gga aac tcg gct tct gat atc tac tct tgg ggg cct tgg  
 891  
 Leu Thr Asn Gly Asn Ser Ala Ser Asp Ile Tyr Ser Trp Gly Pro Trp  
 235 240 245 250  
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 938  
 Asn Gln Arg

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Val Pro Met Arg Asn His Glu Ala Thr Glu Arg Gly Asn Thr Asn Asn  
 20 25 30

Asn Leu Arg Ala Leu Pro Lys Ala Val Gln Pro Val Ser Ser Ile Glu  
 35 40 45

Gly Glu Met Ala Lys Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn  
 50 55 60

Lys Pro Lys Pro Pro Ile Ile Val Thr His Asp Ser Pro Asn Ser Leu  
 65 70 75 80

Arg Ala Asn Ala Val Glu Ile Ser Ser Gly Cys Asp Ile Cys Glu Thr  
 85 90 95

Leu Ser Asp Phe Ala Arg Arg Lys Gln Arg Gly Leu Cys Ile Leu Ser  
 100 105 110

Ala Asn Gly Cys Val Thr Asn Val Thr Leu Arg Gln Pro Ala Ser Ser  
 115 120 125

Gly Ala Ile Val Thr Leu His Gly Arg Tyr Glu Ile Leu Ser Leu Leu  
 130 135 140



Gly Ser Ile Leu Pro Pro Pro Ala Pro Leu Gly Ile Thr Gly Leu Thr  
145 150 155 160

Ile Tyr Leu Ala Gly Pro Gln Gly Gln Val Val Gly Gly Gly Val Val  
165 170 175

Gly Gly Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe  
180 185 190

Met Asn Ala Val Phe Asp Arg Leu Pro Met Asp Asp Asp Glu Ala Ala  
195 200 205

Ser Met Gln Asn Gln Gln Tyr Tyr Gln Asn Gly Arg Ser Arg Pro Leu  
210 215 220

Asp Asp Ile His Gly Leu Pro Gln Asn Leu Leu Thr Asn Gly Asn Ser  
225 230 235 240

Ala Ser Asp Ile Tyr Ser Trp Gly Pro Trp Asn Gln Arg  
245 250

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1 5 10 15  
ata aat atg gac cac cat cac gcc ttt gca tca cat tca tac aac tca  
96  
Ile Asn Met Asp His His His Ala Phe Ala Ser His Ser Tyr Asn Ser  
20 25 30  
gtt ttc ata agc aaa aag gca atg gaa gag tca cga tcc tac aga aag  
144  
Val Phe Ile Ser Lys Lys Ala Met Glu Glu Ser Arg Ser Tyr Arg Lys  
35 40 45  
gag agg aag cag aca aag aag aaa acg ggt cgt ggg tca gga tcc agg  
192  
Glu Arg Lys Gln Thr Lys Lys Lys Thr Gly Arg Gly Ser Gly Ser Arg  
50 55 60  
tcg atc cat ata aag atg agg aag ctt cga gtg ctt ata ccg ggt gga  
240  
Ser Ile His Ile Lys Met Arg Lys Leu Arg Val Leu Ile Pro Gly Gly  
65 70 75 80  
cga aga ttg aac caa ccg gat ctg ctt cta tca aag act gct gat tat  
288  
Arg Arg Leu Asn Gln Pro Asp Leu Leu Leu Ser Lys Thr Ala Asp Tyr



	85	90	95
att atg cat ttg gag ttg agg att agc att cta cat ttg ttg gtc aga			
336			
Ile Met His Leu Glu Leu Arg Ile Ser Ile Leu His Leu Leu Val Arg			
	100	105	110
tat tac tta aag aag aaa aga tca aac ctt tcg tca tca cca aac gaa			
384			
Tyr Tyr Leu Lys Lys Lys Arg Ser Asn Leu Ser Ser Ser Pro Asn Glu			
	115	120	125
tct aat caa aac cca gaa ttt tcc gac tcc gat act tac caa aga cag			
432			
Ser Asn Gln Asn Pro Glu Phe Ser Asp Ser Asp Thr Tyr Gln Arg Gln			
	130	135	140
ctt caa cag ctc ttt cat ctc cat gat tca ggt cta gat caa gct tta			
480			
Leu Gln Gln Leu Phe His Leu His Asp Ser Gly Leu Asp Gln Ala Leu			
145	150	155	160
atc gat gct ctt cct gtg ttt ctt tac aaa gag atc aaa ggt acg aaa			
528			
Ile Asp Ala Leu Pro Val Phe Leu Tyr Lys Glu Ile Lys Gly Thr Lys			
	165	170	175
gag cct ttt gat tgt gca gtg tgt ctc tgt gaa ttc tcg gaa gat gat			
576			
Glu Pro Phe Asp Cys Ala Val Cys Leu Cys Glu Phe Ser Glu Asp Asp			
	180	185	190
aag ctt aga ttg ctt ccg aat tgt agt cac gct ttt cac ata gat tgt			
624			
Lys Leu Arg Leu Leu Pro Asn Cys Ser His Ala Phe His Ile Asp Cys			
	195	200	205
atc gat act tgg ctt ctc tcg aat tcg act tgt cca ctt tgt aga gga			
672			
Ile Asp Thr Trp Leu Leu Ser Asn Ser Thr Cys Pro Leu Cys Arg Gly			
	210	215	220
acc ctt ttc tct tta ggt cat caa ttt gaa tac cct gat ttc aat ttc			
720			
Thr Leu Phe Ser Leu Gly His Gln Phe Glu Tyr Pro Asp Phe Asn Phe			
225	230	235	240
ggg ttt ttc gcc gga gat gat gga gga gga gga gtt agg gtt tct ccg			
768			
Gly Phe Phe Ala Gly Asp Asp Gly Gly Gly Gly Val Arg Val Ser Pro			
	245	250	255
gtt cag aaa cca gct gag aat gag att ggg aag aga gtg ttt tca gtg			
816			
Val Gln Lys Pro Ala Glu Asn Glu Ile Gly Lys Arg Val Phe Ser Val			
	260	265	270
agg ctt ggt aag ttt agg agc agt aat att gtc aac aat ggt gaa gta			
864			
Arg Leu Gly Lys Phe Arg Ser Ser Asn Ile Val Asn Asn Gly Glu Val			
	275	280	285



gta gta gga gga gga gga gag aca agt agt agt agt ctt gat aat aga  
912

Val Val Gly Gly Gly Gly Glu Thr Ser Ser Ser Ser Leu Asp Asn Arg  
290 295 300

aga tgt ttc tca atg ggg tct tat cag tac ata gtg gct gaa tca gat  
960

Arg Cys Phe Ser Met Gly Ser Tyr Gln Tyr Ile Val Ala Glu Ser Asp  
305 310 315 320

ctg gtt gtt gct ttg tgt cct aat aat gaa gga ttg aag aat aat aag  
1008

Leu Val Val Ala Leu Cys Pro Asn Asn Glu Gly Leu Lys Asn Asn Lys  
325 330 335

gat gtt gaa ggg aag aag att aat atg aga agt aaa ggt gag agc ttt  
1056

Asp Val Glu Gly Lys Lys Ile Asn Met Arg Ser Lys Gly Glu Ser Phe  
340 345 350

tct gtg tca aag att tgg caa tgg tct aat aag aga tca aag ttt cct  
1104

Ser Val Ser Lys Ile Trp Gln Trp Ser Asn Lys Arg Ser Lys Phe Pro  
355 360 365

aat aat cat cca tca gag act aat ctt gtg gtt ggt ggt tct tct tct  
1152

Asn Asn His Pro Ser Glu Thr Asn Leu Val Val Gly Gly Ser Ser Ser  
370 375 380

tct tct tct tat gtt tgt tct gga tct gat ggg tta tca ttg aat gga  
1200

Ser Ser Ser Tyr Val Cys Ser Gly Ser Asp Gly Leu Ser Leu Asn Gly  
385 390 395 400

agg aga ttt cag ggt cca tga  
1221

Arg Arg Phe Gln Gly Pro  
405

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Ile Asn Met Asp His His His Ala Phe Ala Ser His Ser Tyr Asn Ser  
20 25 30

Val Phe Ile Ser Lys Lys Ala Met Glu Glu Ser Arg Ser Tyr Arg Lys  
35 40 45

Glu Arg Lys Gln Thr Lys Lys Lys Thr Gly Arg Gly Ser Gly Ser Arg  
50 55 60



Ser Ile His Ile Lys Met Arg Lys Leu Arg Val Leu Ile Pro Gly Gly  
 65 70 75 80  
 Arg Arg Leu Asn Gln Pro Asp Leu Leu Leu Ser Lys Thr Ala Asp Tyr  
 85 90 95  
 Ile Met His Leu Glu Leu Arg Ile Ser Ile Leu His Leu Leu Val Arg  
 100 105 110  
 Tyr Tyr Leu Lys Lys Lys Arg Ser Asn Leu Ser Ser Ser Pro Asn Glu  
 115 120 125  
 Ser Asn Gln Asn Pro Glu Phe Ser Asp Ser Asp Thr Tyr Gln Arg Gln  
 130 135 140  
 Leu Gln Gln Leu Phe His Leu His Asp Ser Gly Leu Asp Gln Ala Leu  
 145 150 155 160  
 Ile Asp Ala Leu Pro Val Phe Leu Tyr Lys Glu Ile Lys Gly Thr Lys  
 165 170 175  
 Glu Pro Phe Asp Cys Ala Val Cys Leu Cys Glu Phe Ser Glu Asp Asp  
 180 185 190  
 Lys Leu Arg Leu Leu Pro Asn Cys Ser His Ala Phe His Ile Asp Cys  
 195 200 205  
 Ile Asp Thr Trp Leu Leu Ser Asn Ser Thr Cys Pro Leu Cys Arg Gly  
 210 215 220  
 Thr Leu Phe Ser Leu Gly His Gln Phe Glu Tyr Pro Asp Phe Asn Phe  
 225 230 235 240  
 Gly Phe Phe Ala Gly Asp Asp Gly Gly Gly Gly Val Arg Val Ser Pro  
 245 250 255  
 Val Gln Lys Pro Ala Glu Asn Glu Ile Gly Lys Arg Val Phe Ser Val  
 260 265 270  
 Arg Leu Gly Lys Phe Arg Ser Ser Asn Ile Val Asn Asn Gly Glu Val  
 275 280 285  
 Val Val Gly Gly Gly Gly Glu Thr Ser Ser Ser Ser Leu Asp Asn Arg  
 290 295 300  
 Arg Cys Phe Ser Met Gly Ser Tyr Gln Tyr Ile Val Ala Glu Ser Asp



305                                      310                                      315                                      320  
 Leu Val Val Ala Leu Cys Pro Asn Asn Glu Gly Leu Lys Asn Asn Lys  
    325                                      330                                      335  
 Asp Val Glu Gly Lys Lys Ile Asn Met Arg Ser Lys Gly Glu Ser Phe  
    340                                      345                                      350  
 Ser Val Ser Lys Ile Trp Gln Trp Ser Asn Lys Arg Ser Lys Phe Pro  
    355                                      360                                      365  
 Asn Asn His Pro Ser Glu Thr Asn Leu Val Val Gly Gly Ser Ser Ser  
    370                                      375                                      380  
 Ser Ser Ser Tyr Val Cys Ser Gly Ser Asp Gly Leu Ser Leu Asn Gly  
    385                                      390                                      395                                      400  
 Arg Arg Phe Gln Gly Pro  
    405

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 <221> CDS <222> (32)..(1216) <223> G1766

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Met Asn Ser Phe Ser Gln Val  
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cct cct ggc ttc aga ttt cat cct act gat gaa gaa ctt gta gac tac  
 100

Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Asp Tyr  
    10                                      15                                      20

tac ttg agg aaa aaa gtt gca tca aag aga ata gaa atc gat atc atc  
 148

Tyr Leu Arg Lys Lys Val Ala Ser Lys Arg Ile Glu Ile Asp Ile Ile  
    25                                      30                                      35

aag gat gtt gat ctt tac aag att gag cca tgt gat ctt caa gag tta  
 196

Lys Asp Val Asp Leu Tyr Lys Ile Glu Pro Cys Asp Leu Gln Glu Leu  
 40                                      45                                      50                                      55

tgc aag ata gga aac gaa gag cag agc gaa tgg tac ttc ttt agt cat  
 244

Cys Lys Ile Gly Asn Glu Glu Gln Ser Glu Trp Tyr Phe Phe Ser His  
    60                                      65                                      70

aaa gac aag aag tat ccc acg gga act cga acc aat aga gcc acg aaa  
 292

Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Lys  
    75                                      80                                      85



gca gga ttt tgg aaa gcc act gga aga gac aag gct ata tat ata aga  
 340  
 Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ala Ile Tyr Ile Arg  
 90 95 100

cat agt ctt atc ggt atg agg aaa aca ctt gtg ttt tac aaa gga aga  
 388  
 His Ser Leu Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg  
 105 110 115

gcc cca aat ggt cag aaa tcc gat tgg atc atg cac gaa tat cgc tta  
 436  
 Ala Pro Asn Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu  
 120 125 130 135

gaa aca agt gaa aat gga acc cct cag gaa gaa gga tgg gta gta tgt  
 484  
 Glu Thr Ser Glu Asn Gly Thr Pro Gln Glu Glu Gly Trp Val Val Cys  
 140 145 150

agg gta ttc aag aag aaa ttg gca gcg aca gtg agg aaa atg gga gat  
 532  
 Arg Val Phe Lys Lys Lys Leu Ala Ala Thr Val Arg Lys Met Gly Asp  
 155 160 165

tac cat tca tca cca tcg cag cat tgg tac gat gat cag ctc tct ttt  
 580  
 Tyr His Ser Ser Pro Ser Gln His Trp Tyr Asp Asp Gln Leu Ser Phe  
 170 175 180

atg gcc tcc gag atc att tct agt tct cca cga cag ttt ctt ccc aat  
 628  
 Met Ala Ser Glu Ile Ile Ser Ser Ser Pro Arg Gln Phe Leu Pro Asn  
 185 190 195

cat cat tat aac cgc cac cat cac cag cag aca ttg cct tgt ggc ctc  
 676  
 His His Tyr Asn Arg His His His Gln Gln Thr Leu Pro Cys Gly Leu  
 200 205 210 215

aat gca ttc aac aac aac aat cct aac ttg caa tgc aag caa gag ctc  
 724  
 Asn Ala Phe Asn Asn Asn Asn Pro Asn Leu Gln Cys Lys Gln Glu Leu  
 220 225 230

gag tta cat tac aat caa atg gta caa cat caa caa caa aac cat cat  
 772  
 Glu Leu His Tyr Asn Gln Met Val Gln His Gln Gln Gln Asn His His  
 235 240 245

ctt cgt gaa tct atg ttt ctc cag ctt cct cag ctc gaa agc cct acc  
 820  
 Leu Arg Glu Ser Met Phe Leu Gln Leu Pro Gln Leu Glu Ser Pro Thr  
 250 255 260

agt aat tgc aat tct gac aac aac aat aac aca aga aat att agt aac  
 868  
 Ser Asn Cys Asn Ser Asp Asn Asn Asn Asn Thr Arg Asn Ile Ser Asn  
 265 270 275



ttg cag aaa tca tca aat ata tct cat gag gaa caa ttg caa caa ggg  
916

Leu Gln Lys Ser Ser Asn Ile Ser His Glu Glu Gln Leu Gln Gln Gly  
280 285 290 295

aat caa agt ttc agc tct ctg tat tac gat caa gga gta gag caa atg  
964

Asn Gln Ser Phe Ser Ser Leu Tyr Tyr Asp Gln Gly Val Glu Gln Met  
300 305 310

act act gac tgg aga gtt ctc gat aaa ttt gtt gct tca cag ctt agc  
1012

Thr Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala Ser Gln Leu Ser  
315 320 325

aat gat gaa gag gct gca gcc gtg gtt tct tct tct tct cat caa aac  
1060

Asn Asp Glu Glu Ala Ala Ala Val Val Ser Ser Ser Ser His Gln Asn  
330 335 340

aac gtc aag att gac acg aga aac acg ggt tat cat gtg ata gat gag  
1108

Asn Val Lys Ile Asp Thr Arg Asn Thr Gly Tyr His Val Ile Asp Glu  
345 350 355

gga ata aat ttg ccg gag aat gat tct gaa agg gtt gtt gaa atg gga  
1156

Gly Ile Asn Leu Pro Glu Asn Asp Ser Glu Arg Val Val Glu Met Gly  
360 365 370 375

gaa gag tat tca aat gct cat gct gct tct act tct tca agt tgt cag  
1204

Glu Glu Tyr Ser Asn Ala His Ala Ala Ser Thr Ser Ser Ser Cys Gln  
380 385 390

att gat ctc tag aaatagtgat agagagatga aaaagatgca aggtgaatat  
1256

Ile Asp Leu

atatgaaaat acatgcacac tagtggttatt tatacttaaa gatggaaggg gaaaaacaag  
1316

gagttatttc ctggatttat ggaggttttg tacataataa aaacctacaa ccatatggta  
1376

ttttcttttg aaaaaaaaaa aaaaaaaaaa aaaa  
1410

<210> 262 <211> 394 <212> PRT <213> Arabidopsis thaliana <400>  
262

Met Asn Ser Phe Ser Gln Val Pro Pro Gly Phe Arg Phe His Pro Thr  
1 5 10 15

Asp Glu Glu Leu Val Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys  
20 25 30



Arg Ile Glu Ile Asp Ile Ile Lys Asp Val Asp Leu Tyr Lys Ile Glu  
35 40 45

Pro Cys Asp Leu Gln Glu Leu Cys Lys Ile Gly Asn Glu Glu Gln Ser  
50 55 60

Glu Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr  
65 70 75 80

Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg  
85 90 95

Asp Lys Ala Ile Tyr Ile Arg His Ser Leu Ile Gly Met Arg Lys Thr  
100 105 110

Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp  
115 120 125

Ile Met His Glu Tyr Arg Leu Glu Thr Ser Glu Asn Gly Thr Pro Gln  
130 135 140

Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Lys Leu Ala Ala  
145 150 155 160

Thr Val Arg Lys Met Gly Asp Tyr His Ser Ser Pro Ser Gln His Trp  
165 170 175

Tyr Asp Asp Gln Leu Ser Phe Met Ala Ser Glu Ile Ile Ser Ser Ser  
180 185 190

Pro Arg Gln Phe Leu Pro Asn His His Tyr Asn Arg His His His Gln  
195 200 205

Gln Thr Leu Pro Cys Gly Leu Asn Ala Phe Asn Asn Asn Asn Pro Asn  
210 215 220

Leu Gln Cys Lys Gln Glu Leu Glu Leu His Tyr Asn Gln Met Val Gln  
225 230 235 240

His Gln Gln Gln Asn His His Leu Arg Glu Ser Met Phe Leu Gln Leu  
245 250 255

Pro Gln Leu Glu Ser Pro Thr Ser Asn Cys Asn Ser Asp Asn Asn Asn  
260 265 270

Asn Thr Arg Asn Ile Ser Asn Leu Gln Lys Ser Ser Asn Ile Ser His



275                      280                      285

Glu Glu Gln Leu Gln Gln Gly Asn Gln Ser Phe Ser Ser Leu Tyr Tyr  
 290                      295                      300

Asp Gln Gly Val Glu Gln Met Thr Thr Asp Trp Arg Val Leu Asp Lys  
 305                      310                      315                      320

Phe Val Ala Ser Gln Leu Ser Asn Asp Glu Glu Ala Ala Ala Val Val  
 325                      330                      335

Ser Ser Ser Ser His Gln Asn Asn Val Lys Ile Asp Thr Arg Asn Thr  
 340                      345                      350

Gly Tyr His Val Ile Asp Glu Gly Ile Asn Leu Pro Glu Asn Asp Ser  
 355                      360                      365

Glu Arg Val Val Glu Met Gly Glu Glu Tyr Ser Asn Ala His Ala Ala  
 370                      375                      380

Ser Thr Ser Ser Ser Cys Gln Ile Asp Leu  
 385                      390

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<400> 263  
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 48  
 Met Gln Val Phe Gln Arg Lys Glu Asp Ser Ser Trp Gly Asn Ser Met  
 1                      5                      10                      15

cct aca aca aat tca aat att caa gga tct gaa tct ttc agc ttg act  
 96  
 Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr  
 20                      25                      30

aag gat atg ata atg tct aca aca caa tta ccc gcg atg aaa cat tcg  
 144  
 Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser  
 35                      40                      45

ggt ttg cag ctg caa aat caa gat tca acc tca tca caa tct act gaa  
 192  
 Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu  
 50                      55                      60

gaa gaa tca ggc ggc ggt gaa gtt gca agc ttt gga gaa tat aag cgt  
 240  
 Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg  
 65                      70                      75                      80



tat gga tgc agc att gtt aat aac aat ctc tca ggt tac atc gaa aac  
 288  
 Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn  
                     85                    90                    95

ttg gga aag cct att gaa aat tat act aag tca att act acc tcg tcg  
 336  
 Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser  
                     100                    105                    110

atg gtg tct caa gac tct gtg ttt cct gct cct act tct ggt caa ata  
 384  
 Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile  
                     115                    120                    125

tct tgg tct ctt caa tgt gct gaa acg tca cat ttc aat ggt ttc ttg  
 432  
 Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu  
                     130                    135                    140

gct cct gaa tat gca tca aca cca acg gcg ctg cca cat tta gag atg  
 480  
 Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met  
 145                    150                    155                    160

atg ggt ttg gtt tct tca aga gtg cca ttg cct cat cac att caa gag  
 528  
 Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu  
                     165                    170                    175

aat gaa cca ata ttt gtc aat gcg aaa cag tat cat gcg att ctc cgt  
 576  
 Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg  
                     180                    185                    190

cgc agg aag cac cgt gct aaa ctc gaa gct cag aac aaa ctc atc aaa  
 624  
 Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys  
                     195                    200                    205

tgc cgt aaa ccg tac ctt cat gag tct cgc cat ctt cat gct tta aag  
 672  
 Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys  
                     210                    215                    220

aga gct aga ggc tcc ggt gga cgt ttc ctc aat aca aag aag ctt caa  
 720  
 Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln  
 225                    230                    235                    240

gaa tca tca aac tca ctg tgt tct tct caa atg gca aat gga caa aat  
 768  
 Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn  
                     245                    250                    255

ttc tct atg agc cct cac ggt ggt gga agc gga atc ggg tct agt tcg  
 816  
 Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser  
                     260                    265                    270



atc tca ccg agc tcc aat tca aac tgt atc aac atg ttc caa aac ccg  
864

Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro  
275 280 285

cag ttc aga ttc tca ggt tat ccg tca aca cac cat gcc tca gct ctc  
912

Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu  
290 295 300

atg tca ggg act tga

927

Met Ser Gly Thr

305

<210> 264 <211> 308 <212> PRT <213> Arabidopsis thaliana <400>  
264

Met Gln Val Phe Gln Arg Lys Glu Asp Ser Ser Trp Gly Asn Ser Met  
1 5 10 15

Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr  
20 25 30

Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser  
35 40 45

Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu  
50 55 60

Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg  
65 70 75 80

Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn  
85 90 95

Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser  
100 105 110

Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile  
115 120 125

Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu  
130 135 140

Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met  
145 150 155 160

Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu  
165 170 175



Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg  
 180 185 190

Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys  
 195 200 205

Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys  
 210 215 220

Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln  
 225 230 235 240

Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn  
 245 250 255

Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser  
 260 265 270

Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro  
 275 280 285

Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu  
 290 295 300

Met Ser Gly Thr  
 305

<210> 265 <211> 450 <212> DNA <213> Arabidopsis thaliana <220>  
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<400> 265  
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 53

Met Asp Gln Gly Gly Arg Gly Val Gly  
 1 5

gcc gag cat gga aag tac cgg gga gtt cgg aga cga cct tgg gga aaa  
 101

Ala Glu His Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys  
 10 15 20 25

tat gca gca gag ata cga gat tcg agg aag cac ggt gaa cgt gtg tgg  
 149

Tyr Ala Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp  
 30 35 40

ctt gga acg ttc gat acg gca gag gaa gcg gct aga gcc tat gac caa  
 197

Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Gln  
 45 50 55



gct gct tac tcc atg aga ggc caa gca gca atc ctt aac ttc cct cat  
 245  
 Ala Ala Tyr Ser Met Arg Gly Gln Ala Ala Ile Leu Asn Phe Pro His  
           60                          65                          70

gag tat aac atg ggg agt ggt gtc tct tct tcc acc gcc atg gct gga  
 293  
 Glu Tyr Asn Met Gly Ser Gly Val Ser Ser Ser Thr Ala Met Ala Gly  
           75                          80                          85

tct tcc tcc gcc tcc gcc tcc gct tct tct tct tct agg caa gtt ttt  
 341  
 Ser Ser Ser Ala Ser Ala Ser Ala Ser Ser Ser Ser Arg Gln Val Phe  
           90                          95                          100                          105

gaa ttt gag tac ttg gat gat agt gtt ttg gag gag ctc ctt gag gaa  
 389  
 Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Glu Glu Leu Leu Glu Glu  
                           110                          115                          120

gga gag aaa cct aac aag ggc aag aag aaa tga gcgagatata attcatgatt  
 442  
 Gly Glu Lys Pro Asn Lys Gly Lys Lys Lys  
                           125                          130

atttctaa  
 450

<210> 266 <211> 131 <212> PRT <213> Arabidopsis thaliana <400>  
 266

Met Asp Gln Gly Gly Arg Gly Val Gly Ala Glu His Gly Lys Tyr Arg  
 1                          5                          10                          15

Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp  
           20                          25                          30

Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly Thr Phe Asp Thr Ala  
           35                          40                          45

Glu Glu Ala Ala Arg Ala Tyr Asp Gln Ala Ala Tyr Ser Met Arg Gly  
           50                          55                          60

Gln Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Ser Gly  
 65                          70                          75                          80

Val Ser Ser Ser Thr Ala Met Ala Gly Ser Ser Ser Ala Ser Ala Ser  
           85                          90                          95

Ala Ser Ser Ser Ser Arg Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp  
           100                          105                          110



Ser Val Leu Glu Glu Leu Leu Glu Glu Gly Glu Lys Pro Asn Lys Gly  
 115 120 125

Lys Lys Lys  
 130

<210> 267 <211> 1716 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (169)..(1497) <223> G1804

<400> 267  
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 60

aaggaggaga acctccataa caagaagcgg attctctcag ttttccggcg gcggaggaac  
 120

acaaagccac cggttttttag acacacagat ttcattttca gttgttaa atg gta act  
 177

Met Val Thr  
 1

aga gaa acg aag ttg acg tca gag cga gaa gta gag tcg tcc atg gcg  
 225

Arg Glu Thr Lys Leu Thr Ser Glu Arg Glu Val Glu Ser Ser Met Ala  
 5 10 15

caa gcg aga cat aat gga gga ggt ggt ggt gag aat cat ccg ttt act  
 273

Gln Ala Arg His Asn Gly Gly Gly Gly Glu Asn His Pro Phe Thr  
 20 25 30 35

tct ttg gga aga caa tcc tct atc tac tca ttg acc ctt gac gag ttc  
 321

Ser Leu Gly Arg Gln Ser Ser Ile Tyr Ser Leu Thr Leu Asp Glu Phe  
 40 45 50

caa cat gct tta tgt gag aac ggc aag aac ttt ggg tcc atg aac atg  
 369

Gln His Ala Leu Cys Glu Asn Gly Lys Asn Phe Gly Ser Met Asn Met  
 55 60 65

gac gag ttt ctt gtc tct att tgg aac gca gag gag aat aat aac aat  
 417

Asp Glu Phe Leu Val Ser Ile Trp Asn Ala Glu Glu Asn Asn Asn Asn  
 70 75 80

caa caa caa gca gca gca gct gca ggt tca cat tct gtt ccg gct aat  
 465

Gln Gln Gln Ala Ala Ala Ala Ala Gly Ser His Ser Val Pro Ala Asn  
 85 90 95

cac aat ggt ttc aac aac aac aat aac aat gga ggc gag ggt ggt gtt  
 513

His Asn Gly Phe Asn Asn Asn Asn Asn Asn Gly Gly Glu Gly Gly Val  
 100 105 110 115

ggt gtc ttt agt ggt ggt tct aga ggc aac gaa gat gct aac aat aag  
 561

Gly Val Phe Ser Gly Gly Ser Arg Gly Asn Glu Asp Ala Asn Asn Lys



	120	125	130
aga ggg ata gcg aac gag tct agt ctt cct cga caa ggc tct ttg aca			
609			
Arg Gly Ile Ala Asn Glu Ser Ser Leu Pro Arg Gln Gly Ser Leu Thr			
	135	140	145
ctt cca gct ccg ctt tgt agg aag act gtt gat gag gtt tgg tct gag			
657			
Leu Pro Ala Pro Leu Cys Arg Lys Thr Val Asp Glu Val Trp Ser Glu			
	150	155	160
ata cat aga ggt ggt ggt agc ggt aat gga gga gac agc aat gga cgt			
705			
Ile His Arg Gly Gly Gly Ser Gly Asn Gly Gly Asp Ser Asn Gly Arg			
	165	170	175
agt agt agt agt aat gga cag aac aat gct cag aac ggc ggt gag act			
753			
Ser Ser Ser Ser Asn Gly Gln Asn Asn Ala Gln Asn Gly Gly Glu Thr			
	180	185	190
gcg gct aga caa ccg act ttt gga gag atg aca ctt gag gat ttc ttg			
801			
Ala Ala Arg Gln Pro Thr Phe Gly Glu Met Thr Leu Glu Asp Phe Leu			
	200	205	210
gtg aag gct ggt gtg gtt aga gaa cat ccc act aat cct aaa cct aat			
849			
Val Lys Ala Gly Val Val Arg Glu His Pro Thr Asn Pro Lys Pro Asn			
	215	220	225
cca aac ccg aac caa aac caa aac ccg tct agt gta ata ccc gca gct			
897			
Pro Asn Pro Asn Gln Asn Gln Asn Pro Ser Ser Val Ile Pro Ala Ala			
	230	235	240
gca cag caa cag ctt tat ggt gtg ttt caa gga acc ggt gat cct tca			
945			
Ala Gln Gln Gln Leu Tyr Gly Val Phe Gln Gly Thr Gly Asp Pro Ser			
	245	250	255
ttc ccg ggt caa gct atg ggt gtg ggt gac cca tca ggt tat gct aaa			
993			
Phe Pro Gly Gln Ala Met Gly Val Gly Asp Pro Ser Gly Tyr Ala Lys			
	260	265	270
agg aca gga gga gga ggg tat cag cag gcg cca cca gtt cag gca ggt			
1041			
Arg Thr Gly Gly Gly Gly Tyr Gln Gln Ala Pro Pro Val Gln Ala Gly			
	280	285	290
gtt tgc tat gga ggt ggc gtt ggg ttt gga gcg ggt gga cag caa atg			
1089			
Val Cys Tyr Gly Gly Gly Val Gly Phe Gly Ala Gly Gly Gln Gln Met			
	295	300	305
gga atg gtt gga ccg tta agc ccg gtg tct tca gat gga tta gga cat			
1137			
Gly Met Val Gly Pro Leu Ser Pro Val Ser Ser Asp Gly Leu Gly His			
	310	315	320



gga caa gtg gat aac ata gga ggt cag tat gga gta gat atg gga ggg  
1185

Gly Gln Val Asp Asn Ile Gly Gly Gln Tyr Gly Val Asp Met Gly Gly  
325 330 335

cta agg gga agg aaa aga gta gtg gat ggt cca gtg gag aaa gta gtg  
1233

Leu Arg Gly Arg Lys Arg Val Val Asp Gly Pro Val Glu Lys Val Val  
340 345 350 355

gag aga aga cag agg agg atg atc aag aac cgc gag tct gct gct aga  
1281

Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg  
360 365 370

tct aga gca aga aaa caa gca tat aca gtg gaa ttg gaa gct gaa ctt  
1329

Ser Arg Ala Arg Lys Gln Ala Tyr Thr Val Glu Leu Glu Ala Glu Leu  
375 380 385

aac cag ttg aaa gaa gag aat gcg cag cta aaa cat gca ttg gcg gag  
1377

Asn Gln Leu Lys Glu Glu Asn Ala Gln Leu Lys His Ala Leu Ala Glu  
390 395 400

ttg gag agg aag agg aag caa cag tat ttt gag agt ttg aag tca agg  
1425

Leu Glu Arg Lys Arg Lys Gln Gln Tyr Phe Glu Ser Leu Lys Ser Arg  
405 410 415

gca caa ccg aaa ttg ccg aaa tcg aac ggg aga ttg cgg aca ttg atg  
1473

Ala Gln Pro Lys Leu Pro Lys Ser Asn Gly Arg Leu Arg Thr Leu Met  
420 425 430 435

agg aac ccg agt tgt cca ctc taa acaacaata ggaagatgga gaagaagtcg  
1527

Arg Asn Pro Ser Cys Pro Leu  
440

gagacagaac gagggaaaaa ctgatgattt tctacgttgt tgttttgtct ttgaggaatg  
1587

aggttataga atctttatac ttgatgttt tctgtgttg taggaggaac accatctgat  
1647

ctgctttact agtgttccct gtgaacaaag aaagtgattc tgtgtttcaa catcatcaat  
1707

ctttggaaa  
1716

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268

Met Val Thr Arg Glu Thr Lys Leu Thr Ser Glu Arg Glu Val Glu Ser  
1 5 10 15



Ser Met Ala Gln Ala Arg His Asn Gly Gly Gly Gly Gly Glu Asn His  
 20 25 30

Pro Phe Thr Ser Leu Gly Arg Gln Ser Ser Ile Tyr Ser Leu Thr Leu  
 35 40 45

Asp Glu Phe Gln His Ala Leu Cys Glu Asn Gly Lys Asn Phe Gly Ser  
 50 55 60

Met Asn Met Asp Glu Phe Leu Val Ser Ile Trp Asn Ala Glu Glu Asn  
 65 70 75 80

Asn Asn Asn Gln Gln Gln Ala Ala Ala Ala Gly Ser His Ser Val  
 85 90 95

Pro Ala Asn His Asn Gly Phe Asn Asn Asn Asn Asn Gly Gly Glu  
 100 105 110

Gly Gly Val Gly Val Phe Ser Gly Gly Ser Arg Gly Asn Glu Asp Ala  
 115 120 125

Asn Asn Lys Arg Gly Ile Ala Asn Glu Ser Ser Leu Pro Arg Gln Gly  
 130 135 140

Ser Leu Thr Leu Pro Ala Pro Leu Cys Arg Lys Thr Val Asp Glu Val  
 145 150 155 160

Trp Ser Glu Ile His Arg Gly Gly Gly Ser Gly Asn Gly Gly Asp Ser  
 165 170 175

Asn Gly Arg Ser Ser Ser Ser Asn Gly Gln Asn Asn Ala Gln Asn Gly  
 180 185 190

Gly Glu Thr Ala Ala Arg Gln Pro Thr Phe Gly Glu Met Thr Leu Glu  
 195 200 205

Asp Phe Leu Val Lys Ala Gly Val Val Arg Glu His Pro Thr Asn Pro  
 210 215 220

Lys Pro Asn Pro Asn Pro Asn Gln Asn Gln Asn Pro Ser Ser Val Ile  
 225 230 235 240

Pro Ala Ala Ala Gln Gln Gln Leu Tyr Gly Val Phe Gln Gly Thr Gly  
 245 250 255

Asp Pro Ser Phe Pro Gly Gln Ala Met Gly Val Gly Asp Pro Ser Gly



260 265 270  
 Tyr Ala Lys Arg Thr Gly Gly Gly Tyr Gln Gln Ala Pro Pro Val  
 275 280 285  
 Gln Ala Gly Val Cys Tyr Gly Gly Gly Val Gly Phe Gly Ala Gly Gly  
 290 295 300  
 Gln Gln Met Gly Met Val Gly Pro Leu Ser Pro Val Ser Ser Asp Gly  
 305 310 315 320  
 Leu Gly His Gly Gln Val Asp Asn Ile Gly Gly Gln Tyr Gly Val Asp  
 325 330 335  
 Met Gly Gly Leu Arg Gly Arg Lys Arg Val Val Asp Gly Pro Val Glu  
 340 345 350  
 Lys Val Val Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser  
 355 360 365  
 Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Val Glu Leu Glu  
 370 375 380  
 Ala Glu Leu Asn Gln Leu Lys Glu Glu Asn Ala Gln Leu Lys His Ala  
 385 390 395 400  
 Leu Ala Glu Leu Glu Arg Lys Arg Lys Gln Gln Tyr Phe Glu Ser Leu  
 405 410 415  
 Lys Ser Arg Ala Gln Pro Lys Leu Pro Lys Ser Asn Gly Arg Leu Arg  
 420 425 430  
 Thr Leu Met Arg Asn Pro Ser Cys Pro Leu  
 435 440  
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 <221> CDS <222> (1)..(1662) <223> G1807  
 <400> 269  
 atg ggt gat aca gag aag tgt aac agt gat atg atc cag aga ctt cat  
 48  
 Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His  
 1 5 10 15  
 tca tct ttc ggc act act tct tct tcc att ccc aaa aat ccc att tct  
 96  
 Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser  
 20 25 30



cag ctc gat tta aac cct aat ttc atc cgc tca tca gct cct caa ttc  
144

Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe  
35 40 45

tcc aag cct ttc agt gac agt ggc aaa cga atc ggt gtt cct ccg tcg  
192

Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser  
50 55 60

cac ccc aac tta atc cca ccg act tct ccg ttt tct cag atc ccg acc  
240

His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr  
65 70 75 80

acc cga caa ccc ggt tcg cat aat ttt aac ccg gga gga gct aat cat  
288

Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His  
85 90 95

tca cgg tca atg tca cag ccc aac tct ttc ttc tct ttt gac tcc tta  
336

Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu  
100 105 110

cct ccg tta agc cct tct ccg ttt cga gat cac gat gtt tca atg gag  
384

Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu  
115 120 125

gat aga gat tcc ggc gtg ttt aac agc aac cat tcg ttg cct cca tcg  
432

Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser  
130 135 140

ccg ttc acg agg tgt aat tcg acc tct tct agc tcc ttg aga gtc ggt  
480

Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly  
145 150 155 160

gag agt tta cct ccg aga aag tct cat aga cgc tcc aac agt gat atc  
528

Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile  
165 170 175

ccc agt ggg ttt aat tcg atg cct ttg atc cct ccg aga cca ttg gag  
576

Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu  
180 185 190

agg tct ttt tct ggt ggg gag tgt gct gat tgg tca aag tct aat cct  
624

Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro  
195 200 205

ttt gtg aag aag gaa tcg agc tgc gaa agg gaa ggt gtc gga gag aga  
672

Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg  
210 215 220



gaa gct atg gat gat ctc ttc tca gca tat atg aat ctt gaa aac att  
 720  
 Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile  
 225 230 235 240  
 gat gtg ttg aac tcc tct gaa gct gat gat agc aag aac ggt aat gag  
 768  
 Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu  
 245 250 255  
 aat agg gat gat atg gag agc agc aga gca agc ggg acc aag act aac  
 816  
 Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn  
 260 265 270  
 ggt agt gat acg gaa gga gag agc agc agt gtc aat gag agt gcc aat  
 864  
 Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn  
 275 280 285  
 aat aat atg aat tct tct ggt gaa aag aga gag agc gtg aag aga aga  
 912  
 Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg  
 290 295 300  
 gcg gct gga gga gat att gct cct acc acc aga cat tac agg agt gtt  
 960  
 Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val  
 305 310 315 320  
 tca gtg gac agt tgt ttc atg gag aag ttg tct ttt ggt gat gaa tct  
 1008  
 Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser  
 325 330 335  
 cta aag ccg cct cct tct cct gga tct atg tca agg aaa gtt tcc cct  
 1056  
 Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro  
 340 345 350  
 acc aat tcg gtt gat ggg aac tcg ggt gct gct ttt agc atc gag ttc  
 1104  
 Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe  
 355 360 365  
 aat aac ggt gag ttt act gca gcg gaa atg aag aag atc atg gca aat  
 1152  
 Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn  
 370 375 380  
 gat aaa cta gca gag atg gcc atg tct gac cct aaa cgt gtc aaa agg  
 1200  
 Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg  
 385 390 395 400  
 aat gat cct ctt ttc aga atc tta gcg aac cgt caa tcc gca gca cgg  
 1248  
 Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg  
 405 410 415



tca aag gag agg aag atg cgg tac ata gta gaa ttg gaa cac aaa gtg  
1296

Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val  
420 425 430

cag act ctt cag acc gag gct acc aca ttg tct gct cag ctc aca ctt  
1344

Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu  
435 440 445

ttg cag cgc gat atg atg ggg ttg aca aat cag aac aat gag ctt aag  
1392

Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys  
450 455 460

ttc cgg ctt caa gca atg gag caa caa gcg cgt ctt cgc gat gct ctg  
1440

Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu  
465 470 475 480

aac gaa gca ctg aat gga gaa gtc cag cga ctg aaa ctg gca atc ggt  
1488

Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly  
485 490 495

gag agc agt cag aac gaa tca gag aga tca aag atg caa tca ctc aac  
1536

Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn  
500 505 510

gct gag atg ttc cag caa ctc aac atc agc cag tta aga cag cag cca  
1584

Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro  
515 520 525

caa cag atg cag caa cag tct cat cag cag aac cac cag aat gga acc  
1632

Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr  
530 535 540

atg gca aca aaa tct gaa tca aat gaa tag

1662

Met Ala Thr Lys Ser Glu Ser Asn Glu  
545 550

<210> 270 <211> 553 <212> PRT <213> Arabidopsis thaliana <400>  
270

Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His  
1 5 10 15

Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser  
20 25 30

Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe  
35 40 45



Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser  
 50 55 60  
 His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr  
 65 70 75 80  
 Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His  
 85 90 95  
 Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu  
 100 105 110  
 Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu  
 115 120 125  
 Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser  
 130 135 140  
 Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly  
 145 150 155 160  
 Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile  
 165 170 175  
 Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu  
 180 185 190  
 Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro  
 195 200 205  
 Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg  
 210 215 220  
 Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile  
 225 230 235 240  
 Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu  
 245 250 255  
 Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn  
 260 265 270  
 Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn  
 275 280 285  
 Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg



290	295	300
Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val		
305	310	315 320
Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser		
	325	330 335
Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro		
	340	345 350
Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe		
	355	360 365
Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn		
	370	375 380
Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg		
385	390	395 400
Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg		
	405	410 415
Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val		
	420	425 430
Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu		
	435	440 445
Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys		
	450	455 460
Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu		
465	470	475 480
Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly		
	485	490 495
Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn		
	500	505 510
Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro		
	515	520 525
Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr		
	530	535 540



Met Ala Thr Lys Ser Glu Ser Asn Glu  
545 550

<210> 271 <211> 969 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (1)..(969) <223> G1835

<400> 271  
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48  
Met Ile Gly Thr Ser Phe Pro Glu Asp Leu Asp Cys Gly Asn Phe Phe  
1 5 10 15  
gac aac atg gat gat ctc atg gac ttt ccc ggt gga gat atc gat gtc  
96  
Asp Asn Met Asp Asp Leu Met Asp Phe Pro Gly Gly Asp Ile Asp Val  
20 25 30  
ggt ttc ggc ata ggt gac tcc gac tct ttc cct acc atc tgg acc act  
144  
Gly Phe Gly Ile Gly Asp Ser Asp Ser Phe Pro Thr Ile Trp Thr Thr  
35 40 45  
cat cac gac acg tgg cct gcc gct tct gat cct ctc ttc tct tcc aac  
192  
His His Asp Thr Trp Pro Ala Ala Ser Asp Pro Leu Phe Ser Ser Asn  
50 55 60  
acc aac tct gat tca tca cct gag ctc tat gtt ccg ttt gag gac att  
240  
Thr Asn Ser Asp Ser Ser Pro Glu Leu Tyr Val Pro Phe Glu Asp Ile  
65 70 75 80  
gtt aag gtg gaa aga cct cca agc ttt gta gag gaa aca ttg gtt gag  
288  
Val Lys Val Glu Arg Pro Pro Ser Phe Val Glu Glu Thr Leu Val Glu  
85 90 95  
aag aag gaa gat tcg ttt tcg aca aac act gat tca tca tct tct cat  
336  
Lys Lys Glu Asp Ser Phe Ser Thr Asn Thr Asp Ser Ser Ser Ser His  
100 105 110  
agc caa ttc agg agc tca agt cca gtg tcg gtt ctc gag agc agc tcc  
384  
Ser Gln Phe Arg Ser Ser Ser Pro Val Ser Val Leu Glu Ser Ser Ser  
115 120 125  
tcc tcg tct caa acc acc aac aca acc tcc ctt gtt ctc cct gga aag  
432  
Ser Ser Ser Gln Thr Thr Asn Thr Thr Ser Leu Val Leu Pro Gly Lys  
130 135 140  
cac ggt cgt cca cgc aca aaa cgc cct cgt cca cct gtc cag gat aaa  
480  
His Gly Arg Pro Arg Thr Lys Arg Pro Arg Pro Pro Val Gln Asp Lys  
145 150 155 160



gat aga gtc aaa gac aat gtg tgc ggt ggt gac tcg cgc ctc atc att  
 528  
 Asp Arg Val Lys Asp Asn Val Cys Gly Gly Asp Ser Arg Leu Ile Ile  
 165 170 175  
  
 aga ata ccg aaa cag ttt ctc tct gat cac aac aag atg atc aac aag  
 576  
 Arg Ile Pro Lys Gln Phe Leu Ser Asp His Asn Lys Met Ile Asn Lys  
 180 185 190  
  
 aag aag aag aag aag gcc aag att act tct tcc tct tct tcg tcc ggg  
 624  
 Lys Lys Lys Lys Lys Ala Lys Ile Thr Ser Ser Ser Ser Ser Ser Gly  
 195 200 205  
  
 att gat ctt gaa gtc aat gga aac aac gtc gat tcg tat tct tca gag  
 672  
 Ile Asp Leu Glu Val Asn Gly Asn Asn Val Asp Ser Tyr Ser Ser Glu  
 210 215 220  
  
 caa tat ccg ctt agg aaa tgt atg cac tgt gag gtc acc aag act cca  
 720  
 Gln Tyr Pro Leu Arg Lys Cys Met His Cys Glu Val Thr Lys Thr Pro  
 225 230 235 240  
  
 cag tgg agg ctt ggt cca atg ggt cca aag aca ctt tgc aat gcg tgc  
 768  
 Gln Trp Arg Leu Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys  
 245 250 255  
  
 ggt gta cgt tac aaa tca ggg agg ctt ttc ccg gag tac cgt cca gct  
 816  
 Gly Val Arg Tyr Lys Ser Gly Arg Leu Phe Pro Glu Tyr Arg Pro Ala  
 260 265 270  
  
 gct agt cca aca ttt act cca gct ctt cac tca aac tca cac aag aaa  
 864  
 Ala Ser Pro Thr Phe Thr Pro Ala Leu His Ser Asn Ser His Lys Lys  
 275 280 285  
  
 gtg gct gaa atg aga aac aag aga tgc agt gat ggt agc tac ata acc  
 912  
 Val Ala Glu Met Arg Asn Lys Arg Cys Ser Asp Gly Ser Tyr Ile Thr  
 290 295 300  
  
 gaa gag aat gat ctg caa ggg ctg att ccg aac aat gcc tac att ggc  
 960  
 Glu Glu Asn Asp Leu Gln Gly Leu Ile Pro Asn Asn Ala Tyr Ile Gly  
 305 310 315 320  
  
 gta gac taa  
 969  
 Val Asp

<210> 272 <211> 322 <212> PRT <213> Arabidopsis thaliana <400>  
 272

Met Ile Gly Thr Ser Phe Pro Glu Asp Leu Asp Cys Gly Asn Phe Phe  
 1 5 10 15



Asp Asn Met Asp Asp Leu Met Asp Phe Pro Gly Gly Asp Ile Asp Val  
 20 25 30

Gly Phe Gly Ile Gly Asp Ser Asp Ser Phe Pro Thr Ile Trp Thr Thr  
 35 40 45

His His Asp Thr Trp Pro Ala Ala Ser Asp Pro Leu Phe Ser Ser Asn  
 50 55 60

Thr Asn Ser Asp Ser Ser Pro Glu Leu Tyr Val Pro Phe Glu Asp Ile  
 65 70 75 80

Val Lys Val Glu Arg Pro Pro Ser Phe Val Glu Glu Thr Leu Val Glu  
 85 90 95

Lys Lys Glu Asp Ser Phe Ser Thr Asn Thr Asp Ser Ser Ser Ser His  
 100 105 110

Ser Gln Phe Arg Ser Ser Ser Pro Val Ser Val Leu Glu Ser Ser Ser  
 115 120 125

Ser Ser Ser Gln Thr Thr Asn Thr Thr Ser Leu Val Leu Pro Gly Lys  
 130 135 140

His Gly Arg Pro Arg Thr Lys Arg Pro Arg Pro Pro Val Gln Asp Lys  
 145 150 155 160

Asp Arg Val Lys Asp Asn Val Cys Gly Gly Asp Ser Arg Leu Ile Ile  
 165 170 175

Arg Ile Pro Lys Gln Phe Leu Ser Asp His Asn Lys Met Ile Asn Lys  
 180 185 190

Lys Lys Lys Lys Lys Ala Lys Ile Thr Ser Ser Ser Ser Ser Ser Gly  
 195 200 205

Ile Asp Leu Glu Val Asn Gly Asn Asn Val Asp Ser Tyr Ser Ser Glu  
 210 215 220

Gln Tyr Pro Leu Arg Lys Cys Met His Cys Glu Val Thr Lys Thr Pro  
 225 230 235 240

Gln Trp Arg Leu Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys  
 245 250 255



Gly Val Arg Tyr Lys Ser Gly Arg Leu Phe Pro Glu Tyr Arg Pro Ala  
                   260                  265                  270

Ala Ser Pro Thr Phe Thr Pro Ala Leu His Ser Asn Ser His Lys Lys  
                   275                  280                  285

Val Ala Glu Met Arg Asn Lys Arg Cys Ser Asp Gly Ser Tyr Ile Thr  
                   290                  295                  300

Glu Glu Asn Asp Leu Gln Gly Leu Ile Pro Asn Asn Ala Tyr Ile Gly  
                   305                  310                  315                  320

Val Asp

<210> 273 <211> 668 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (47)..(610) <223> G1836

<400> 273  
 ataacaagcc tagaactacta gaaacttcaa aaaagaaaaa aatctt atg gag aac  
 55

Met Glu Asn  
 1

aac aac ggc aac aac cag ctg cca ccg aaa ggt aac gag caa ctg aag  
 103  
 Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu Gln Leu Lys  
                   5                  10                  15

agt ttc tgg tca aaa gag atg gaa ggt aac tta gat ttc aaa aat cac  
 151  
 Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe Lys Asn His  
                   20                  25                  30                  35

gac ctt cct ata act cgt atc aag aag att atg aag tat gat ccg gat  
 199  
 Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr Asp Pro Asp  
                   40                  45                  50

gtg act atg ata gct agt gag gct cca atc ctc ctc tcg aaa gca tgt  
 247  
 Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser Lys Ala Cys  
                   55                  60                  65

gag atg ttt atc atg gat ctc acg atg cgt tcg tgg ctc cat gct cag  
 295  
 Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu His Ala Gln  
                   70                  75                  80

gaa agc aaa cga gtc acg cta cag aaa tct aat gtc gat gcc gca gtg  
 343  
 Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp Ala Ala Val  
                   85                  90                  95



gct caa act gtt atc ttt gat ttc ttg ctt gat gat gac att gag gta  
 391  
 Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp Ile Glu Val  
 100 105 110 115

aag aga gag tct gtt gcc gcc gct gct gat cct gtg gcc atg cca cct  
 439  
 Lys Arg Glu Ser Val Ala Ala Ala Ala Asp Pro Val Ala Met Pro Pro  
 120 125 130

att gac gat gga gag ctg cct cca gga atg gta att gga act cct gtt  
 487  
 Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly Thr Pro Val  
 135 140 145

tgt tgt agt ctt gga atc cac caa cca caa caa atg cag gca tgg  
 535  
 Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met Gln Ala Trp  
 150 155 160

cct gga gct tgg acc tcg gtg tct ggt gag gag gaa gaa gcg cgt ggg  
 583  
 Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu Ala Arg Gly  
 165 170 175

aaa aaa gga ggt gac gac gga aac taa taagtggaat acgttttagg  
 630  
 Lys Lys Gly Gly Asp Asp Gly Asn  
 180 185

gtattttcaa gggaatatgt agtaaatagt catggatc  
 668

<210> 274 <211> 187 <212> PRT <213> Arabidopsis thaliana <400>  
 274

Met Glu Asn Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu  
 1 5 10 15

Gln Leu Lys Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe  
 20 25 30

Lys Asn His Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr  
 35 40 45

Asp Pro Asp Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser  
 50 55 60

Lys Ala Cys Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu  
 65 70 75 80

His Ala Gln Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp  
 85 90 95



Ala Ala Val Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp  
 100 105 110

Ile Glu Val Lys Arg Glu Ser Val Ala Ala Ala Asp Pro Val Ala  
 115 120 125

Met Pro Pro Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly  
 130 135 140

Thr Pro Val Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met  
 145 150 155 160

Gln Ala Trp Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu  
 165 170 175

Ala Arg Gly Lys Lys Gly Gly Asp Asp Gly Asn  
 180 185

<210> 275 <211> 897 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(897) <223> G1900

<400> 275  
 atg ctg gaa act aaa gat cct gcg ata aag ctc ttt ggt atg aaa att  
 48  
 Met Leu Glu Thr Lys Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile  
 1 5 10 15

cct ttc ccg acg gtt tta gag gtt gct gat gaa gaa gaa gaa aag aac  
 96  
 Pro Phe Pro Thr Val Leu Glu Val Ala Asp Glu Glu Glu Glu Lys Asn  
 20 25 30

caa aac aag aca tta act gat caa tcg gag aaa gac aaa acc cta aag  
 144  
 Gln Asn Lys Thr Leu Thr Asp Gln Ser Glu Lys Asp Lys Thr Leu Lys  
 35 40 45

aaa cca acc aag att ctt cca tgt cca aga tgc aac agc atg gag act  
 192  
 Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Met Glu Thr  
 50 55 60

aag ttc tgt tac tac aac aac tac aac gta aac caa cct cgc cat ttt  
 240  
 Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe  
 65 70 75 80

tgt aaa gct tgt cag aga tat tgg acc tca ggt ggg acc atg aga agt  
 288  
 Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ser Gly Gly Thr Met Arg Ser  
 85 90 95

gtt cca atc gga gca gga cgg cgc aag aac aag aac aac tca cca act  
 336  
 Val Pro Ile Gly Ala Gly Arg Arg Lys Asn Lys Asn Asn Ser Pro Thr



100	105	110
tca cat tac cac cat gtg act atc tcc gaa aca aat ggt ccg gtc ctt		
384		
Ser His Tyr His His Val Thr Ile Ser Glu Thr Asn Gly Pro Val Leu		
115	120	125
agt ttc agc ctc gga gat gat caa aag gtc tcg agt aat agg ttt ggt		
432		
Ser Phe Ser Ser Leu Gly Asp Asp Gln Lys Val Ser Ser Asn Arg Phe Gly		
130	135	140
aat caa aag cta gtt gct agg ata gag aac aat gac gag cgc tct aat		
480		
Asn Gln Lys Leu Val Ala Arg Ile Glu Asn Asn Asp Glu Arg Ser Asn		
145	150	155
aac aac act tcg aac ggt ttg aat tgt ttt ccg gga gtt tcg tgg ccg		
528		
Asn Asn Thr Ser Asn Gly Leu Asn Cys Phe Pro Gly Val Ser Trp Pro		
165	170	175
tac acg tgg aat cct gcg ttt tac ccg gtt tac cct tat tgg agc atg		
576		
Tyr Thr Trp Asn Pro Ala Phe Tyr Pro Val Tyr Pro Tyr Trp Ser Met		
180	185	190
cca gtg ttg tct tct ccg gta agt tca agt cct act tct act ctt ggt		
624		
Pro Val Leu Ser Ser Pro Val Ser Ser Ser Pro Thr Ser Thr Leu Gly		
195	200	205
aag cat tcg aga gac gaa gac gag acg gtg aag caa aaa cag agg aat		
672		
Lys His Ser Arg Asp Glu Asp Glu Thr Val Lys Gln Lys Gln Arg Asn		
210	215	220
gga tct gta ttg gtt cca aag act ttg aga att gat gat cct aat gaa		
720		
Gly Ser Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu		
225	230	235
gct gca aag agt tcg ata tgg aca aca ctt ggg atc aag aac gaa gtt		
768		
Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Val		
245	250	255
atg ttc aat ggg ttt ggt tcg aag aaa gag gtt aag ctc agt aac aaa		
816		
Met Phe Asn Gly Phe Gly Ser Lys Lys Glu Val Lys Leu Ser Asn Lys		
260	265	270
gaa gaa aca gag acc tca ctt gtt ctt tgt gca aac cct gct gcg tta		
864		
Glu Glu Thr Glu Thr Ser Leu Val Leu Cys Ala Asn Pro Ala Ala Leu		
275	280	285
tca aga tca atc aat ttc cat gag cag atg tga		
897		
Ser Arg Ser Ile Asn Phe His Glu Gln Met		
290	295	



<210> 276 <211> 298 <212> PRT <213> Arabidopsis thaliana <400>  
276

Met Leu Glu Thr Lys Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile  
1 5 10 15

Pro Phe Pro Thr Val Leu Glu Val Ala Asp Glu Glu Glu Glu Lys Asn  
20 25 30

Gln Asn Lys Thr Leu Thr Asp Gln Ser Glu Lys Asp Lys Thr Leu Lys  
35 40 45

Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Met Glu Thr  
50 55 60

Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe  
65 70 75 80

Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ser Gly Gly Thr Met Arg Ser  
85 90 95

Val Pro Ile Gly Ala Gly Arg Arg Lys Asn Lys Asn Asn Ser Pro Thr  
100 105 110

Ser His Tyr His His Val Thr Ile Ser Glu Thr Asn Gly Pro Val Leu  
115 120 125

Ser Phe Ser Leu Gly Asp Asp Gln Lys Val Ser Ser Asn Arg Phe Gly  
130 135 140

Asn Gln Lys Leu Val Ala Arg Ile Glu Asn Asn Asp Glu Arg Ser Asn  
145 150 155 160

Asn Asn Thr Ser Asn Gly Leu Asn Cys Phe Pro Gly Val Ser Trp Pro  
165 170 175

Tyr Thr Trp Asn Pro Ala Phe Tyr Pro Val Tyr Pro Tyr Trp Ser Met  
180 185 190

Pro Val Leu Ser Ser Pro Val Ser Ser Ser Pro Thr Ser Thr Leu Gly  
195 200 205

Lys His Ser Arg Asp Glu Asp Glu Thr Val Lys Gln Lys Gln Arg Asn  
210 215 220



Gly Ser Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu  
 225 230 235 240

Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Val  
 245 250 255

Met Phe Asn Gly Phe Gly Ser Lys Lys Glu Val Lys Leu Ser Asn Lys  
 260 265 270

Glu Glu Thr Glu Thr Ser Leu Val Leu Cys Ala Asn Pro Ala Ala Leu  
 275 280 285

Ser Arg Ser Ile Asn Phe His Glu Gln Met  
 290 295

<210> 277 <211> 1200 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(1200) <223> G1903

<400> 277  
 atg tct aaa tct aga gat acg gag ata aag ttg ttt ggg agg aca atc  
 48  
 Met Ser Lys Ser Arg Asp Thr Glu Ile Lys Leu Phe Gly Arg Thr Ile  
 1 5 10 15  
 aca tct ctt tta gat gtg aat tgt tat gat ccg tcg tcg ttg tcc cct  
 96  
 Thr Ser Leu Leu Asp Val Asn Cys Tyr Asp Pro Ser Ser Leu Ser Pro  
 20 25 30  
 gtt cac gat gtt tct tct gat cca agc aag gag gat tcg tct tct tct  
 144  
 Val His Asp Val Ser Ser Asp Pro Ser Lys Glu Asp Ser Ser Ser Ser  
 35 40 45  
 tca tct tct tgt tct cca act att gga cca atc agg gtt ccg gtt aaa  
 192  
 Ser Ser Ser Cys Ser Pro Thr Ile Gly Pro Ile Arg Val Pro Val Lys  
 50 55 60  
 aaa agt gag caa gag agt aac aaa ttc aaa gat cca tat ata tta tcc  
 240  
 Lys Ser Glu Gln Glu Ser Asn Lys Phe Lys Asp Pro Tyr Ile Leu Ser  
 65 70 75 80  
 gat cta aac gaa cca cca aaa gca gta tct gag att tca tca cca aga  
 288  
 Asp Leu Asn Glu Pro Pro Lys Ala Val Ser Glu Ile Ser Ser Pro Arg  
 85 90 95  
 agt tcc aag aac aac tgt gat caa cag agc gag atc aca aca aca act  
 336  
 Ser Ser Lys Asn Asn Cys Asp Gln Gln Ser Glu Ile Thr Thr Thr Thr  
 100 105 110  
 acc aca agt act aca tca gga gag aaa tca acg gct ctc aag aaa ccg  
 384



Thr Thr Ser Thr Thr Ser Gly Glu Lys Ser Thr Ala Leu Lys Lys Pro  
 115 120 125  
 gac aag ctt att cca tgt cct aga tgt gaa agc gca aac acc aaa ttc  
 432  
 Asp Lys Leu Ile Pro Cys Pro Arg Cys Glu Ser Ala Asn Thr Lys Phe  
 130 135 140  
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 480  
 Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg Tyr Phe Cys Arg  
 145 150 155 160  
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 528  
 Asn Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met Arg Asn Val Pro  
 165 170 175  
 gtt ggc tca ggt cgt cgc aag aac aaa gga tgg cct tct tca aac cat  
 576  
 Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Pro Ser Ser Asn His  
 180 185 190  
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 624  
 Tyr Leu Gln Val Thr Ser Glu Asp Cys Asp Asn Asn Asn Ser Gly Thr  
 195 200 205  
 atc ctt agt ttc ggt tct tcg gag tct tcg gtt aca gag act ggt aag  
 672  
 Ile Leu Ser Phe Gly Ser Ser Glu Ser Ser Val Thr Glu Thr Gly Lys  
 210 215 220  
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 720  
 His Gln Ser Gly Asp Thr Ala Lys Ile Ser Ala Asp Ser Val Ser Gln  
 225 230 235 240  
 gaa aat aaa agc tac caa ggg ttt ctt cct ccg caa gta atg tta cct  
 768  
 Glu Asn Lys Ser Tyr Gln Gly Phe Leu Pro Pro Gln Val Met Leu Pro  
 245 250 255  
 aat aat tct tct cct tgg cct tac caa tgg agt cca acg ggt cct aac  
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 260 265 270  
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 864  
 Ala Ser Phe Tyr Pro Val Pro Phe Tyr Trp Gly Cys Thr Val Pro Ile  
 275 280 285  
 tac cct acc tca gag act tca tca tgt tta gga aaa cgg tca aga gat  
 912  
 Tyr Pro Thr Ser Glu Thr Ser Ser Cys Leu Gly Lys Arg Ser Arg Asp  
 290 295 300  
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 960  
 Gln Thr Glu Gly Arg Ile Asn Asp Thr Asn Thr Thr Ile Thr Thr Thr



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305          310          315          320
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1008
Arg Ala Arg Leu Val Ser Glu Ser Leu Arg Met Asn Ile Glu Ala Ser
          325          330          335

aag agc gct gtg tgg tct aag tta ccg aca aaa ccc gag aaa aaa acg
1056
Lys Ser Ala Val Trp Ser Lys Leu Pro Thr Lys Pro Glu Lys Lys Thr
          340          345          350

caa gga ttc agt ttg ttc aat gga ttt gac aca aag gga aac agc aac
1104
Gln Gly Phe Ser Leu Phe Asn Gly Phe Asp Thr Lys Gly Asn Ser Asn
          355          360          365

aga agt agc ttg gtc tcc gaa act tct cac agt cta caa gca aac cct
1152
Arg Ser Ser Leu Val Ser Glu Thr Ser His Ser Leu Gln Ala Asn Pro
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          35          40          45

Ser Ser Ser Cys Ser Pro Thr Ile Gly Pro Ile Arg Val Pro Val Lys
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Lys Ser Glu Gln Glu Ser Asn Lys Phe Lys Asp Pro Tyr Ile Leu Ser
65          70          75          80

Asp Leu Asn Glu Pro Pro Lys Ala Val Ser Glu Ile Ser Ser Pro Arg
          85          90          95

Ser Ser Lys Asn Asn Cys Asp Gln Gln Ser Glu Ile Thr Thr Thr Thr
          100          105          110

Thr Thr Ser Thr Thr Ser Gly Glu Lys Ser Thr Ala Leu Lys Lys Pro
          115          120          125

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Asp Lys Leu Ile Pro Cys Pro Arg Cys Glu Ser Ala Asn Thr Lys Phe  
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Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg Tyr Phe Cys Arg  
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 165 170 175

Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Pro Ser Ser Asn His  
 180 185 190

Tyr Leu Gln Val Thr Ser Glu Asp Cys Asp Asn Asn Asn Ser Gly Thr  
 195 200 205

Ile Leu Ser Phe Gly Ser Ser Glu Ser Ser Val Thr Glu Thr Gly Lys  
 210 215 220

His Gln Ser Gly Asp Thr Ala Lys Ile Ser Ala Asp Ser Val Ser Gln  
 225 230 235 240

Glu Asn Lys Ser Tyr Gln Gly Phe Leu Pro Pro Gln Val Met Leu Pro  
 245 250 255

Asn Asn Ser Ser Pro Trp Pro Tyr Gln Trp Ser Pro Thr Gly Pro Asn  
 260 265 270

Ala Ser Phe Tyr Pro Val Pro Phe Tyr Trp Gly Cys Thr Val Pro Ile  
 275 280 285

Tyr Pro Thr Ser Glu Thr Ser Ser Cys Leu Gly Lys Arg Ser Arg Asp  
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Gln Thr Glu Gly Arg Ile Asn Asp Thr Asn Thr Thr Ile Thr Thr Thr  
 305 310 315 320

Arg Ala Arg Leu Val Ser Glu Ser Leu Arg Met Asn Ile Glu Ala Ser  
 325 330 335

Lys Ser Ala Val Trp Ser Lys Leu Pro Thr Lys Pro Glu Lys Lys Thr  
 340 345 350

Gln Gly Phe Ser Leu Phe Asn Gly Phe Asp Thr Lys Gly Asn Ser Asn  
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 104

Asp Thr Ala Lys Gln Met Arg Asp Glu Glu Leu Phe Lys Ala Ala Glu  
 10 15 20

tgg gga gat tca tgc ttg ttc atg tca tta tct gaa gaa cag ctc tct  
 152

Trp Gly Asp Ser Ser Leu Phe Met Ser Leu Ser Glu Glu Gln Leu Ser  
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aaa tct ctc aat ttc aga aac gaa gat ggt cgc tct ctc ctc cat gtc  
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Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg Ser Leu Leu His Val  
 40 45 50

gct gct tcc ttc ggc cat tct caa ata gtg aag ttg tta tca agt tca  
 248

Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys Leu Leu Ser Ser Ser  
 55 60 65

gat gaa gca aag act gta atc aat agc aag gat gat gaa gga tgg gct  
 296

Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp Asp Glu Gly Trp Ala  
 70 75 80 85

cct ttg cat tcc gct gct agc atc ggt aat gct gag ctc gtt gag gtg  
 344

Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala Glu Leu Val Glu Val  
 90 95 100

ctt ttg acc aga ggt gct gat gtc aat gcc aaa aat aac ggt ggt cgc  
 392

Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys Asn Asn Gly Gly Arg  
 105 110 115

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Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg Leu Glu Ile Ala Gln  
 120 125 130

ctt tta tta aca cac ggt gca aag att aac atc aca gac aag gtt ggt  
 488

Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile Thr Asp Lys Val Gly



135                      140                      145  
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 Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly Lys Leu Glu Val Cys  
 150                      155                      160                      165  
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 584  
 Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp Ala Thr Asp Lys Met  
 170                      175                      180  
 ggt caa act gca ctc atg cat tca gtt atc tgc gat gac aaa cag gtt  
 632  
 Gly Gln Thr Ala Leu Met His Ser Val Ile Cys Asp Asp Lys Gln Val  
 185                      190                      195  
 gcg ttc ctg ctt ata aga cat ggt gca gat gtg gat gta gaa gac aag  
 680  
 Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val Asp Val Glu Asp Lys  
 200                      205                      210  
 gaa ggc tac act gtt cta ggc cga gct acc aat gaa ttc cga cct gca  
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 Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn Glu Phe Arg Pro Ala  
 215                      220                      225  
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 774  
 Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly  
 230                      235                      240  
 gattacttta aaacttacta actctgagag ttgtttagtt acttaaaagg atttttcttt  
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 20                      25                      30  
 Glu Glu Gln Leu Ser Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg  
 35                      40                      45  
 Ser Leu Leu His Val Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys  
 50                      55                      60  
 Leu Leu Ser Ser Ser Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp  
 65                      70                      75                      80



Asp Glu Gly Trp Ala Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala  
85 90 95

Glu Leu Val Glu Val Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys  
100 105 110

Asn Asn Gly Gly Arg Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg  
115 120 125

Leu Glu Ile Ala Gln Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile  
130 135 140

Thr Asp Lys Val Gly Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly  
145 150 155 160

Lys Leu Glu Val Cys Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp  
165 170 175

Ala Thr Asp Lys Met Gly Gln Thr Ala Leu Met His Ser Val Ile Cys  
180 185 190

Asp Asp Lys Gln Val Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val  
195 200 205

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210 215 220

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115

Met Glu Ala  
1

cgt cca gtt cat aga tca ggt tcg aga gac ctc aca cgc act tct tca  
163

Arg Pro Val His Arg Ser Gly Ser Arg Asp Leu Thr Arg Thr Ser Ser  
5 10 15

atc cca tct aca caa aaa cct tca cca gta gaa gat agt ttc atg aga  
211

Ile Pro Ser Thr Gln Lys Pro Ser Pro Val Glu Asp Ser Phe Met Arg



498



atg cgt tgg acg cca gag ctt cac gag gct ttt gtt gag gct gtc aac  
 835  
 Met Arg Trp Thr Pro Glu Leu His Glu Ala Phe Val Glu Ala Val Asn  
 230 235 240

agt ctt ggc ggt agt gaa aga gct act cct aaa ggg gta ctg aag att  
 883  
 Ser Leu Gly Gly Ser Glu Arg Ala Thr Pro Lys Gly Val Leu Lys Ile  
 245 250 255

atg aaa gtt gaa ggc ttg act ata tat cat gtt aaa agc cat tta cag  
 931  
 Met Lys Val Glu Gly Leu Thr Ile Tyr His Val Lys Ser His Leu Gln  
 260 265 270 275

aaa tat agg aca gct aga tat cgg cca gaa cca tca gaa act ggt tcg  
 979  
 Lys Tyr Arg Thr Ala Arg Tyr Arg Pro Glu Pro Ser Glu Thr Gly Ser  
 280 285 290

cca gaa agg aag ttg aca ccg ctt gaa cat ata aca tct ctt gat ttg  
 1027  
 Pro Glu Arg Lys Leu Thr Pro Leu Glu His Ile Thr Ser Leu Asp Leu  
 295 300 305

aaa ggt ggg ata ggt att aca gag gct cta cga ctt cag atg gaa gta  
 1075  
 Lys Gly Gly Ile Gly Ile Thr Glu Ala Leu Arg Leu Gln Met Glu Val  
 310 315 320

cag aag caa ctc cat gag cag ctc gag att caa aga aac ctg caa ctc  
 1123  
 Gln Lys Gln Leu His Glu Gln Leu Glu Ile Gln Arg Asn Leu Gln Leu  
 325 330 335

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 340 345 350 355

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 1219  
 Asn Ser Gly Leu Thr Lys Gly Thr Ala Ser Thr Ser Asp Ser Ala Ala  
 360 365 370

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 1267  
 Lys Ser Glu Gln Glu Asp Lys Lys Thr Ala Asp Ser Lys Glu Val Pro  
 375 380 385

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 1315  
 Glu Glu Glu Thr Arg Lys Cys Glu Glu Leu Glu Ser Pro Gln Pro Lys  
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 1366  
 Arg Pro Lys Ile Asp Asn  
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Phe Met Arg Ser Asp Asn Asn Ser Gln Leu Met Ser Arg Pro Leu Gly  
35 40 45

Gln Thr Tyr His Leu Leu Ser Ser Ser Asn Gly Gly Ala Val Gly His  
50 55 60

Ile Cys Ser Ser Ser Ser Ser Gly Phe Ala Thr Asn Leu His Tyr Ser  
65 70 75 80

Thr Met Val Ser His Glu Lys Gln Gln His Tyr Thr Gly Ser Ser Ser  
85 90 95

Asn Asn Ala Val Gln Thr Pro Ser Asn Asn Asp Ser Ala Trp Cys His  
100 105 110

Asp Ser Leu Pro Gly Gly Phe Leu Asp Phe His Glu Thr Asn Pro Ala  
115 120 125

Ile Gln Asn Asn Cys Gln Ile Glu Asp Gly Gly Ile Ala Ala Ala Phe  
130 135 140

Asp Asp Ile Gln Lys Arg Ser Asp Trp His Glu Trp Ala Asp His Leu  
145 150 155 160

Ile Thr Asp Asp Asp Pro Leu Met Ser Thr Asn Trp Asn Asp Leu Leu  
165 170 175

Leu Glu Thr Asn Ser Asn Ser Asp Ser Lys Asp Gln Lys Thr Leu Gln  
180 185 190

Ile Pro Gln Pro Gln Ile Val Gln Gln Gln Pro Ser Pro Ser Val Glu  
195 200 205



Leu Arg Pro Val Ser Thr Thr Ser Ser Asn Ser Asn Asn Gly Thr Gly  
 210 215 220

Lys Ala Arg Met Arg Trp Thr Pro Glu Leu His Glu Ala Phe Val Glu  
 225 230 235 240

Ala Val Asn Ser Leu Gly Gly Ser Glu Arg Ala Thr Pro Lys Gly Val  
 245 250 255

Leu Lys Ile Met Lys Val Glu Gly Leu Thr Ile Tyr His Val Lys Ser  
 260 265 270

His Leu Gln Lys Tyr Arg Thr Ala Arg Tyr Arg Pro Glu Pro Ser Glu  
 275 280 285

Thr Gly Ser Pro Glu Arg Lys Leu Thr Pro Leu Glu His Ile Thr Ser  
 290 295 300

Leu Asp Leu Lys Gly Gly Ile Gly Ile Thr Glu Ala Leu Arg Leu Gln  
 305 310 315 320

Met Glu Val Gln Lys Gln Leu His Glu Gln Leu Glu Ile Gln Arg Asn  
 325 330 335

Leu Gln Leu Arg Ile Glu Glu Gln Gly Lys Tyr Leu Gln Met Met Phe  
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Glu Lys Gln Asn Ser Gly Leu Thr Lys Gly Thr Ala Ser Thr Ser Asp  
 355 360 365

Ser Ala Ala Lys Ser Glu Gln Glu Asp Lys Lys Thr Ala Asp Ser Lys  
 370 375 380

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113

Met Asn Ile Val Ser Trp Lys Asp Ala  
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161  
Asn Asp Glu Val Ala Gly Gly Ala Thr Thr Arg Arg Glu Arg Glu Val  
10 15 20 25

aaa gag gat caa gaa gaa acc gaa gtc aga gcc acc agt ggc aaa acc  
209  
Lys Glu Asp Gln Glu Glu Thr Glu Val Arg Ala Thr Ser Gly Lys Thr  
30 35 40

gta att aaa aag cag cct aca tcg atc tct tct tct tct tct tct tgg  
257  
Val Ile Lys Lys Gln Pro Thr Ser Ile Ser Ser Ser Ser Ser Ser Trp  
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305  
Met Lys Ser Lys Asp Pro Arg Ile Val Arg Val Ser Arg Ala Phe Gly  
60 65 70

ggc aaa gac cgt cac agc aaa gtg tgt acg tta cgt gga cta cgt gac  
353  
Gly Lys Asp Arg His Ser Lys Val Cys Thr Leu Arg Gly Leu Arg Asp  
75 80 85

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401  
Arg Arg Val Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu  
90 95 100 105

caa gaa cgg ctc ggt gtt gac cag cct agc aaa gcc gtt gac tgg ttg  
449  
Gln Glu Arg Leu Gly Val Asp Gln Pro Ser Lys Ala Val Asp Trp Leu  
110 115 120

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497  
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125 130 135

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545  
Ser Pro Glu Asn Phe Ser Ile Phe Asn His His Gln Ser Phe Leu Asn  
140 145 150

ctt ggt caa cgg ccc ggt caa gat ccg acc caa ctc ggg ttt aaa atc  
593  
Leu Gly Gln Arg Pro Gly Gln Asp Pro Thr Gln Leu Gly Phe Lys Ile  
155 160 165

aat gga tgt gta caa aag tct act act act agc cgc gaa gaa aac gat  
641  
Asn Gly Cys Val Gln Lys Ser Thr Thr Thr Ser Arg Glu Glu Asn Asp  
170 175 180 185



aga gag aaa gga gaa aac gat gtc gtt tac aca aac aat cat cat gtt  
689

Arg Glu Lys Gly Glu Asn Asp Val Val Tyr Thr Asn Asn His His Val  
190 195 200

ggg tct tat gga act tat cac aac ctg gaa cat cat cat cat cac  
737

Gly Ser Tyr Gly Thr Tyr His Asn Leu Glu His His His His His His  
205 210 215

caa cat ttg agt tta cag gca gat tat cat agt cat caa cta cat agt  
785

Gln His Leu Ser Leu Gln Ala Asp Tyr His Ser His Gln Leu His Ser  
220 225 230

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833

Leu Val Pro Phe Pro Ser Gln Ile Leu Val Cys Pro Met Thr Thr Ser  
235 240 245

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881

Pro Thr Thr Thr Thr Ile Gln Ser Leu Phe Pro Ser Ser Ser Ser Ala  
250 255 260 265

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923

Gly Ser Gly Thr Met Glu Thr Leu Asp Pro Arg Gln Met  
270 275

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983

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35 40 45

Ser Ile Ser Ser Ser Ser Ser Ser Trp Met Lys Ser Lys Asp Pro Arg  
50 55 60



Ile Val Arg Val Ser Arg Ala Phe Gly Gly Lys Asp Arg His Ser Lys  
65 70 75 80

Val Cys Thr Leu Arg Gly Leu Arg Asp Arg Arg Val Arg Leu Ser Val  
85 90 95

Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Glu Arg Leu Gly Val Asp  
100 105 110

Gln Pro Ser Lys Ala Val Asp Trp Leu Leu Asp Ala Ala Lys Glu Glu  
115 120 125

Ile Asp Glu Leu Pro Pro Leu Pro Ile Ser Pro Glu Asn Phe Ser Ile  
130 135 140

Phe Asn His His Gln Ser Phe Leu Asn Leu Gly Gln Arg Pro Gly Gln  
145 150 155 160

Asp Pro Thr Gln Leu Gly Phe Lys Ile Asn Gly Cys Val Gln Lys Ser  
165 170 175

Thr Thr Thr Ser Arg Glu Glu Asn Asp Arg Glu Lys Gly Glu Asn Asp  
180 185 190

Val Val Tyr Thr Asn Asn His His Val Gly Ser Tyr Gly Thr Tyr His  
195 200 205

Asn Leu Glu His His His His His His Gln His Leu Ser Leu Gln Ala  
210 215 220

Asp Tyr His Ser His Gln Leu His Ser Leu Val Pro Phe Pro Ser Gln  
225 230 235 240

Ile Leu Val Cys Pro Met Thr Thr Ser Pro Thr Thr Thr Thr Ile Gln  
245 250 255

Ser Leu Phe Pro Ser Ser Ser Ser Ala Gly Ser Gly Thr Met Glu Thr  
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Leu Asp Pro Arg Gln Met  
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112

Met Asp Asn Ser Asp Ile Leu Met  
1 5

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160

Asn Met Met Met Gln Gln Met Glu Lys Leu Pro Glu His Phe Ser Asn  
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tca aac cct aac cct aat ccc cat aac att atg atg ctt tct gaa tcc  
208

Ser Asn Pro Asn Pro Asn Pro His Asn Ile Met Met Leu Ser Glu Ser  
25 30 35 40

aac acc cac ccg ttc ttc ttc aac ccc act cat tct cat ctc cca ttt  
256

Asn Thr His Pro Phe Phe Phe Asn Pro Thr His Ser His Leu Pro Phe  
45 50 55

gac caa acc atg cct cac cac caa ccc ggt tta aat ttc ccg tac gcc  
304

Asp Gln Thr Met Pro His His Gln Pro Gly Leu Asn Phe Arg Tyr Ala  
60 65 70

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352

Pro Ser Pro Ser Ser Ser Leu Pro Glu Lys Arg Gly Gly Cys Ser Asp  
75 80 85

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400

Asn Ala Asn Met Ala Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val  
90 95 100

atg cag cct ata cat att gat ccg gaa tcc gta aag cca cca aag aga  
448

Met Gln Pro Ile His Ile Asp Pro Glu Ser Val Lys Pro Pro Lys Arg  
105 110 115 120

aag aac gtg agg atc tct aag gat cca cag agc gtg gca gct ccg cat  
496

Lys Asn Val Arg Ile Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His  
125 130 135

cga agg gag agg ata agc gag ccg att ccg att ctt cag ccg ctt gtt  
544

Arg Arg Glu Arg Ile Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val  
140 145 150

ccc ggt ggg act aag atg gat acg gcg tcg atg ctc gat gag gct atc  
592

Pro Gly Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile  
155 160 165

cat tac gtt aag ttt ctc aag aag caa gtg cag tcg ctg gag gaa cat  
640

His Tyr Val Lys Phe Leu Lys Lys Gln Val Gln Ser Leu Glu Glu His



170                      175                      180  
 gcg gtg gtt aac ggc gga gga atg acg gcg gtg gcc gga gga gca ctt  
 688  
 Ala Val Val Asn Gly Gly Gly Met Thr Ala Val Ala Gly Gly Ala Leu  
 185                      190                      195                      200  
 gcg ggt act gtt ggt gga gga tat gga gga aaa ggg tgt ggc att atg  
 736  
 Ala Gly Thr Val Gly Gly Gly Tyr Gly Gly Lys Gly Cys Gly Ile Met  
                     205                      210                      215  
 cgg tct gat cat cac cag atg ctt gga aat gca cag att ctt aga tga  
 784  
 Arg Ser Asp His His Gln Met Leu Gly Asn Ala Gln Ile Leu Arg  
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 904  
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                     20                      25                      30  
 Asn Ile Met Met Leu Ser Glu Ser Asn Thr His Pro Phe Phe Phe Asn  
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 Pro Thr His Ser His Leu Pro Phe Asp Gln Thr Met Pro His His Gln  
                     50                      55                      60  
 Pro Gly Leu Asn Phe Arg Tyr Ala Pro Ser Pro Ser Ser Ser Leu Pro  
 65                      70                      75                      80  
 Glu Lys Arg Gly Gly Cys Ser Asp Asn Ala Asn Met Ala Ala Met Arg  
                     85                      90                      95  
 Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His Ile Asp Pro  
                     100                      105                      110



Glu Ser Val Lys Pro Pro Lys Arg Lys Asn Val Arg Ile Ser Lys Asp  
 115 120 125

Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile Ser Glu Arg  
 130 135 140

Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys Met Asp Thr  
 145 150 155 160

Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe Leu Lys Lys  
 165 170 175

Gln Val Gln Ser Leu Glu Glu His Ala Val Val Asn Gly Gly Gly Met  
 180 185 190

Thr Ala Val Ala Gly Gly Ala Leu Ala Gly Thr Val Gly Gly Gly Tyr  
 195 200 205

Gly Gly Lys Gly Cys Gly Ile Met Arg Ser Asp His His Gln Met Leu  
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 120

aggtttaaag attttagcaa ag atg gcg aat tca gga aat tat gga aag agg  
 172

Met Ala Asn Ser Gly Asn Tyr Gly Lys Arg  
 1 5 10

ccc ttt cga ggc gat gaa tcg gat gaa aag aaa gaa gcc gat gat gat  
 220

Pro Phe Arg Gly Asp Glu Ser Asp Glu Lys Lys Glu Ala Asp Asp Asp  
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gag aac ata ttc cct ttc ttc tct gcc cga tcc caa tat gac atg cgt  
 268

Glu Asn Ile Phe Pro Phe Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg  
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gcc atg gtc tca gcc ttg act caa gtc att gga aac caa agc agc tct  
 316

Ala Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Ser Ser Ser  
 45 50 55



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 His Asp Asn Asn Gln His Gln Pro Val Val Tyr Asn Gln Gln Asp Pro  
 60 65 70  
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 412  
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 75 80 85 90  
 cac tat aga ggg gta aga caa cga cca tgg gga aag tgg gca gct gaa  
 460  
 His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu  
 95 100 105  
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 Ile Arg Asp Pro Gln Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu  
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 556  
 Thr Ala Glu Ala Ala Ala Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe  
 125 130 135  
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 604  
 Lys Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala  
 140 145 150  
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 652  
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 155 160 165 170  
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 796  
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 220 225 230  
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 235 240 245 250



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934

Leu Arg Phe Gly Asp Ser Ser Pro Pro Asn Ser Gly Phe  
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Thr Gln Val Ile Gly Asn Gln Ser Ser Ser His Asp Asn Asn Gln His  
50 55 60

Gln Pro Val Val Tyr Asn Gln Gln Asp Pro Asn Pro Pro Ala Pro Pro  
65 70 75 80

Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg His Tyr Arg Gly Val Arg  
85 90 95

Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Gln Lys  
100 105 110

Ala Ala Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala  
115 120 125

Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys  
130 135 140

Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala Ser Asn Thr Ser Thr Thr  
145 150 155 160

Thr Gly Pro Pro Asn Tyr Tyr Ser Ser Asn Asn Gln Ile Tyr Tyr Ser  
165 170 175

Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro Tyr Phe Asn Gln Tyr Tyr  
180 185 190



Tyr Asn Gln Tyr Leu His Gln Gly Gly Asn Ser Asn Asp Ala Leu Ser  
 195 200 205

Tyr Ser Leu Ala Gly Gly Glu Thr Gly Gly Ser Met Tyr Asn His Gln  
 210 215 220

Thr Leu Ser Thr Thr Asn Ser Ser Ser Ser Gly Gly Ser Ser Arg Gln  
 225 230 235 240

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 114

Met Glu Gly Leu Glu Ser Val  
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tac gct caa gct atg tat gga atg aca cga gag agc aaa atc atg gag  
 162

Tyr Ala Gln Ala Met Tyr Gly Met Thr Arg Glu Ser Lys Ile Met Glu  
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cat caa gga tca gat ttg att tgg gga gga aat gag cta atg gct cga  
 210

His Gln Gly Ser Asp Leu Ile Trp Gly Gly Asn Glu Leu Met Ala Arg  
 25 30 35

gaa ctc tgt tct tct tct tat cac cac caa ctc att aat ccg aat  
 258

Glu Leu Cys Ser Ser Ser Ser Tyr His His Gln Leu Ile Asn Pro Asn  
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ctt agc agc tgt ttc atg tct gat ctt gga gtc tta ggt gag att caa  
 306

Leu Ser Ser Cys Phe Met Ser Asp Leu Gly Val Leu Gly Glu Ile Gln  
 60 65 70

cag cag caa cat gtt ggc aac aga gct agc tcg ata gat cca tca tca  
 354

Gln Gln Gln His Val Gly Asn Arg Ala Ser Ser Ile Asp Pro Ser Ser  
 75 80 85

ctc gat tgt ttg tta tct gcg acg tcg aat agc aac aac acc tcg acg  
 402



Leu Asp Cys Leu Leu Ser Ala Thr Ser Asn Ser Asn Asn Thr Ser Thr  
 90 95 100  
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 Glu Asp Asp Glu Gly Ile Ser Val Leu Phe Ser Asp Cys Gln Thr Leu  
 105 110 115  
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 Trp Ser Phe Gly Gly Val Ser Ser Ala Glu Ser Glu Asn Arg Glu Ile  
 120 125 130 135  
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 546  
 Thr Thr Glu Thr Thr Thr Thr Ile Lys Pro Lys Pro Leu Lys Arg Asn  
 140 145 150  
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 594  
 Arg Gly Gly Asp Gly Gly Thr Thr Glu Thr Thr Thr Thr Thr Thr Lys  
 155 160 165  
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 Pro Lys Ser Leu Lys Arg Asn Arg Gly Asp Glu Thr Gly Ser His Phe  
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 Ile Tyr Asp Glu Asn Gln Ser Lys Ser Lys Lys Pro Arg Thr Glu Lys  
 200 205 210 215  
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 786  
 Glu Arg Gly Gly Ser Ser Asn Ile Ser Phe Gln His Ser Thr Cys Leu  
 220 225 230  
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 834  
 Ser Asp Asn Val Glu Pro Asp Ala Glu Ala Ile Ala Gln Met Lys Glu  
 235 240 245  
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 Met Ile Tyr Arg Ala Ala Ala Phe Arg Pro Val Asn Phe Gly Leu Glu  
 250 255 260  
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 930  
 Ile Val Glu Lys Pro Lys Arg Lys Asn Val Lys Ile Ser Thr Asp Pro  
 265 270 275  
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 Gln Thr Val Ala Ala Arg Gln Arg Arg Glu Arg Ile Ser Glu Lys Ile



280                      285                      290                      295  
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 Ser Met Leu Asp Glu Ala Ala Asn Tyr Leu Lys Phe Leu Arg Ala Gln  
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 Val Lys Ala Leu Glu Asn Leu Arg Pro Lys Leu Asp Gln Thr Asn Leu  
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 1170  
 Ser Phe Ser Ser Ala Pro Thr Ser Phe Pro Leu Phe His Pro Ser Phe  
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 1335  
  
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                                  20                      25                      30  
  
 Gly Asn Glu Leu Met Ala Arg Glu Leu Cys Ser Ser Ser Ser Tyr His  
                                  35                      40                      45  
  
 His Gln Leu Ile Asn Pro Asn Leu Ser Ser Cys Phe Met Ser Asp Leu  
                                  50                      55                      60



Gly Val Leu Gly Glu Ile Gln Gln Gln Gln His Val Gly Asn Arg Ala  
 65 70 75 80  
 Ser Ser Ile Asp Pro Ser Ser Leu Asp Cys Leu Leu Ser Ala Thr Ser  
 85 90 95  
 Asn Ser Asn Asn Thr Ser Thr Glu Asp Asp Glu Gly Ile Ser Val Leu  
 100 105 110  
 Phe Ser Asp Cys Gln Thr Leu Trp Ser Phe Gly Gly Val Ser Ser Ala  
 115 120 125  
 Glu Ser Glu Asn Arg Glu Ile Thr Thr Glu Thr Thr Thr Thr Ile Lys  
 130 135 140  
 Pro Lys Pro Leu Lys Arg Asn Arg Gly Gly Asp Gly Gly Thr Thr Glu  
 145 150 155 160  
 Thr Thr Thr Thr Thr Thr Lys Pro Lys Ser Leu Lys Arg Asn Arg Gly  
 165 170 175  
 Asp Glu Thr Gly Ser His Phe Ser Leu Val His Pro Gln Asp Asp Ser  
 180 185 190  
 Glu Lys Gly Gly Phe Lys Leu Ile Tyr Asp Glu Asn Gln Ser Lys Ser  
 195 200 205  
 Lys Lys Pro Arg Thr Glu Lys Glu Arg Gly Gly Ser Ser Asn Ile Ser  
 210 215 220  
 Phe Gln His Ser Thr Cys Leu Ser Asp Asn Val Glu Pro Asp Ala Glu  
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 245 250 255  
 Pro Val Asn Phe Gly Leu Glu Ile Val Glu Lys Pro Lys Arg Lys Asn  
 260 265 270  
 Val Lys Ile Ser Thr Asp Pro Gln Thr Val Ala Ala Arg Gln Arg Arg  
 275 280 285  
 Glu Arg Ile Ser Glu Lys Ile Arg Val Leu Gln Thr Leu Val Pro Gly  
 290 295 300



Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ala Asn Tyr  
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Leu Lys Phe Leu Arg Ala Gln Val Lys Ala Leu Glu Asn Leu Arg Pro  
 325 330 335

Lys Leu Asp Gln Thr Asn Leu Ser Phe Ser Ser Ala Pro Thr Ser Phe  
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Pro Leu Phe His Pro Ser Phe Leu Pro Leu Gln Asn Pro Asn Gln Ile  
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His His Pro Glu Cys  
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 97

Thr Asn Gln Thr His Asn Asn Ala Lys Glu Ile Arg Tyr Arg Gly Val  
 15 20 25

agg aag cgt cct tgg ggc cgt tat gcc gcc gag atc cga gat ccg ggc  
 145

Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly  
 30 35 40

aag aaa acc cgc gtc tgg ctt ggc act ttc gat acg gct gaa gag gcg  
 193

Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala  
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gcg cgt gct tac gat acg gcg gcg cgt gat ttt cgt ggt gct aag gct  
 241

Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe Arg Gly Ala Lys Ala  
 65 70 75

aag acc aat ttc cca act ttt ctc gag ctg agt gac cag aag gtc cct  
 289

Lys Thr Asn Phe Pro Thr Phe Leu Glu Leu Ser Asp Gln Lys Val Pro  
 80 85 90

acc ggt ttc gcg cgt agc cct agc cag agc agc acg ctc gac tgt gct  
 337

Thr Gly Phe Ala Arg Ser Pro Ser Gln Ser Ser Thr Leu Asp Cys Ala  
 95 100 105

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 385



Ser Pro Pro Thr Leu Val Val Pro Ser Ala Thr Ala Gly Asn Val Pro  
 110 115 120

ccg cag ctc gag ctt agt ctc ggc gga gga ggc ggc ggc tcg tgt tat  
 433

Pro Gln Leu Glu Leu Ser Leu Gly Gly Gly Gly Gly Gly Ser Cys Tyr  
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 481

Gln Ile Pro Met Ser Arg Pro Val Tyr Phe Leu Asp Leu Met Gly Ile  
 145 150 155

ggc aac gta ggt cgt ggt cag cct cct cct gtg aca tcg gcg ttt aga  
 529

Gly Asn Val Gly Arg Gly Gln Pro Pro Pro Val Thr Ser Ala Phe Arg  
 160 165 170

tcg ccg gtg gtg cat gtt gcg acg aag atg gct tgt ggt gcc caa agc  
 577

Ser Pro Val Val His Val Ala Thr Lys Met Ala Cys Gly Ala Gln Ser  
 175 180 185

gac tct gat tcg tca tcg gtc gtt gat ttc gaa ggt ggg atg gag aag  
 625

Asp Ser Asp Ser Ser Ser Val Val Asp Phe Glu Gly Gly Met Glu Lys  
 190 195 200

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 673

Arg Ser Gln Leu Leu Asp Leu Asp Leu Asn Leu Pro Pro Pro Ser Glu  
 205 210 215 220

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Gln Ala

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 842

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 Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly Lys Lys Thr Arg  
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 Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr  
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 Asp Thr Ala Ala Arg Asp Phe Arg Gly Ala Lys Ala Lys Thr Asn Phe  
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 Pro Thr Phe Leu Glu Leu Ser Asp Gln Lys Val Pro Thr Gly Phe Ala  
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 Arg Ser Pro Ser Gln Ser Ser Thr Leu Asp Cys Ala Ser Pro Pro Thr  
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 Leu Val Val Pro Ser Ala Thr Ala Gly Asn Val Pro Pro Gln Leu Glu  
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 Leu Ser Leu Gly Gly Gly Gly Gly Gly Ser Cys Tyr Gln Ile Pro Met  
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 Ser Arg Pro Val Tyr Phe Leu Asp Leu Met Gly Ile Gly Asn Val Gly  
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 Arg Gly Gln Pro Pro Pro Val Thr Ser Ala Phe Arg Ser Pro Val Val  
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 Ser Ser Val Val Asp Phe Glu Gly Gly Met Glu Lys Arg Ser Gln Leu  
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113

Met Asp Ser Ser Cys Ile Asp Glu Ile Ser Ser  
1 5 10

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161

Ser Thr Ser Glu Ser Phe Ser Ala Thr Thr Ala Lys Lys Leu Ser Pro  
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209

Pro Pro Ala Ala Ala Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser  
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257

Ser Val Val Leu Asp Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys  
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cta cca tct tca aaa tac aaa ggt gtt gtt cct cag cct aac gga aga  
305

Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg  
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tgg gga gct cag atc tac gag aag cac caa cga gta tgg ctc ggg act  
353

Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr  
80 85 90

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401

Phe Asn Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys  
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449

Arg Phe Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu  
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497

Asp Gly Asp Leu Ala Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val  
125 130 135

gac atg ttg aga aaa cac act tac gcc gac gag ctt gaa cag aac aat  
545

Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn  
140 145 150 155

aaa cgg cag ttg ttt ctc tcc gtc gac gct aac gga aaa cgt aac gga  
593

Lys Arg Gln Leu Phe Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly  
160 165 170

tcg agt act act caa aac gac aaa gtt tta aag acg tgt gaa gtt ctt  
641

Ser Ser Thr Thr Gln Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu  
175 180 185



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 689  
 Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu  
 190 195 200

gtg ata cct aaa caa cac gcc gag aaa cac ttt ccg tta ccg tca ccg  
 737  
 Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro Ser Pro  
 205 210 215

tca ccg gca gtg act aaa gga gtt ttg atc aac ttc gaa gac gtt aac  
 785  
 Ser Pro Ala Val Thr Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn  
 220 225 230 235

ggt aaa gtg tgg agg ttc cgt tac tca tac tgg aac agt agt caa agt  
 833  
 Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser  
 240 245 250

tac gtg ttg acc aag gga tgg agt cga ttc gtc aag gag aag aat ctt  
 881  
 Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu  
 255 260 265

cga gcc ggt gat gtt gtt act ttc gag aga tcg acc gga cta gag cgg  
 929  
 Arg Ala Gly Asp Val Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg  
 270 275 280

cag tta tat att gat tgg aaa gtt cgg tct ggt ccg aga gaa aac ccg  
 977  
 Gln Leu Tyr Ile Asp Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro  
 285 290 295

gtt cag gtg gtg gtt cgg ctt ttc gga gtt gat atc ttt aat gtg acc  
 1025  
 Val Gln Val Val Val Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr  
 300 305 310 315

acc gtg aag cca aac gac gtc gtg gcc gtt tgc ggt gga aag aga tct  
 1073  
 Thr Val Lys Pro Asn Asp Val Val Ala Val Cys Gly Gly Lys Arg Ser  
 320 325 330

cga gat gtt gat gat atg ttt gcg tta cgg tgt tcc aag aag cag gcg  
 1121  
 Arg Asp Val Asp Asp Met Phe Ala Leu Arg Cys Ser Lys Lys Gln Ala  
 335 340 345

ata atc aat gct ttg tga catatttcct tttccgattt tatgctttcg  
 1169  
 Ile Ile Asn Ala Leu  
 350

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 1229

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 1246



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20 25 30

Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp  
35 40 45

Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys  
50 55 60

Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile  
65 70 75 80

Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Gln Glu  
85 90 95

Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe Arg Gly Arg  
100 105 110

Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly Asp Leu Ala  
115 120 125

Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys  
130 135 140

His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn Lys Arg Gln Leu Phe  
145 150 155 160

Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly Ser Ser Thr Thr Gln  
165 170 175

Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu Phe Glu Lys Ala Val  
180 185 190

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln  
195 200 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Pro Ser Pro Ala Val Thr  
210 215 220

Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg



520



aaa gct gcc att ctc aac ttc cct cac gag tat aac atg gga acc gga  
 295  
 Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Thr Gly  
 70 75 80 85  
 tcc tca tcc act gcg gct aat tct tct tcc tcg tcg cag caa gtt ttt  
 343  
 Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser Ser Gln Gln Val Phe  
 90 95 100  
 gag ttt gag tac ttg gac gat agc gtt ttg gat gaa ctt ctt gaa tat  
 391  
 Glu Phe Glu Tyr Leu Asp Asp Ser Val Ileu Asp Glu Leu Leu Glu Tyr  
 105 110 115  
 gga gag aac tat aac aag act cat aat atc aac atg ggc aag agg caa  
 439  
 Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn Met Gly Lys Arg Gln  
 120 125 130  
 taa aggggaataca atcggtatta actgaaagtt atgtgaaaga ccattttcag  
 492  
 ttataacaaa taaaataaaa tcccaagcgt acaaagctgt ttctaaaaaa aaaaaaaaaa  
 552  
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 553

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Gln Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala  
 20 25 30

Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly  
 35 40 45

Thr Phe Asp Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala  
 50 55 60

Tyr Ser Met Arg Gly Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr  
 65 70 75 80

Asn Met Gly Thr Gly Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser  
 85 90 95

Ser Gln Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Asp  
 100 105 110



Glu Leu Leu Glu Tyr Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn  
 115 120 125

Met Gly Lys Arg Gln  
 130

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 120

acttaaacct tatccagttt cttgaaacag agtactctga tca atg aac tca ttt  
 175

Met Asn Ser Phe  
 1

tca gct ttt tct gaa atg ttt ggc tcc gat tac gag cct caa ggc gga  
 223

Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu Pro Gln Gly Gly  
 5 10 15 20

gat tat tgt ccg acg ttg gcc acg agt tgt ccg aag aaa ccg gcg ggc  
 271

Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly  
 25 30 35

cgt aag aag ttt cgt gag act cgt cac cca att tac aga gga gtt cgt  
 319

Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg  
 40 45 50

caa aga aac tcc ggt aag tgg gtt tct gaa gtg aga gag cca aac aag  
 367

Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg Glu Pro Asn Lys  
 55 60 65

aaa acc agg att tgg ctc ggg act ttc caa acc gct gag atg gca gct  
 415

Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala  
 70 75 80

cgt gct cac gac gtc gct gca tta gcc ctc cgt ggc cga tca gca tgt  
 463

Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys  
 85 90 95 100

ctc aac ttc gct gac tcg gct tgg cgg cta cga atc ccg gag tca aca  
 511

Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr  
 105 110 115

tgc gcc aag gat atc caa aaa gcg gct gct gaa gcg gcg ttg gct ttt  
 559

Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Ala Phe



120 125 130  
 caa gat gag acg tgt gat acg acg acc acg aat cat ggc ctg gac atg  
 607  
 Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His Gly Leu Asp Met  
 135 140 145  
 gag gag acg atg gtg gaa gct att tat aca ccg gaa cag agc gaa ggt  
 655  
 Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Glu Gly  
 150 155 160  
 gcg ttt tat atg gat gag gag aca atg ttt ggg atg ccg act ttg ttg  
 703  
 Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met Pro Thr Leu Leu  
 165 170 175 180  
 gat aat atg gct gaa ggc atg ctt tta ccg ccg cct gtt caa tgg  
 751  
 Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Ser Val Gln Trp  
 185 190 195  
 aat cat aat tat gac ggc gaa gga gat ggt gac gtg tcg ctt tgg agt  
 799  
 Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val Ser Leu Trp Ser  
 200 205 210  
 tac taa tattcgatag tcgtttccat ttttgtacta tagtttgaaa atattctagt  
 855  
 Tyr  
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 20 25 30  
 Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr  
 35 40 45  
 Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg  
 50 55 60  
 Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala  
 65 70 75 80



Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly  
85 90 95

Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile  
100 105 110

Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala  
115 120 125

Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His  
130 135 140

Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu  
145 150 155 160

Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met  
165 170 175

Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro  
180 185 190

Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val  
195 200 205

Ser Leu Trp Ser Tyr  
210

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1 5

tct ccg gtt tcc tca ggc ggt gat tac agt ccg aag ctt gcc acg agc  
103

Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys Leu Ala Thr Ser  
10 15 20

tgc ccc aag aaa cca gcg gga agg aag aag ttt cgt gag act cgt cac  
151

Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His  
25 30 35

cca att tac aga gga gtt cgt caa aga aac tcc ggt aag tgg gtg tgt  
199

Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Cys  
40 45 50 55



gag ttg aga gag cca aac aag aaa acg agg att tgg ctc ggg act ttc  
247

Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
60 65 70

caa acc gct gag atg gca gct cgt gct cac gac gtc gcc gcc ata gct  
295

Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala  
75 80 85

ctc cgt ggc aga tct gcc tgt ctc aat ttc gct gac tcg gct tgg cgg  
343

Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
90 95 100

cta cga atc ccg gaa tca acc tgt gcc aag gaa atc caa aag gcg gcg  
391

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala  
105 110 115

gct gaa gcc gcg ttg aat ttt caa gat gag atg tgt cat atg acg acg  
439

Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr  
120 125 130 135

gat gct cat ggt ctt gac atg gag gag acc ttg gtg gag gct att tat  
487

Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr  
140 145 150

acg ccg gaa cag agc caa gat gcg ttt tat atg gat gaa gag gcg atg  
535

Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met  
155 160 165

ttg ggg atg tct agt ttg ttg gat aac atg gcc gaa ggg atg ctt tta  
583

Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu  
170 175 180

ccg tcg ccg tcg gtt caa tgg aac tat aat ttt gat gtc gag gga gat  
631

Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp Val Glu Gly Asp  
185 190 195

gat gac gtg tcc tta tgg agc tat taa aattcgattt ttatttccat  
678

Asp Asp Val Ser Leu Trp Ser Tyr  
200 205

ttttggtatt atagcttttt atacatttga tcctttttta gaatggatct tcttcttttt  
738

ttggttgtga gaaacgaatg taaatggtaa aagttgttgt caaatgcaaa tgtttttgag  
798

tgcag  
803



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Met Phe Gly Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr  
1 5 10 15

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20 25 30

Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg  
35 40 45

Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr  
50 55 60

Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala  
65 70 75 80

His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn  
85 90 95

Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala  
100 105 110

Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp  
115 120 125

Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu  
130 135 140

Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe  
145 150 155 160

Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn  
165 170 175

Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr  
180 185 190

Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr  
195 200 205

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gacagagatc ttttagttac cttatccagt ttcttgaac agagtactct tctgatca  
118

atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag  
166

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu  
1 5 10 15

tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc  
214

Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser  
20 25 30

tgc ccc aag aaa ccg gcg ggt cgt aag aag ttt cgt gag act cgt cac  
262

Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His  
35 40 45

cca ata tac aga gga gtt cgt cgg aga aac tcc ggt aag tgg gtt tgt  
310

Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys  
50 55 60

gag gtt aga gaa cca aac aag aaa aca agg att tgg ctc gga aca ttt  
358

Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
65 70 75 80

caa acc gct gag atg gca gct cga gct cac gac gtt gcc gct tta gcc  
406

Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala  
85 90 95

ctt cgt ggc cga tca gcc tgt ctc aat ttc gct gac tcg gct tgg aga  
454

Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
100 105 110

ctc cga atc ccg gaa tca act tgc gct aag gac atc caa aag gcg gcg  
502

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala  
115 120 125

gct gaa gct gcg ttg gcg ttt cag gat gag atg tgt gat gcg acg acg  
550

Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr  
130 135 140

gat cat ggc ttc gac atg gag gag acg ttg gtg gag gct att tac acg  
598

Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr  
145 150 155 160

gcg gaa cag agc gaa aat gcg ttt tat atg cac gat gag gcg atg ttt  
646

Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe  
165 170 175

gag atg ccg agt ttg ttg gct aat atg gca gaa ggg atg ctt ttg ccg  
694



Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro  
 180 185 190

ctt ccg tcc gta cag tgg aat cat aat cat gaa gtc gac ggc gat gat  
 742

Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp  
 195 200 205

gac gac gta tcg tta tgg agt tat taa aactcagatt attatttcca  
 789

Asp Asp Val Ser Leu Trp Ser Tyr  
 210 215

tttttagtac gatacttttt attttattat tatttttaga tcctttttta gaatggaatc  
 849

tacattatgt ttgtaaaact gagaaacgag tgtaaattaa attgattcag tttcagtat  
 908

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Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser  
 20 25 30

Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His  
 35 40 45

Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys  
 50 55 60

Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
 65 70 75 80

Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala  
 85 90 95

Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
 100 105 110

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala  
 115 120 125

Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr  
 130 135 140

Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr  
 145 150 155 160



Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe  
 165 170 175

Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro  
 180 185 190

Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp  
 195 200 205

Asp Asp Val Ser Leu Trp Ser Tyr  
 210 215

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ggg aag att gtg atc cag aag atc gat gat.tcc acg agt aga caa gtc  
 106

Gly Lys Ile Val Ile Gln Lys Ile Asp Asp Ser Thr Ser Arg Gln Val  
 5 10 15

act ttc tcc aaa aga aga aag ggt ctc atc aag aaa gct aaa gaa ctt  
 154

Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala Lys Glu Leu  
 20 25 30 35

gct att ctc tgc gac gcc gag gtc tgt ctc atc att ttc tcc aac act  
 202

Ala Ile Leu Cys Asp Ala Glu Val Cys Leu Ile Ile Phe Ser Asn Thr  
 40 45 50

gac aag ctc tat gac ttt gcc agc tcc agt gtg aaa tct act att gaa  
 250

Asp Lys Leu Tyr Asp Phe Ala Ser Ser Ser Val Lys Ser Thr Ile Glu  
 55 60 65

cga ttc aat acg gct aag atg gag gag caa gaa cta atg aac cct gca  
 298

Arg Phe Asn Thr Ala Lys Met Glu Glu Gln Glu Leu Met Asn Pro Ala  
 70 75 80

tca gaa gtt aag ttt tgg cag aga gag gct gaa act cta agg caa gaa  
 346

Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Glu Thr Leu Arg Gln Glu  
 85 90 95

ttg cac tca ttg caa gaa aat tat cgg caa cta acg gga gtg gaa tta  
 394

Leu His Ser Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly Val Glu Leu  
 100 105 110 115



aat ggt ttg agc gtt aag gag tta caa aac ata gag agt caa ctt gaa  
442

Asn Gly Leu Ser Val Lys Glu Leu Gln Asn Ile Glu Ser Gln Leu Glu  
120 125 130

atg agt tta cgt gga att cgt atg aaa agg gaa caa att ttg acc aat  
490

Met Ser Leu Arg Gly Ile Arg Met Lys Arg Glu Gln Ile Leu Thr Asn  
135 140 145

gaa att aaa gag cta acc aga aag agg aat ctt gtt cat cat gaa aac  
538

Glu Ile Lys Glu Leu Thr Arg Lys Arg Asn Leu Val His His Glu Asn  
150 155 160

ctc gaa ttg tcg aga aaa gta caa agg att cat caa gaa aat gtc gaa  
586

Leu Glu Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu Asn Val Glu  
165 170 175

cta tac aag aag gct tat gga acg tcg aac aca aat gga ttg gga cat  
634

Leu Tyr Lys Lys Ala Tyr Gly Thr Ser Asn Thr Asn Gly Leu Gly His  
180 185 190 195

cat gag cta gta gat gca gtt tat gaa tcc cat gaa cag gtt agg ctg  
682

His Glu Leu Val Asp Ala Val Tyr Glu Ser His Ala Gln Val Arg Leu  
200 205 210

cag cta agc cag cct gag cag tcc cat tat aag aca tct tca aac agc  
730

Gln Leu Ser Gln Pro Glu Gln Ser His Tyr Lys Thr Ser Ser Asn Ser  
215 220 225

taa gatcatataa gagatatata acaaattggt cgttcttgat tatctcaaaa  
783

ccctttcaaaa tatatatatcg tgcattat ataggaagac tcgtttgact atgtcaatat  
843

atatgttttc atgcaggagt aagtgtgagt gtaatcatgt cggagagcaa accaaaggtt  
903

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959

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20 25 30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Cys Leu Ile Ile Phe



35                      40                      45  
 Ser Asn Thr Asp Lys Leu Tyr Asp Phe Ala Ser Ser Ser Val Lys Ser  
 50                      55                      60  
 Thr Ile Glu Arg Phe Asn Thr Ala Lys Met Glu Glu Gln Glu Leu Met  
 65                      70                      75                      80  
 Asn Pro Ala Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Glu Thr Leu  
 85                      90                      95  
 Arg Gln Glu Leu His Ser Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly  
 100                      105                      110  
 Val Glu Leu Asn Gly Leu Ser Val Lys Glu Leu Gln Asn Ile Glu Ser  
 115                      120                      125  
 Gln Leu Glu Met Ser Leu Arg Gly Ile Arg Met Lys Arg Glu Gln Ile  
 130                      135                      140  
 Leu Thr Asn Glu Ile Lys Glu Leu Thr Arg Lys Arg Asn Leu Val His  
 145                      150                      155                      160  
 His Glu Asn Leu Glu Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu  
 165                      170                      175  
 Asn Val Glu Leu Tyr Lys Lys Ala Tyr Gly Thr Ser Asn Thr Asn Gly  
 180                      185                      190  
 Leu Gly His His Glu Leu Val Asp Ala Val Tyr Glu Ser His Ala Gln  
 195                      200                      205  
 Val Arg Leu Gln Leu Ser Gln Pro Glu Gln Ser His Tyr Lys Thr Ser  
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 tcaattgggtt ttggtgtag tcttttgggg agagag atg ggg aga ggg aag ata  
 114  
 Met Gly Arg Gly Lys Ile



1

5

gtt ata cga agg atc gat aac tct aca agt aga caa gtg act ttc tcc  
 162  
 Val Ile Arg Arg Ile Asp Asn Ser Thr Ser Arg Gln Val Thr Phe Ser  
           10                          15                          20

aag aga agg agt ggt ttg ctt aag aag gct aaa gag tta tcg atc ctt  
 210  
 Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Ile Leu  
           25                          30                          35

tgt gat gca gaa gtt ggt gtt atc ata ttc tct agc acc gga aag ctc  
 258  
 Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser Ser Thr Gly Lys Leu  
           40                          45                          50

tac gac tac gca agc aat tca agt atg aaa aca atc att gag cgg tac  
 306  
 Tyr Asp Tyr Ala Ser Asn Ser Ser Met Lys Thr Ile Ile Glu Arg Tyr  
           55                          60                          65                          70

aac aga gta aaa gag gag cag cat caa ctt ctg aat cat gcc tca gag  
 354  
 Asn Arg Val Lys Glu Glu Gln His Gln Leu Leu Asn His Ala Ser Glu  
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ata aag ttt tgg caa aga gag gtt gca agt ttg cag cag cag ctc caa  
 402  
 Ile Lys Phe Trp Gln Arg Glu Val Ala Ser Leu Gln Gln Gln Leu Gln  
                           90                          95                          100

cat cta caa gaa tgc cac agg aaa cta gtg gga gag gaa ctt tct gga  
 450  
 His Leu Gln Glu Cys His Arg Lys Leu Val Gly Glu Glu Leu Ser Gly  
                           105                          110                          115

atg aat gct aac gac cta caa aat ctt gaa gac cag cta gta aca agt  
 498  
 Met Asn Ala Asn Asp Leu Gln Asn Leu Glu Asp Gln Leu Val Thr Ser  
           120                          125                          130

cta aaa ggt gtt cgt ctc aaa aag gat caa ctt atg aca aat gaa atc  
 546  
 Leu Lys Gly Val Arg Leu Lys Lys Asp Gln Leu Met Thr Asn Glu Ile  
           135                          140                          145                          150

aga gaa ctt aat cgt aag gga caa atc atc caa aaa gag aat cac gag  
 594  
 Arg Glu Leu Asn Arg Lys Gly Gln Ile Ile Gln Lys Glu Asn His Glu  
                           155                          160                          165

cta caa aat att gta gat ata atg cgt aag gaa aat att aaa ttg caa  
 642  
 Leu Gln Asn Ile Val Asp Ile Met Arg Lys Glu Asn Ile Lys Leu Gln  
                           170                          175                          180

aag aag gtt cat gga aga aca aat gtg att gaa ggc aat tca agt gta  
 690  
 Lys Lys Val His Gly Arg Thr Asn Val Ile Glu Gly Asn Ser Ser Val  
           185                          190                          195



gat cca ata agc aat gga acc aca aca tat gca cca ccg caa ctt caa  
738

Asp Pro Ile Ser Asn Gly Thr Thr Thr Tyr Ala Pro Pro Gln Leu Gln  
200 205 210

ctc ata caa cta caa cca gct cct aga gaa aaa tca atc aga cta ggg  
786

Leu Ile Gln Leu Gln Pro Ala Pro Arg Glu Lys Ser Ile Arg Leu Gly  
215 220 225 230

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841

Leu Gln Leu Ser

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901

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961

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1098

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Lys Glu Leu Ser Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe  
35 40 45

Ser Ser Thr Gly Lys Leu Tyr Asp Tyr Ala Ser Asn Ser Ser Met Lys  
50 55 60

Thr Ile Ile Glu Arg Tyr Asn Arg Val Lys Glu Glu Gln His Gln Leu  
65 70 75 80

Leu Asn His Ala Ser Glu Ile Lys Phe Trp Gln Arg Glu Val Ala Ser  
85 90 95

Leu Gln Gln Gln Leu Gln His Leu Gln Glu Cys His Arg Lys Leu Val  
100 105 110



Gly Glu Glu Leu Ser Gly Met Asn Ala Asn Asp Leu Gln Asn Leu Glu  
 115 120 125

Asp Gln Leu Val Thr Ser Leu Lys Gly Val Arg Leu Lys Lys Asp Gln  
 130 135 140

Leu Met Thr Asn Glu Ile Arg Glu Leu Asn Arg Lys Gly Gln Ile Ile  
 145 150 155 160

Gln Lys Glu Asn His Glu Leu Gln Asn Ile Val Asp Ile Met Arg Lys  
 165 170 175

Glu Asn Ile Lys Leu Gln Lys Lys Val His Gly Arg Thr Asn Val Ile  
 180 185 190

Glu Gly Asn Ser Ser Val Asp Pro Ile Ser Asn Gly Thr Thr Thr Tyr  
 195 200 205

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 114

Met Asp Arg Gly Trp  
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tct ggt ctc act ctt gat tca tct tct ctt gat ctt tta aac cct aat  
 162

Ser Gly Leu Thr Leu Asp Ser Ser Ser Leu Asp Leu Leu Asn Pro Asn  
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cgt att tct cat aag aat cac cga cgt ttc tca aat cct ttg gcg atg  
 210

Arg Ile Ser His Lys Asn His Arg Arg Phe Ser Asn Pro Leu Ala Met  
 25 30 35

tct aga att gac gaa gaa gat gat cag aag acg aga ata tca acc aac  
 258

Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr Arg Ile Ser Thr Asn  
 40 45 50



ggt agt gaa ttt agg ttt ccg gtg agt ctc tca ggt att cgt gat cgt  
 306  
 Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser Gly Ile Arg Asp Arg  
 55 60 65

gaa gat gaa gat ttt tca tct ggc gtt gct gga gat aat gac cgt gaa  
 354  
 Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly Asp Asn Asp Arg Glu  
 70 75 80 85

gtt ccc ggc gaa gtg gat ttc ttc tcc gac aag aaa tct agg gtt tgt  
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 Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys Lys Ser Arg Val Cys  
 90 95 100

cgt gaa gac gac gaa gga ttt cgt gtg aag aag gaa gaa caa gat gat  
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 Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys Glu Glu Gln Asp Asp  
 105 110 115

cga acg gac gta aat acc ggt ttg aat ctt cga aca act ggt aat aca  
 498  
 Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg Thr Thr Gly Asn Thr  
 120 125 130

aag agt gat gag tca atg atc gat gat gga gaa tct tcc gaa atg gaa  
 546  
 Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu Ser Ser Glu Met Glu  
 135 140 145

gat aag cgt gcg aaa aat gag ttg gtg aaa tta caa gat gag ttg aag  
 594  
 Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu Gln Asp Glu Leu Lys  
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 Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu Leu Leu Thr Gln Val  
 170 175 180

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 185 190 195

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 200 205 210

gag gag acg ata gta cca agg caa ttt att gat tta ggc cct acg aga  
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 215 220 225

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 250 255 260

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 Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Lys Ile Gln  
 265 270 275

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 Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp Gln Thr Ala Glu Ala  
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 295 300 305

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 Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg Ser  
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 1218  
 Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro  
 360 365 370

gcc gcg gta gcc atg gct tct acc acc acg gcg gcg gct aac atg ttg  
 1266  
 Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala Ala Ala Asn Met Leu  
 375 380 385

cta tcc ggg tca atg tct agt cac gac ggg atg atg aac cct aca aat  
 1314  
 Leu Ser Gly Ser Met Ser Ser His Asp Gly Met Met Asn Pro Thr Asn  
 390 395 400 405

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 1362  
 Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr Ser Met Ala Thr Ile  
 410 415 420

tca gcc tcc gcg ccg ttt cca acc gtc aca tta gac ctc acc cac tca  
 1410  
 Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu Asp Leu Thr His Ser  
 425 430 435



cct ccg cct cct aat ggt tcc aat cct tcc tct tcc gcg gct acc aac  
1458

Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser Ser Ala Ala Thr Asn  
440 445 450

aac aac cac aac tca ctg atg cag cgg ccg caa caa caa caa cag caa  
1506

Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln Gln Gln Gln Gln  
455 460 465

atg acg aac tta cct ccg gga atg cta cct cat gta ata ggc cag gca  
1554

Met Thr Asn Leu Pro Pro Gly Met Leu Pro His Val Ile Gly Gln Ala  
470 475 480 485

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1602

Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln Phe Ser Gly Gly Ser  
490 495 500

ccc tcg acg gca gcg ttt tct cag tca cac gcg gtg gct gat aca ata  
1650

Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala Val Ala Asp Thr Ile  
505 510 515

acg gca ctc aca gct gac ccg aat ttc acg gcg gct ctt gca gcc gtt  
1698

Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Val  
520 525 530

att tct tct atg atc aat ggt acg aac cac cac gac ggc gaa gga aac  
1746

Ile Ser Ser Met Ile Asn Gly Thr Asn His His Asp Gly Glu Gly Asn  
535 540 545

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1801

Asn Lys Asn Gln  
550

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Asn Pro Leu Ala Met Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr  
 35 40 45

Arg Ile Ser Thr Asn Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser  
 50 55 60

Gly Ile Arg Asp Arg Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly  
 65 70 75 80

Asp Asn Asp Arg Glu Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys  
 85 90 95

Lys Ser Arg Val Cys Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys  
 100 105 110

Glu Glu Gln Asp Asp Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg  
 115 120 125

Thr Thr Gly Asn Thr Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu  
 130 135 140

Ser Ser Glu Met Glu Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu  
 145 150 155 160

Gln Asp Glu Leu Lys Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu  
 165 170 175

Leu Leu Thr Gln Val Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu  
 180 185 190

Val Ser Leu Met Gln Gln Gln Gln Gln Asn Asn Lys Val Ile Glu  
 195 200 205

Ala Ala Glu Lys Pro Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp  
 210 215 220

Leu Gly Pro Thr Arg Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser  
 225 230 235 240

Ser Ser Glu Asp Arg Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg  
 245 250 255

Arg Ser Asn Gly Lys Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu  
 260 265 270

Ser Asn Lys Ile Gln Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp



275	280	285
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Gly Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg 325 330 335		
Cys Thr Met Ala Thr Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys 340 345 350		
Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn 355 360 365		
His Pro Leu Pro Pro Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala 370 375 380		
Ala Ala Asn Met Leu Leu Ser Gly Ser Met Ser Ser His Asp Gly Met 385 390 395 400		
Met Asn Pro Thr Asn Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr 405 410 415		
Ser Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu 420 425 430		
Asp Leu Thr His Ser Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser 435 440 445		
Ser Ala Ala Thr Asn Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln 450 455 460		
Gln Gln Gln Gln Gln Met Thr Asn Leu Pro Pro Gly Met Leu Pro His 465 470 475 480		
Val Ile Gly Gln Ala Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln 485 490 495		
Phe Ser Gly Gly Ser Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala 500 505 510		
Val Ala Asp Thr Ile Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala 515 520 525		



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 165

Met Ser Asn Glu Thr Arg Asp Leu Tyr Asn Tyr Gln Tyr Pro Ser Ser  
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 213

Phe Ser Leu His Glu Met Met Asn Leu Pro Thr Ser Asn Pro Ser Ser  
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tat gga aac ctc cca tca caa aac ggt ttt aat cca tct act tat tcc  
 261

Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser  
 35 40 45

ttc acc gat tgt ctc caa agt tct cca gca gcg tat gaa tct cta ctt  
 309

Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu  
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cag aaa act ttt ggt ctt tct ccc tct tcc tca gag gtt ttc aat tct  
 357

Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser  
 65 70 75 80

tcg atc gat caa gaa ccg aac cgt gat gtt act aat gac gta atc aat  
 405

Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn  
 85 90 95

ggt ggt gca tgc aac gag act gaa act agg gtt tct cct tct aat tct  
 453

Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser  
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 501

Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg  
 115 120 125



agg aaa cga gag tta gtc ggt gaa gaa gat caa att tcc aaa aaa gtt  
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 Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val  
 130 135 140  
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 Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg  
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 Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala  
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 885  
 Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His  
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 Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser  
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 1029  
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 290 295 300  
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Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser  
35 40 45

Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu  
50 55 60

Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser  
65 70 75 80

Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn  
85 90 95

Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser  
100 105 110

Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg  
115 120 125

Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val  
130 135 140

Gly Lys Thr Lys Lys Thr Glu Val Lys Lys Gln Arg Glu Pro Arg Val  
145 150 155 160

Ser Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg  
165 170 175

Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg  
180 185 190

Ser Tyr Tyr Arg Cys Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val  
195 200 205



Glu Arg Ser Phe Gln Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Gly  
210 215 220

Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala  
225 230 235 240

Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His  
245 250 255

Asp Met Phe Arg Thr Ala Ala Tyr Thr Asn Gly Gly Ser Val Ala Ala  
260 265 270

Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser  
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120

ttatttcttt gacctctcaa aaca atg ggt aga tca ccg tgt tgt gac aaa  
171

Met Gly Arg Ser Pro Cys Cys Asp Lys  
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ttg ggt ttg aag aaa gga cct tgg aca cca gag gag gat cag aaa ctt  
219

Leu Gly Leu Lys Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu  
10 15 20 25

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267

Leu Ala Tyr Ile Glu Glu His Gly His Gly Ser Trp Arg Ser Leu Pro  
30 35 40

gag aaa gct ggt ctc cat cga tgc gga aag agt tgt aga cta aga tgg  
315

Glu Lys Ala Gly Leu His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp  
45 50 55

act aac tac cta aga cct gac atc aaa aga ggc aaa ttc aac tta caa  
363



Thr Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Lys Phe Asn Leu Gln  
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 75 80 85  
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 459  
 Ser Ala Ile Ala Thr His Leu Pro Lys Arg Thr Asp Asn Glu Ile Lys  
 90 95 100 105  
 aac tat tgg aac act cat ttg aag aaa cgg tta gtg aaa atg ggg att  
 507  
 Asn Tyr Trp Asn Thr His Leu Lys Lys Arg Leu Val Lys Met Gly Ile  
 110 115 120  
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 555  
 Asp Pro Val Thr His Lys Pro Lys Asn Glu Thr Pro Leu Ser Ser Leu  
 125 130 135  
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 603  
 Gly Leu Ser Lys Asn Ala Ala Ile Leu Ser His Thr Ala Gln Trp Glu  
 140 145 150  
 agt gca agg ctt gaa gct gaa gca aga cta gct aga gaa tca aag ctt  
 651  
 Ser Ala Arg Leu Glu Ala Glu Ala Arg Leu Ala Arg Glu Ser Lys Leu  
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 699  
 Leu His Leu Gln His Tyr Gln Thr Lys Thr Ser Ser Gln Pro His His  
 170 175 180 185  
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 747  
 His His Gly Phe Thr His Lys Ser Leu Leu Pro Asn Trp Thr Thr Lys  
 190 195 200  
 cca cac gaa gat caa caa cag ctt gaa tct ccg aca tct aca gtg tca  
 795  
 Pro His Glu Asp Gln Gln Gln Leu Glu Ser Pro Thr Ser Thr Val Ser  
 205 210 215  
 ttc tct gag atg aag gaa tca atc ccg gcg aag ata gag ttt gtc gga  
 843  
 Phe Ser Glu Met Lys Glu Ser Ile Pro Ala Lys Ile Glu Phe Val Gly  
 220 225 230  
 tca tca act ggt gtg act ctg atg aaa gaa cct gaa cac gat tgg atc  
 891  
 Ser Ser Thr Gly Val Thr Leu Met Lys Glu Pro Glu His Asp Trp Ile  
 235 240 245  
 aat tca acg atg cac gag ttt gaa act acg cag atg gga gaa gga atc  
 939  
 Asn Ser Thr Met His Glu Phe Glu Thr Thr Gln Met Gly Glu Gly Ile



250                      255                      260                      265  
 gaa gaa ggg ttc acg ggt ctc ttg ctc ggt ggt gat tca atc gac cgg  
 987  
 Glu Glu Gly Phe Thr Gly Leu Leu Leu Gly Gly Asp Ser Ile Asp Arg  
                     270                      275                      280  
 agt ttt tcc ggc gat aaa aac gag acg gcc ggc gag agt agt ggt ggt  
 1035  
 Ser Phe Ser Gly Asp Lys Asn Glu Thr Ala Gly Glu Ser Ser Gly Gly  
                     285                      290                      295  
 gac tgc aac tac tat gag gac aac aag aac tac ttg gac agc att ttc  
 1083  
 Asp Cys Asn Tyr Tyr Glu Asp Asn Lys Asn Tyr Leu Asp Ser Ile Phe  
                     300                      305                      310  
 aac ttt gta gat cct tca ccg tcg gat tca ccg atg ttc tga  
 1125  
 Asn Phe Val Asp Pro Ser Pro Ser Asp Ser Pro Met Phe  
                     315                      320                      325  
 atctaagggt tgatatttgt tgggaatggt ttgattctt ttttagttt ctagtttttg  
 1185  
 tgcttaaaact ctgattagac aatttttaaa ctaatccaat ttttgcgcta aaaaaaaaaa  
 1245  
 aaaaaaa  
 1252

<210> 312 <211> 326 <212> PRT <213> Arabidopsis thaliana <400>  
 312

Met Gly Arg Ser Pro Cys Cys Asp Lys Leu Gly Leu Lys Lys Gly Pro  
 1                      5                      10                      15

Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ala Tyr Ile Glu Glu His  
                     20                      25                      30

Gly His Gly Ser Trp Arg Ser Leu Pro Glu Lys Ala Gly Leu His Arg  
                     35                      40                      45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp  
                     50                      55                      60

Ile Lys Arg Gly Lys Phe Asn Leu Gln Glu Glu Gln Thr Ile Ile Gln  
 65                      70                      75                      80

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Ala Ile Ala Thr His Leu  
                     85                      90                      95

Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu  
                     100                      105                      110



Lys Lys Arg Leu Val Lys Met Gly Ile Asp Pro Val Thr His Lys Pro  
 115 120 125

Lys Asn Glu Thr Pro Leu Ser Ser Leu Gly Leu Ser Lys Asn Ala Ala  
 130 135 140

Ile Leu Ser His Thr Ala Gln Trp Glu Ser Ala Arg Leu Glu Ala Glu  
 145 150 155 160

Ala Arg Leu Ala Arg Glu Ser Lys Leu Leu His Leu Gln His Tyr Gln  
 165 170 175

Thr Lys Thr Ser Ser Gln Pro His His His His Gly Phe Thr His Lys  
 180 185 190

Ser Leu Leu Pro Asn Trp Thr Thr Lys Pro His Glu Asp Gln Gln Gln  
 195 200 205

Leu Glu Ser Pro Thr Ser Thr Val Ser Phe Ser Glu Met Lys Glu Ser  
 210 215 220

Ile Pro Ala Lys Ile Glu Phe Val Gly Ser Ser Thr Gly Val Thr Leu  
 225 230 235 240

Met Lys Glu Pro Glu His Asp Trp Ile Asn Ser Thr Met His Glu Phe  
 245 250 255

Glu Thr Thr Gln Met Gly Glu Gly Ile Glu Glu Gly Phe Thr Gly Leu  
 260 265 270

Leu Leu Gly Gly Asp Ser Ile Asp Arg Ser Phe Ser Gly Asp Lys Asn  
 275 280 285

Glu Thr Ala Gly Glu Ser Ser Gly Gly Asp Cys Asn Tyr Tyr Glu Asp  
 290 295 300

Asn Lys Asn Tyr Leu Asp Ser Ile Phe Asn Phe Val Asp Pro Ser Pro  
 305 310 315 320

Ser Asp Ser Pro Met Phe  
 325

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53  
Met Ser Asn Pro Thr Arg Lys Asn Met Glu Arg  
1 5 10

att aaa ggt cca tgg agt cca gaa gaa gat gat ctg ttg cag agg ctt  
101  
Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Asp Leu Leu Gln Arg Leu  
15 20 25

gtt cag aaa cat ggt ccg agg aac tgg tct ttg att agc aaa tca atc  
149  
Val Gln Lys His Gly Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile  
30 35 40

cct gga cgt tcc ggc aaa tct tgt cgt ctc cgg tgg tgt aac cag cta  
197  
Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu  
45 50 55

tct ccg gag gta gag cac cgt gct ttt tcg cag gaa gaa gac gag acg  
245  
Ser Pro Glu Val Glu His Arg Ala Phe Ser Gln Glu Glu Asp Glu Thr  
60 65 70 75

att att cga gct cac gct cgg ttt ggt aac aag tgg gct acg atc tct  
293  
Ile Ile Arg Ala His Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ser  
80 85 90

cgt ctt ctc aat gga cga acc gat aac gct atc aag aat cat tgg aac  
341  
Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn  
95 100 105

tcg acg ctg aag cga aaa tgc agc gtc gaa ggg caa agt tgt gat ttt  
389  
Ser Thr Leu Lys Arg Lys Cys Ser Val Glu Gly Gln Ser Cys Asp Phe  
110 115 120

ggt ggt aat gga ggg tat gat ggt aat tta gga gaa gag caa ccg ttg  
437  
Gly Gly Asn Gly Gly Tyr Asp Gly Asn Leu Gly Glu Glu Gln Pro Leu  
125 130 135

aaa cgt acg gcg agt ggt ggt ggt gtc tcg act ggc ttg tat atg  
485  
Lys Arg Thr Ala Ser Gly Gly Gly Gly Val Ser Thr Gly Leu Tyr Met  
140 145 150 155

agt ccc gga agt cca tcg gga tct gac gtc agc gag caa tct agt ggt  
533  
Ser Pro Gly Ser Pro Ser Gly Ser Asp Val Ser Glu Gln Ser Ser Gly  
160 165 170

ggt gca cac gtg ttt aaa cca acg gtt aga tct gag gtt aca gcg tca  
581  
Gly Ala His Val Phe Lys Pro Thr Val Arg Ser Glu Val Thr Ala Ser  
175 180 185



tcg tct ggt gaa gat cct cca act tat ctt agt ttg tct ctt cct tgg  
629

Ser Ser Gly Glu Asp Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro Trp  
190 195 200

act gac gag acg gtt cga gtc aac gag ccg gtt caa ctt aac cag aat  
677

Thr Asp Glu Thr Val Arg Val Asn Glu Pro Val Gln Leu Asn Gln Asn  
205 210 215

acg gtt atg gac ggt ggt tat acg gcg gag ctg ttt ccg gtt aga aag  
725

Thr Val Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys  
220 225 230 235

gaa gag caa gtg gaa gta gaa gaa gaa gaa gcg aag ggg ata tct ggt  
773

Glu Glu Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly  
240 245 250

gga ttc ggt ggt gag ttc atg acg gtg gtt cag gag atg ata agg acg  
821

Gly Phe Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg Thr  
255 260 265

gag gtg agg agt tac atg gcg gat tta cag cga gga aac gtc ggt ggt  
869

Glu Val Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly  
270 275 280

agt agt tct ggc ggc gga ggt ggc ggt tcg tgt atg cca caa agt gta  
917

Ser Ser Ser Gly Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val  
285 290 295

aac agc cgt cgt gtt ggg ttt aga gag ttt ata gtg aac caa atc gga  
965

Asn Ser Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly  
300 305 310 315

att ggg aag atg gag tag gcggcc

989  
Ile Gly Lys Met Glu  
320

<210> 314 <211> 320 <212> PRT <213> Arabidopsis thaliana <400>  
314

Met Ser Asn Pro Thr Arg Lys Asn Met Glu Arg Ile Lys Gly Pro Trp  
1 5 10 15

Ser Pro Glu Glu Asp Asp Leu Leu Gln Arg Leu Val Gln Lys His Gly  
20 25 30

Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly  
35 40 45



Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu  
50 55 60

His Arg Ala Phe Ser Gln Glu Glu Asp Glu Thr Ile Ile Arg Ala His  
65 70 75 80

Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ser Arg Leu Leu Asn Gly  
85 90 95

Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn Ser Thr Leu Lys Arg  
100 105 110

Lys Cys Ser Val Glu Gly Gln Ser Cys Asp Phe Gly Gly Asn Gly Gly  
115 120 125

Tyr Asp Gly Asn Leu Gly Glu Glu Gln Pro Leu Lys Arg Thr Ala Ser  
130 135 140

Gly Gly Gly Gly Val Ser Thr Gly Leu Tyr Met Ser Pro Gly Ser Pro  
145 150 155 160

Ser Gly Ser Asp Val Ser Glu Gln Ser Ser Gly Gly Ala His Val Phe  
165 170 175

Lys Pro Thr Val Arg Ser Glu Val Thr Ala Ser Ser Ser Gly Glu Asp  
180 185 190

Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro Trp Thr Asp Glu Thr Val  
195 200 205

Arg Val Asn Glu Pro Val Gln Leu Asn Gln Asn Thr Val Met Asp Gly  
210 215 220

Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys Glu Glu Gln Val Glu  
225 230 235 240

Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe Gly Gly Glu  
245 250 255

Phe Met Thr Val Val Gln Glu Met Ile Arg Thr Glu Val Arg Ser Tyr  
260 265 270

Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly Ser Ser Ser Gly Gly  
275 280 285

Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val Asn Ser Arg Arg Val



290 295 300

Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly Ile Gly Lys Met Glu  
 305 310 315 320

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 <221> CDS <222> (1)..(852) <223> G237

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 48  
 Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser  
 1 5 10 15

cct gaa gaa gac gag aag cta agg agc ttc atc ctc tct tat ggc cat  
 96  
 Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His  
 20 25 30

tct tgc tgg acc act gtt ccc atc aaa gct ggg tta caa agg aat ggg  
 144  
 Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly  
 35 40 45

aag agc tgc aga tta aga tgg att aat tac cta aga cca ggg tta aag  
 192  
 Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys  
 50 55 60

agg gat atg att agt gca gaa gaa gaa gag act atc ttg acg ttt cat  
 240  
 Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His  
 65 70 75 80

tct ccc ttg ggt aac aag tgg tgc caa ata gct aaa ttc tta ccg gga  
 288  
 Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly  
 85 90 95

aga aca gac aat gag ata aag aac tat tgg cac tct cat ttg aaa aag  
 336  
 Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys  
 100 105 110

aaa tgg ctc aag tct cag agc tta caa gat gca aaa tct att tcc cct  
 384  
 Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro  
 115 120 125

cct tcg tct tca tca tca tca ctt gtt gct tgt gga gaa aga aat ccg  
 432  
 Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro  
 130 135 140

gaa acc ttg atc tcg aat cac gtg ttc tcc ctc cag aga ctt cta gag  
 480  
 Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu  
 145 150 155 160



aac aaa tct tca tct ccc tca caa gaa agc aac gga aat aac agc cat  
 528  
 Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His  
 165 170 175  
 caa tgt tct tct gct cct gag att cca agg ctt ttc ttc tct gaa tgg  
 576  
 Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp  
 180 185 190  
 ctt tct tct tca tat ccc cac acc gat tat tcc tct gag ttt acc gac  
 624  
 Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp  
 195 200 205  
 tct aag cac agt caa gct cca aat gtc gaa gag act ctc tca gct tat  
 672  
 Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr  
 210 215 220  
 gaa gaa atg ggt gat gtt gat cag ttc cat tac aac gaa atg atg atc  
 720  
 Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile  
 225 230 235 240  
 aac aac agc aac tgg act ctt aac gac att gtg ttt ggt tcc aaa tgt  
 768  
 Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys  
 245 250 255  
 aag aag cag gag cat cat att tat aga gag gct tca gat tgt aat tct  
 816  
 Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser  
 260 265 270  
 tct gct gaa ttc ttt tct cca cca aca acg acg taa attgcgttta  
 862  
 Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr  
 275 280  
 ttgtaatgta aatcaaattt ctaaggcaaa accggaaaaa aaaaaaaaaa aaaaaaaaaa  
 920

<210> 316 <211> 283 <212> PRT <213> Arabidopsis thaliana <400>  
 316

Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser  
 1 5 10 15

Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His  
 20 25 30

Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly  
 35 40 45

Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys  
 50 55 60



Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His  
65 70 75 80

Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly  
85 90 95

Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys  
100 105 110

Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro  
115 120 125

Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro  
130 135 140

Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu  
145 150 155 160

Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His  
165 170 175

Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp  
180 185 190

Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp  
195 200 205

Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr  
210 215 220

Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile  
225 230 235 240

Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys  
245 250 255

Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser  
260 265 270

Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr  
275 280

<210> 317 <211> 723 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (1)..(723) <223> G342



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 48  
 Met Asp Val Tyr Gly Met Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp  
 1 5 10 15  
 ctt ctc gat ttc tcc aac gac gaa atc ttc tct tcc tct tcc acc gtc  
 96  
 Leu Leu Asp Phe Ser Asn Asp Glu Ile Phe Ser Ser Ser Ser Thr Val  
 20 25 30  
 act tcc tcc gcc gct tcc tcc gcc gct tct tcc gaa aac cct ttc agc  
 144  
 Thr Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Glu Asn Pro Phe Ser  
 35 40 45  
 ttt cct tct tcc acc tac act tct cct act ctc ctc acc gac ttc act  
 192  
 Phe Pro Ser Ser Thr Tyr Thr Ser Pro Thr Leu Leu Thr Asp Phe Thr  
 50 55 60  
 cac gat ctc tgc gtt ccc agt gac gac gca gct cat ctc gaa tgg tta  
 240  
 His Asp Leu Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu Trp Leu  
 65 70 75 80  
 tcg cga ttc gtt gac gat tca ttc tcc gat ttc cca gca aat cct tta  
 288  
 Ser Arg Phe Val Asp Asp Ser Phe Ser Asp Phe Pro Ala Asn Pro Leu  
 85 90 95  
 acc atg acc gtt aga ccc gag att tca ttc acc gga aaa cct aga agt  
 336  
 Thr Met Thr Val Arg Pro Glu Ile Ser Phe Thr Gly Lys Pro Arg Ser  
 100 105 110  
 cgc cga tca aga gca cca gca cct tcc gta gct gga act tgg gct ccg  
 384  
 Arg Arg Ser Arg Ala Pro Ala Pro Ser Val Ala Gly Thr Trp Ala Pro  
 115 120 125  
 atg tct gaa tca gag ctt tgt cac tcc gtc gct aaa cct aaa ccg aag  
 432  
 Met Ser Glu Ser Glu Leu Cys His Ser Val Ala Lys Pro Lys Pro Lys  
 130 135 140  
 aaa gtc tac aac gct gaa tcg gtt acg gcg gat gga gcg agg cgg tgc  
 480  
 Lys Val Tyr Asn Ala Glu Ser Val Thr Ala Asp Gly Ala Arg Arg Cys  
 145 150 155 160  
 acg cac tgt gcc tcg gag aaa acg cca cag tgg aga act gga ccg ctt  
 528  
 Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp Arg Thr Gly Pro Leu  
 165 170 175  
 gga cct aaa aca ctt tgt aac gct tgt gga gtt cgt tac aaa tca ggg  
 576  
 Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg Tyr Lys Ser Gly  
 180 185 190



agg ctt gta ccg gaa tac aga ccg gcg tcg agt ccg acg ttt gta ttg  
624

Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro Thr Phe Val Leu  
195 200 205

act cag cat tcg aac tct cat cgg aaa gtt atg gag ctc cgg cga cag  
672

Thr Gln His Ser Asn Ser His Arg Lys Val Met Glu Leu Arg Arg Gln  
210 215 220

aag gaa caa caa gaa tct tgc gtt cga att ccg ccg ttt cag ccg cag  
720

Lys Glu Gln Gln Glu Ser Cys Val Arg Ile Pro Pro Phe Gln Pro Gln  
225 230 235 240

taa  
723

<210> 318 <211> 240 <212> PRT <213> Arabidopsis thaliana <400>  
318

Met Asp Val Tyr Gly Met Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp  
1 5 10 15

Leu Leu Asp Phe Ser Asn Asp Glu Ile Phe Ser Ser Ser Ser Thr Val  
20 25 30

Thr Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Glu Asn Pro Phe Ser  
35 40 45

Phe Pro Ser Ser Thr Tyr Thr Ser Pro Thr Leu Leu Thr Asp Phe Thr  
50 55 60

His Asp Leu Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu Trp Leu  
65 70 75 80

Ser Arg Phe Val Asp Asp Ser Phe Ser Asp Phe Pro Ala Asn Pro Leu  
85 90 95

Thr Met Thr Val Arg Pro Glu Ile Ser Phe Thr Gly Lys Pro Arg Ser  
100 105 110

Arg Arg Ser Arg Ala Pro Ala Pro Ser Val Ala Gly Thr Trp Ala Pro  
115 120 125

Met Ser Glu Ser Glu Leu Cys His Ser Val Ala Lys Pro Lys Pro Lys  
130 135 140

Lys Val Tyr Asn Ala Glu Ser Val Thr Ala Asp Gly Ala Arg Arg Cys  
145 150 155 160



Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp Arg Thr Gly Pro Leu  
165 170 175

Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg Tyr Lys Ser Gly  
180 185 190

Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro Thr Phe Val Leu  
195 200 205

Thr Gln His Ser Asn Ser His Arg Lys Val Met Glu Leu Arg Arg Gln  
210 215 220

Lys Glu Gln Gln Glu Ser Cys Val Arg Ile Pro Pro Phe Gln Pro Gln  
225 230 235 240

<210> 319 <211> 932 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (43)..(759) <223> G350

<400> 319  
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54

Met Ala Leu Glu  
1

act ctt act tct cca aga tta tct tct ccg atg ccg act ctg ttt caa  
102

Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro Thr Leu Phe Gln  
5 10 15 20

gat tca gca cta ggg ttt cat gga agc aaa ggc aaa cga tct aag cga  
150

Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys Arg Ser Lys Arg  
25 30 35

tca aga tct gaa ttc gac cgt cag agt ctc acg gag gat gaa tat atc  
198

Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu Asp Glu Tyr Ile  
40 45 50

gct tta tgt ctc atg ctt ctt gct cgc gac gga gat aga aac cgt gac  
246

Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp Arg Asn Arg Asp  
55 60 65

ctt gac ctg cct tct tct tcg tct tca cct cct ctg ctt cct cct ctt  
294

Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu Leu Pro Pro Leu  
70 75 80

cct act ccg atc tac aag tgt agc gtc tgt gac aag gcg ttt tcg tct  
342

Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys Ala Phe Ser Ser  
85 90 95 100



tac cag gct ctt ggt gga cac aag gca agt cac cgg aaa agc ttt tcg  
 390  
 Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Ser Phe Ser  
                   105                                  110                                  115

ctt act caa tct gcc gga gga gat gag ctg tcg aca tcg tcg gcg ata  
 438  
 Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr Ser Ser Ala Ile  
                   120                                  125                                  130

acc acg tct ggt ata tcc ggt ggc ggg gga gga agt gtg aag tcg cac  
 486  
 Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Gly Ser Val Lys Ser His  
                   135                                  140                                  145

gtt tgc tct atc tgt cat aaa tcg ttc gcc acc ggt caa gct ctc ggc  
 534  
 Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly Gln Ala Leu Gly  
                   150                                  155                                  160

ggc cac aaa cgg tgc cac tac gaa gga aag aac gga ggc ggt gtg agt  
 582  
 Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly Gly Gly Val Ser  
                   165                                  170                                  175                                  180

agt agc gtg tcg aat tct gaa gat gtg ggg tct aca agc cac gtc agc  
 630  
 Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr Ser His Val Ser  
                   185                                  190                                  195

agt ggc cac cgt ggg ttt gac ctc aac ata ccg ccg ata ccg gaa ttc  
 678  
 Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro Ile Pro Glu Phe  
                   200                                  205                                  210

tcg atg gtc aac gga gac gaa gag gtg atg agt cct atg ccg gcg aag  
 726  
 Ser Met Val Asn Gly Asp Glu Glu Val Met Ser Pro Met Pro Ala Lys  
                   215                                  220                                  225

aaa ctc cgg ttt gac ttc ccg gag aaa ccc taa acataaacct aggaaaaact  
 779  
 Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro  
                   230                                  235

ttacagaatt cattttatag gaaattgttt tactgtatat acaaatatcg attttgattg  
 839

atgtttcttct tcaactgaaaa attatgattc ttgtttgtat aattgatgtt tctgaaaaag  
 899

atataacttt ttattaaaaa aaaaaaaaaa aaa  
 932

<210> 320 <211> 238 <212> PRT <213> Arabidopsis thaliana <400>  
 320

Met Ala Leu Glu Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro  
                   1                                  5                                  10                                  15



Thr Leu Phe Gln Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys  
20 25 30

Arg Ser Lys Arg Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu  
35 40 45

Asp Glu Tyr Ile Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp  
50 55 60

Arg Asn Arg Asp Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu  
65 70 75 80

Leu Pro Pro Leu Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys  
85 90 95

Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg  
100 105 110

Lys Ser Phe Ser Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr  
115 120 125

Ser Ser Ala Ile Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Ser  
130 135 140

Val Lys Ser His Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly  
145 150 155 160

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 Lys Pro Arg Thr Ser Pro Ser Glu Phe Ile Val Pro Phe Asp Gln Tyr  
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 1008  
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 325 330 335

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 340 345 350

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 Arg Ser Leu Lys Val Arg Trp Asp Glu Thr Ser Ser Ile Pro Arg Pro  
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 1200  
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 405 410 415

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 1296  
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1680  
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545 550 555 560

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 675 680 685

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Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu  
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Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu  
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Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Pro Arg Phe Gln  
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Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His  
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195 200 205

Leu His Ala Asn Glu Trp Arg Phe Arg His Ile Phe Arg Gly Gln Pro  
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Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn  
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Val Asp Leu Asn Thr Met Lys Pro Leu Phe Val Leu Pro Pro Lys Ile  
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Val His Ser Phe Ser Lys Val Leu Thr Ala Ser Asp Thr Ser Thr His  
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130 135 140



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Val His Gly Tyr Gln Trp Lys Phe Lys His Ile Phe Arg Gly Gln Pro  
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 370 375 380

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 Cys Asn Met Val Lys Arg Ile Phe Ile Trp Ser Lys Glu Glu Val Lys  
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 176

Met Asp Gln  
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 368  
 Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala Gly Lys Asp  
 55 60 65

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 416  
 Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly Gly Gly Gly  
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 85 90 95

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 135 140 145



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 1261



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85 90 95

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser  
100 105 110

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130 135 140

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165 170 175

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180 185 190



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 195 200 205

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Val Val Ile Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu  
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 172

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 268

Arg Lys Val Ser Gly Lys Arg Ser Asp Asp Glu Ser Glu Ile Cys Ala  
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Ile Asp Leu Leu Ala Ser Leu Ala Gly Lys Leu Leu Glu Glu Ser Glu



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460
Pro Cys Lys Ser Glu Phe Phe Asp Pro Gly Asn Pro Ala Ser Lys Ser
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Thr Ser Glu Asn Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu
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556
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Ser Gly Leu Lys Ser Leu Val Gly Ser Ile Thr Glu Glu Thr Cys Val
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Val Asn Glu Asp Ala Gly Ser Glu Gln Gly Ala Asn Thr Phe Ser Leu
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700
Lys Asp Pro Ser Gln Leu His Ser Gln Ser Pro Glu Ser Val Leu Leu
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796
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Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu Asn Asp Cys Ile  
115 120 125

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130 135 140

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 370 375 380  
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 385 390 395 400  
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346  
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586  
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165 170 175



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 1066  
 Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser, Leu Ile  
 325 330 335  
 aga cca ttt cat cat ttg atg agc tcg aat cat gat acg gat cat cat  
 1114  
 Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His  
 340 345 350  
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 1161  
 Ser Ser Asp Asn Glu Ser Asp Ser  
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Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys  
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Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg  
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Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp  
85 90 95

Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu  
100 105 110

Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His  
115 120 125

Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe  
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Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn  
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Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg  
165 170 175

Ala Arg Leu Thr Asp Thr Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu  
180 185 190

Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His  
195 200 205



Gln Gly Phe Asn Thr Asn His Gln Gln Gln Phe Pro Leu Thr Asn Pro  
 210 215 220

Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser  
 225 230 235 240

Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala  
 245 250 255

Ala Asn Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ser Ala  
 260 265 270

Gly Asp Gly Ser Gln Leu Phe Phe Gly Pro Thr Pro Pro Ala Met Ser  
 275 280 285

Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His  
 290 295 300

His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser  
 305 310 315 320

Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile  
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 96

Asn Arg Leu Ser Gly Leu Pro Asp Gln Pro Ser Ser His Ser Phe Thr  
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ccg gta aca cta tac gac ggt ttc aat tac aat ctc tcc tcc gat cat  
 144

Pro Val Thr Leu Tyr Asp Gly Phe Asn Tyr Asn Leu Ser Ser Asp His  
 35 40 45



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 65 70 75 80  
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 Val Leu Gly Tyr Ile Ser Gln Met Leu Asn Glu Glu Asp Met Asp Asp  
 85 90 95  
 aaa gtc tgc atg ctt caa gag tct cta gat ctc gaa gct gct gag aga  
 336  
 Lys Val Cys Met Leu Gln Glu Ser Leu Asp Leu Glu Ala Ala Glu Arg  
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 384  
 Ser Leu Tyr Glu Ala Ile Gly Lys Lys Tyr Pro Pro Ser Pro Glu Arg  
 115 120 125  
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 576  
 Ser Cys Ser Ser Ile Leu Ser Val Pro Gln Ser Asn Gly Leu Ile Thr  
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 624  
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 720  
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598



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 1344  
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cgg gtt gaa gaa act ggt caa agg tta gca gcg tat gcc aaa ctg ttt  
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 500 505 510

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 Gly Val Pro Phe Glu Tyr Lys Ala Ile Ala Lys Lys Trp Asp Ala Ile  
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caa ctt gaa gat ctt gat atc gac agg gat gag att act gtt gtt aat  
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tgc ctg tac cgg gct gag aat ttg cat gat gag tca gtc aaa gta gaa  
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 Cys Leu Tyr Arg Ala Glu Asn Leu His Asp Glu Ser Val Lys Val Glu  
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 565 570 575

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 595 600 605

atg ctt gag aca att gtg cca cga gaa gac gaa gag agg atg ttc ctt  
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 Met Leu Glu Thr Ile Val Pro Arg Glu Asp Glu Glu Arg Met Phe Leu  
 610 615 620



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 1920  
 Glu Met Glu Val Phe Gly Arg Glu Ala Leu Asn Val Ile Ala Cys Glu  
 625 630 635 640  
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 1968  
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 Arg Ala Met Arg Ser Gly Leu Val Gln Val Pro Phe Asp Pro Ser Ile  
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 2112  
 Val Ile Asp Gln Asp Asn Arg Trp Leu Leu Gln Gly Trp Lys Gly Arg  
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 35 40 45  
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 65 70 75 80  
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 85 90 95  
 Lys Val Cys Met Leu Gln Glu Ser Leu Asp Leu Glu Ala Ala Glu Arg  
 100 105 110



Ser Leu Tyr Glu Ala Ile Gly Lys Lys Tyr Pro Pro Ser Pro Glu Arg  
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 130 135 140  
 Pro Gly Asn Tyr Thr Gly Gly Asp Cys Ile Gly Phe Gly Asn Gly Gly  
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 Ser Cys Ser Ser Ile Leu Ser Val Pro Gln Ser Asn Gly Leu Ile Thr  
 180 185 190  
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 195 200 205  
 His Gln Ser Val Trp Leu Phe Arg Arg Glu Ile Glu Glu Ala Asn Arg  
 210 215 220  
 Phe Asn Pro Glu Glu Asn Glu Leu Ile Val Asn Phe Arg Glu Glu Asn  
 225 230 235 240  
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 245 250 255  
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 260 265 270  
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 275 280 285  
 Glu Ser Met Lys Glu Phe Asn Ala Leu Arg Asp Val Leu Lys Lys Gly  
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 305 310 315 320  
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 325 330 335  
 Gly Lys Lys Glu Val Val Asp Leu Arg Ser Leu Leu Ile His Cys Ala  
 340 345 350



Gln Ala Val Ala Ala Asp Asp Arg Arg Cys Ala Gly Gln Leu Leu Lys  
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 Ala His Cys Phe Ala Asn Gly Leu Glu Ala Arg Leu Ala Gly Thr Gly  
 385 390 395 400  
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 405 410 415  
 Val Leu Lys Ala His Gln Leu Phe Leu Ala Cys Cys Pro Phe Arg Lys  
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 Cys Leu Tyr Arg Ala Glu Asn Leu His Asp Glu Ser Val Lys Val Glu  
 545 550 555 560  
 Ser Cys Arg Asp Thr Val Leu Asn Leu Ile Gly Lys Ile Asn Pro Asp  
 565 570 575  
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 580 585 590  
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 602



595                      600                      605  
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     610                      615                      620  
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     625                      630                      635                      640  
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 Arg Ala Met Arg Ser Gly Leu Val Gln Val Pro Phe Asp Pro Ser Ile  
                     660                      665                      670  
 Met Lys Thr Ser Leu His Lys Val His Thr Phe Tyr His Lys Asp Phe  
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 Val Ile Asp Gln Asp Asn Arg Trp Leu Leu Gln Gly Trp Lys Gly Arg  
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 96  
 Lys Lys Gly Leu Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr  
                     20                      25                      30  
 gtc aaa gct cat ggc aaa ggt cac tgg aat cgt att gcc aaa aag act  
 144  
 Val Lys Ala His Gly Lys Gly His Trp Asn Arg Ile Ala Lys Lys Thr  
                     35                      40                      45  
 ggt tta aag aga tgt gga aag agt tgt aga ttg agg tgg atg aat tat  
 192  
 Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr  
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 ctc agc cct aat gtg aaa aga ggc aat ttc acc gag caa gaa gag gat  
 240  
 Leu Ser Pro Asn Val Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Asp  
     65                      70                      75                      80



ctt atc att agg ctc cac aag ttg ctt ggt aat agg tgg tct tta att  
 288  
 Leu Ile Ile Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile  
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gct aaa aga gtg ccg ggt cga acg gat aat caa gtg aag aac tat tgg  
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 Ala Lys Arg Val Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp  
                   100                                  105                                  110

aac acg cat ctt agt aag aaa ctc gga atc aaa gat cag aaa acc aaa  
 384  
 Asn Thr His Leu Ser Lys Lys Leu Gly Ile Lys Asp Gln Lys Thr Lys  
                   115                                  120                                  125

cag agc aat ggt gat att gtt tat caa atc aat ctc ccg aat cct acc  
 432  
 Gln Ser Asn Gly Asp Ile Val Tyr Gln Ile Asn Leu Pro Asn Pro Thr  
                   130                                  135                                  140

gaa aca tca gaa gaa acg aaa atc tcg aat att gtc gat aac aat aat  
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 Glu Thr Ser Glu Glu Thr Lys Ile Ser Asn Ile Val Asp Asn Asn Asn  
                   145                                  150                                  155                                  160

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Val Lys Ala His Gly Lys Gly His Trp Asn Arg Ile Ala Lys Lys Thr  
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Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr  
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Leu Ser Pro Asn Val Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Asp



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			100					105					110					
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96
Pro Pro Pro Gly Thr Thr Ile Ser Ala Ala Gly Gly Gly Ala Ser
20      25      30
tac cac cac ctt ctc caa caa caa caa caa cag ctc caa cta ttc tgg
144
Tyr His His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Leu Phe Trp
35      40      45
acc tac caa cgc caa gag atc gaa caa gtt aac gat ttc aaa aac cat
192
Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His
50      55      60
cag ctt cca cta gct agg ata aaa aag atc atg aaa gcc gat gaa gat
240

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Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp  
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 85 90 95  
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 336  
 Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu  
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 130 135 140  
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 576  
 Ala Gly Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Asn  
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 624  
 Gly Val Tyr Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln  
 195 200 205  
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 672  
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   145                  150                  155                  160  
 Pro Thr Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro  
                   165                  170                  175  
 Ala Gly Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Asn  
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 Gly Val Tyr Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln  
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 Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg  
 85                      90                      95  
 Asp Lys Ala Ile Tyr Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr  
 100                      105                      110



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Met Val Ser

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Phe Ser Asp Gln Asn Pro Thr Phe Pro Trp Gln Ile Asp Gly Ser Ala  
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Thr Val Ser Val Glu Val Asp Gly Phe Leu Cys Asp Ala Asp Val Ile  
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Ser Asn Ser Lys Ala Cys Arg Glu Lys Gln Arg Arg Asp Arg Leu Asn  
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Gln Glu Lys Ile Lys Glu Leu Lys Asp Glu Lys Asn Glu Leu Arg Asp  
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Glu Lys Gln Lys Leu Lys Val Glu Lys Glu Arg Ile Asp Gln Gln Leu  
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Asp Val Ile Lys Glu Pro Ser Ser Arg Lys Arg Ile Lys Thr Glu Ser  
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Cys Thr Gly Ser Asn Ser Lys Ala Cys Arg Glu Lys Gln Arg Arg Asp  
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Arg Thr Pro Lys Thr Asp Lys Val Ala Ile Ile Asn Asp Ala Ile Arg  
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Gly Phe Thr Arg Pro Asn Ser Thr Lys Asp Leu Asp Phe Asp Ala His	60	65	70
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Pro Ser Cys Ala Ala Ala Leu Ser Glu His Thr Pro Cys Glu Asp Ala	90	95	100
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Lys Arg Ser Leu Lys Phe Ser Arg Glu Arg Leu Glu Tyr Arg Gln Arg	105	110	115
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His Cys Pro Glu Arg Glu Glu Ile Leu Lys Cys Arg Ile Pro Ala Pro	120	125	130
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Tyr Gly Tyr Lys Thr Pro Phe Arg Trp Pro Ala Ser Arg Asp Val Ala	140	145	150
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Trp Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn	155	160	165
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Gln Asn Trp Val Arg Tyr Glu Asn Asp Arg Phe Trp Phe Pro Gly Gly	170	175	180
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Gly Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Asp Ile Gly	185	190	195
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Arg Leu Ile Asp Leu Ser Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr	200	205	210
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784			
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Thr Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln	235	240	245



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1755

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1947

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35 40 45

Ser Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser  
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Val Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn  
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Lys Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly  
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Glu Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn  
115 120 125

Gln Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met  
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Gln Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln



165                      170                      175  
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 922  
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 1546  
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 485 490 495



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 Gln Met Gln Leu Val Ala Val Met Arg Gln Gln Glu Asp His His His  
 145 150 155 160



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 195 200 205

Ser Leu Leu Glu Lys Ser Ser Ser Arg Gln Asn Gly Lys Arg Val Leu  
 210 215 220

Val Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Gly Trp Arg Asn Pro  
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Gly Ser Glu Asn Ala Ser Ser Lys Val Ile Glu Gln Ala Ala Ala Glu  
 260 265 270

Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala  
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 305 310 315 320

Val Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg  
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 340 345 350

Pro Ala Ala Met Asn Met Ala Ser Thr Thr Thr Ala Ala Ala Ser Met  
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Leu Leu Ser Gly Ser Thr Met Ser Asn Gln Asp Gly Leu Met Asn Pro  
 370 375 380

Thr Asn Leu Leu Ala Arg Thr Ile Leu Pro Cys Ser Ser Ser Met Ala  
 385 390 395 400



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 405 410 415  
 Glu Ser Pro Asn Gly Asn Asn Pro Thr Asn Asn Pro Leu Met Gln Phe  
 420 425 430  
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 465 470 475 480  
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624

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Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys  
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816

Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val  
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 1392  
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1440

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1488

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485 490 495

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1536

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1728

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Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg  
50 55 60

Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys



[illegible]



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370 375 380

Arg Lys Arg Lys Gln Asn Asn Asp Met Asn Val Met Val Met Asp Arg  
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Ser Ala Gly Tyr Thr Cys Glu Asn Gly Gln Cys Pro His Ser Lys Met  
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Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His  
435 440 445

Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile  
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Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr  
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485 490 495

Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala  
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 120

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 178

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 Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu  
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 Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg  
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 418  
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 562  
 Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr  
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 610  
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 658  
 Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn  
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atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat  
 706  
 Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His  
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 210 215 220

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 435 440 445

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1762

His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe  
515 520 525

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Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser  
530 535 540

aac aat caa acg ttt ttt caa ggg aac aac aac aac aac aat gtg ttt  
1858

Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe  
545 550 555 560

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1906

Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn  
565 570 575

aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca  
1954

Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr  
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2002

Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro  
595 600 605

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2050

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610 615 620

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2105

Ser Ile Trp Phe  
625

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2165

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[illegible]



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Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu  
 305 310 315 320

Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser  
 325 330 335

His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser  
 340 345 350

Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu  
 355 360 365

Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg  
 370 375 380

Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu  
 385 390 395 400

Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser  
 405 410 415

Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro  
 420 425 430

Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val  
 435 440 445

Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile  
 450 455 460

Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu  
 465 470 475 480

Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met  
 485 490 495

Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn  
 500 505 510



His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe  
515 520 525

Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser  
530 535 540

Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe  
545 550 555 560

Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn  
565 570 575

Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr  
580 585 590

Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro  
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110

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158

Ile Gln Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro Thr  
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206

Cys Gly Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro  
35 40 45

ctt gat act atc act act act act act act gtt tgt ttt gcg gct cct  
254

Leu Asp Thr Ile Thr Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro  
50 55 60



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 494  
 Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu  
 130 135 140  
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 Ala Ala His Ile Arg Cys Ala Ala Ala Ala Ala Ala Ala Thr Arg Gly  
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 638  
 Ala Ala Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val  
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 686  
 Tyr Asp Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu  
 195 200 205  
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 Asn Ser Asp Gly Glu Ser Leu Trp Ser Tyr  
 240 245



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35 40 45

Thr Ile Thr Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro Ser Ser  
50 55 60

Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Thr Asp Thr Asp  
65 70 75 80

Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile Arg Cys Arg  
85 90 95

Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr Thr Arg  
100 105 110

Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Tyr  
115 120 125

Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu Asn Phe  
130 135 140

Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Leu Ser Ser Ser Ala Ala  
145 150 155 160

His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg Gly Ala Ala  
165 170 175

Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val Tyr Asp  
180 185 190



Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu Leu Leu  
 195 200 205

Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met Val Ala  
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 146

Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser  
 35 40 45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag  
 194

Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu  
 50 55 60

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 242

Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro  
 65 70 75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg  
 290

Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp  
 80 85 90 95

ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc  
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Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile  
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 386

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 115 120 125



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 Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg  
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 225 230 235  
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 260 265 270  
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 290 295 300  
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 305 310 315



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 320 325 330 335  
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 35 40 45

Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser  
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Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn  
 65 70 75 80

Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu  
 85 90 95

Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala  
 100 105 110

Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln  
 115 120 125

Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys



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 Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn  
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 Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro  
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 225                      230                      235                      240  
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 245                      250                      255  
 Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser  
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 Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe  
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 Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val  
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 Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile  
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 Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val  
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cgt cac ttg cta gga gga gga gga gag aac gag ctg cga ctc aat gag  
153  
Arg His Leu Leu Gly Gly Gly Gly Glu Asn Glu Leu Arg Leu Asn Glu  
20 25 30  
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201  
Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu Pro Leu  
35 40 45 50  
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249  
Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu Lys Asp  
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297  
Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu Phe Asp  
70 75 80  
ttt ccg gcg gtt aaa gtc gag cca act gag aac ttt acg gcg atg gag  
345  
Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala Met Glu  
85 90 95  
gag aaa cca aag aaa gcg ata ccg gtt acg gag acg gca gtg aag gcg  
393  
Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val Lys Ala  
100 105 110  
aag cat tac aga gga gtg agg cag aga ccg tgg ggg aaa ttc gcg gcg  
441  
Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala Ala  
115 120 125 130  
gag ata cgt gat ccg gcg aag aat gga gct agg gtt tgg tta ggg acg  
489  
Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly Thr  
135 140 145  
ttt gag acg gcg gaa gat gcg gct tta gct tac gat ata gct gct ttt  
537  
Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala Ala Phe  
150 155 160  
agg atg cgt ggt tcc cgc gct tta ttg aat ttt ccg ttg agg gtt aat  
585  
Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val Asn  
165 170 175



tcc ggt gaa cct gac ccg gtt cgg atc acg tct aag aga tct tct tcg  
633

Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser Ser Ser  
180 185 190

tcg tcg tcg tcg tcg tcc tct tct acg tcg tcg tct gaa aac ggg aag  
681

Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn Gly Lys  
195 200 205 210

ttg aaa cga agg aga aaa gca gag aat ctg acg tcg gag gtg gtg cag  
729

Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val Val Gln  
215 220 225

gtg aag tgt gag gtt ggt gat gag aca cgt gtt gat gag tta ttg gtt  
777

Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu Leu Val  
230 235 240

tca taa gtttgatctt gtgtgttttg tagttgaata gttttgctat aaatgttgag  
833

Ser

gcaccaagta aaagtgttcc cgtgatgtaa attagttact aaacagagcc atatattctc  
893

aatcaaaaaa aaaaaaaaaa  
913

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Ile Thr Arg His Leu Leu Gly Gly Gly Glu Asn Glu Leu Arg Leu  
20 25 30

Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu  
35 40 45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu  
50 55 60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu  
65 70 75 80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala  
85 90 95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val



100                      105                      110  
 Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe  
           115                      120                      125  
 Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu  
           130                      135                      140  
 Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala  
 145                      150                      155                      160  
 Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg  
                          165                      170                      175  
 Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser  
                          180                      185                      190  
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn  
           195                      200                      205  
 Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val  
           210                      215                      220  
 Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu  
 225                      230                      235                      240  
 Leu Val Ser

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cttca atg gca caa ctc cct cct aaa atc ccc aac atg aca caa cat tgg  
 110

Met Ala Gln Leu Pro Pro Lys Ile Pro Asn Met Thr Gln His Trp  
   1                          5                          10                          15

cct gat ttc tct tcc caa aag ctc tct cct ttc tct acc cca acc gca  
 158

Pro Asp Phe Ser Ser Gln Lys Leu Ser Pro Phe Ser Thr Pro Thr Ala  
                           20                          25                          30

acc gct gtc gcc acc gct aca acc acc gta caa aac ccc tca tgg gtc  
 206

Thr Ala Val Ala Thr Ala Thr Thr Thr Val Gln Asn Pro Ser Trp Val  
           35                          40                          45



gac gaa ttc ctc gac ttc tca gcg tct cgc cgt ggc aac cac cgt cgt  
 254  
 Asp Glu Phe Leu Asp Phe Ser Ala Ser Arg Arg Gly Asn His Arg Arg  
 50 55 60  
 tcc atc agc gac tct atc gca ttc ctc gaa gct cca aca gtc agc atc  
 302  
 Ser Ile Ser Asp Ser Ile Ala Phe Leu Glu Ala Pro Thr Val Ser Ile  
 65 70 75  
 gaa gac cac caa ttc gac agg ttc gat gac gaa cag ttc atg tcg atg  
 350  
 Glu Asp His Gln Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met  
 80 85 90 95  
 ttc acc gac gac gac aac ctt cat agc aat cct tcc cat atc aac aac  
 398  
 Phe Thr Asp Asp Asp Asn Leu His Ser Asn Pro Ser His Ile Asn Asn  
 100 105 110  
 aaa aat aac aat gtg ggg ccc acg gga tct tcc tcg aac aca tcc acg  
 446  
 Lys Asn Asn Asn Val Gly Pro Thr Gly Ser Ser Ser Asn Thr Ser Thr  
 115 120 125  
 ccg tcc aat agc ttc aac gac gat aac aaa gaa tta cca ccg tcc gat  
 494  
 Pro Ser Asn Ser Phe Asn Asp Asp Asn Lys Glu Leu Pro Pro Ser Asp  
 130 135 140  
 cat aac atg aac aat aat atc aac aac aac tat aac gat gaa gtc caa  
 542  
 His Asn Met Asn Asn Asn Ile Asn Asn Asn Tyr Asn Asp Glu Val Gln  
 145 150 155  
 agc caa tgc aag atg gag cca gaa gat ggt acg gcg tcg aat aac aat  
 590  
 Ser Gln Cys Lys Met Glu Pro Glu Asp Gly Thr Ala Ser Asn Asn Asn  
 160 165 170 175  
 tcc ggt gat agc tcc ggc aac cgg att ctc gat ccc aaa agg gtt aag  
 638  
 Ser Gly Asp Ser Ser Gly Asn Arg Ile Leu Asp Pro Lys Arg Val Lys  
 180 185 190  
 aga ata tta gca aat cgg caa tca gca cag aga tca agg gtg agg aaa  
 686  
 Arg Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys  
 195 200 205  
 ctg caa tac ata tca gag ctc gaa cgt agc gtc act tcg ttg cag gcg  
 734  
 Leu Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Ala  
 210 215 220  
 gaa gtg tca gtg tta tcg cca aga gtt gca ttc ttg gat cat caa cgt  
 782  
 Glu Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg  
 225 230 235



tta ctt ctt aac gtt gac aac agc gct ctc aag caa cga atc gct gct  
830

Leu Leu Leu Asn Val Asp Asn Ser Ala Leu Lys Gln Arg Ile Ala Ala  
240 245 250 255

tta tct caa gac aag ctt ttc aaa gac gca cat caa gaa gca ttg aag  
878

Leu Ser Gln Asp Lys Leu Phe Lys Asp Ala His Gln Glu Ala Leu Lys  
260 265 270

aga gaa ata gag aga ctt cga caa gtg tat aat caa caa agc ctc acg  
926

Arg Glu Ile Glu Arg Leu Arg Gln Val Tyr Asn Gln Gln Ser Leu Thr  
275 280 285

aat gtg gaa aat gca aat cat tta tcg gcg acc gga gcc ggt gct act  
974

Asn Val Glu Asn Ala Asn His Leu Ser Ala Thr Gly Ala Gly Ala Thr  
290 295 300

ccg gcc gtc gac atc aag tcg tcc gtt gaa aca gag cag ctc ctc aat  
1022

Pro Ala Val Asp Ile Lys Ser Ser Val Glu Thr Glu Gln Leu Leu Asn  
305 310 315

gtc tca taa attaaccatc atgcatcatc atcaacattt ctctctttta  
1071

Val Ser  
320

gcttcttggc aaaagttctt gactataaaa tctcttttcgg gtaagaaatt caggagatat  
1131

acattttttta ttctaatacac attgtttttta agttgtgatg aattcagttt gatgtatctt  
1191

atattttttg tttatgtcgt ctttttttct tgggggttgat ggaagggaat catcaattgt  
1251

tgtttgatca aagaactagt tgaatttttt tttttttttt  
1291

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366

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Asp Phe Ser Ser Gln Lys Leu Ser Pro Phe Ser Thr Pro Thr Ala Thr  
20 25 30

Ala Val Ala Thr Ala Thr Thr Thr Val Gln Asn Pro Ser Trp Val Asp  
35 40 45

Glu Phe Leu Asp Phe Ser Ala Ser Arg Arg Gly Asn His Arg Arg Ser  
50 55 60



Ile Ser Asp Ser Ile Ala Phe Leu Glu Ala Pro Thr Val Ser Ile Glu  
 65 70 75 80

Asp His Gln Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met Phe  
 85 90 95

Thr Asp Asp Asp Asn Leu His Ser Asn Pro Ser His Ile Asn Asn Lys  
 100 105 110

Asn Asn Asn Val Gly Pro Thr Gly Ser Ser Ser Asn Thr Ser Thr Pro  
 115 120 125

Ser Asn Ser Phe Asn Asp Asp Asn Lys Glu Leu Pro Pro Ser Asp His  
 130 135 140

Asn Met Asn Asn Asn Ile Asn Asn Asn Tyr Asn Asp Glu Val Gln Ser  
 145 150 155 160

Gln Cys Lys Met Glu Pro Glu Asp Gly Thr Ala Ser Asn Asn Asn Ser  
 165 170 175

Gly Asp Ser Ser Gly Asn Arg Ile Leu Asp Pro Lys Arg Val Lys Arg  
 180 185 190

Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys Leu  
 195 200 205

Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Ala Glu  
 210 215 220

Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg Leu  
 225 230 235 240

Leu Leu Asn Val Asp Asn Ser Ala Leu Lys Gln Arg Ile Ala Ala Leu  
 245 250 255

Ser Gln Asp Lys Leu Phe Lys Asp Ala His Gln Glu Ala Leu Lys Arg  
 260 265 270

Glu Ile Glu Arg Leu Arg Gln Val Tyr Asn Gln Gln Ser Leu Thr Asn  
 275 280 285

Val Glu Asn Ala Asn His Leu Ser Ala Thr Gly Ala Gly Ala Thr Pro  
 290 295 300



Ala Val Asp Ile Lys Ser Ser Val Glu Thr Glu Gln Leu Leu Asn Val  
 305 310 315 320

Ser

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tttcaataaa atagaaaaaa acatatacaa atctacagag aagagaagct ttattttaat  
 120

cttgtgtgtg tgtgtgtgtt ttatataatt tttatttttt ttcaaattaa aatctcttct  
 180

ttgcttttga tgtgggc atg gct ggt ctt gat cta ggc aca gct ttt cgt  
 230

Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg  
 1 5 10

tac gtt aat cac cag ctc cat cgt ccc gat ctc cac ctt cac cac aat  
 278

Tyr Val Asn His Gln Leu His Arg Pro Asp Leu His Leu His His Asn  
 15 20 25

tcc tcc tcc gat gac gtc act ccc gga gcc ggg atg ggt cat ttc acc  
 326

Ser Ser Ser Asp Asp Val Thr Pro Gly Ala Gly Met Gly His Phe Thr  
 30 35 40

gtc gac gac gaa gac aac aac aac aac cat caa ggt ctt gac tta gcc  
 374

Val Asp Asp Glu Asp Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala  
 45 50 55

tct ggt gga gga tca gga agc tct gga gga gga gga ggt cac ggc ggg  
 422

Ser Gly Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly  
 60 65 70 75

gga gga gac gtc gtt ggt cgt cgt cca cgt ggc aga cca ccg gga tcc  
 470

Gly Gly Asp Val Val Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser  
 80 85 90

aag aac aaa ccg aaa cct ccg gta att atc acg cgc gag agc gca aac  
 518

Lys Asn Lys Pro Lys Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn  
 95 100 105

act cta aga gct cac att ctt gaa gta aca aac ggc tgc gat gtt ttc  
 566

Thr Leu Arg Ala His Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe  
 110 115 120



gac tgc gtt gcg act tat gct cgt cgg aga cag cga ggg atc tgc gtt  
 614  
 Asp Cys Val Ala Thr Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val  
 125 130 135  
 ctg agc ggt agc gga acg gtc acg aac gtc agc ata cgt cag cca tct  
 662  
 Leu Ser Gly Ser Gly Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser  
 140 145 150 155  
 gcg gct gga gcg gtt gtg acg cta caa gga acg ttc gag att ctt tct  
 710  
 Ala Ala Gly Ala Val Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser  
 160 165 170  
 ctc tcc gga tcg ttt ctt cct cct ccg gca cct ccc gga gca acg agt  
 758  
 Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser  
 175 180 185  
 ttg aca att ttc tta gcc gga gga caa ggt cag gtg gtt gga gga agc  
 806  
 Leu Thr Ile Phe Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser  
 190 195 200  
 gtt gtg ggt gag ctt acg gcg gct gga ccg gtg att gtg att gca gct  
 854  
 Val Val Gly Glu Leu Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala  
 205 210 215  
 tcg ttt act aat gtt gct tat gag aga ctt cct tta gaa gaa gat gag  
 902  
 Ser Phe Thr Asn Val Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu  
 220 225 230 235  
 cag cag caa cag ctt gga gga gga tct aac ggc gga ggt aat ttg ttt  
 950  
 Gln Gln Gln Gln Leu Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe  
 240 245 250  
 ccg gag gtg gca gct gga gga gga gga gga ctt ccg ttc ttt aat tta  
 998  
 Pro Glu Val Ala Ala Gly Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu  
 255 260 265  
 ccg atg aat atg caa cca aat gtg caa ctt ccg gtg gaa ggt tgg ccg  
 1046  
 Pro Met Asn Met Gln Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro  
 270 275 280  
 ggg aat tcc ggt gga aga ggt cct ttc tga tgtgtatata ttgataatca  
 1096  
 Gly Asn Ser Gly Gly Arg Gly Pro Phe  
 285 290  
 ttatatatat accggcggag aagcttttcc ggcgaagaat ttgcgagagt gaagaaaggt  
 1156  
 tagaaaagct tttaatggac taatgaattt caaattatca tcgtgatttc ggacattgtc  
 1216



ttgttcacatca tgtaagcctt aggtttatatt tttgtcgttt gtagaatttt atgtttgaat  
1276

cctttttttt ttctgtgaaa ctctattgtg ttcgtctgcy aaggaaaaaa aaattctcaa  
1336

aaaaaa  
1342

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Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg Tyr Val Asn His Gln  
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Leu His Arg Pro Asp Leu His Leu His Asn Ser Ser Ser Asp Asp  
20 25 30

Val Thr Pro Gly Ala Gly Met Gly His Phe Thr Val Asp Asp Glu Asp  
35 40 45

Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala Ser Gly Gly Gly Ser  
50 55 60

Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly Gly Gly Asp Val Val  
65 70 75 80

Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys  
85 90 95

Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His  
100 105 110

Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe Asp Cys Val Ala Thr  
115 120 125

Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Ser Gly  
130 135 140

Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser Ala Ala Gly Ala Val  
145 150 155 160

Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe  
165 170 175

Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu  
180 185 190



Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Glu Leu  
 195 200 205

Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala Ser Phe Thr Asn Val  
 210 215 220

Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu Gln Gln Gln Gln Leu  
 225 230 235 240

Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe Pro Glu Val Ala Ala  
 245 250 255

Gly Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Asn Met Gln  
 260 265 270

Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro Gly Asn Ser Gly Gly  
 275 280 285

Arg Gly Pro Phe  
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 1 5 10 15

ggt ctg aaa caa cat gaa act cct ctt cct cct cct ggt tac cca cca  
 96  
 Gly Leu Lys Gln His Glu Thr Pro Leu Pro Pro Pro Gly Tyr Pro Pro  
 20 25 30

cgg tct gaa aac cct aat ctt ttt ccg gtg ggt caa tcc agc act tcc  
 144  
 Arg Ser Glu Asn Pro Asn Leu Phe Pro Val Gly Gln Ser Ser Thr Ser  
 35 40 45

tcc gcc gcc gcc gcg gtg aaa cct tct gag aat gtt gct cct cct ttt  
 192  
 Ser Ala Ala Ala Ala Val Lys Pro Ser Glu Asn Val Ala Pro Pro Phe  
 50 55 60

agc tta aca atg ccg gtg gag aat tct tct tct gag ttg aag aag aag  
 240  
 Ser Leu Thr Met Pro Val Glu Asn Ser Ser Ser Glu Leu Lys Lys Lys  
 65 70 75 80

aga ggg aga cca aga aag tat aac cct gac ggc tca ctc gct gtg act  
 288  
 Arg Gly Arg Pro Arg Lys Tyr Asn Pro Asp Gly Ser Leu Ala Val Thr  
 85 90 95



ctc tct cct atg cct atc tca tcc tcc gtt ccg ttg acg tcg gag ttt  
 336  
 Leu Ser Pro Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe  
 100 105 110  
 ggt tct cgg aaa cga gga aga ggt cga gga aga ggc aga gga aga gga  
 384  
 Gly Ser Arg Lys Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly  
 115 120 125  
 cga gga cgt gga caa gga caa gga agc aga gag ccc aat aac aac aac  
 432  
 Arg Gly Arg Gly Gln Gly Gln Gly Ser Arg Glu Pro Asn Asn Asn Asn  
 130 135 140  
 aac gac aac aat tgg ctc aag aat cct cag atg ttc gaa ttt aac aac  
 480  
 Asn Asp Asn Asn Trp Leu Lys Asn Pro Gln Met Phe Glu Phe Asn Asn  
 145 150 155 160  
 aac act cct act tct ggt gga gga gga cct gct gaa att gtc agt cca  
 528  
 Asn Thr Pro Thr Ser Gly Gly Gly Gly Pro Ala Glu Ile Val Ser Pro  
 165 170 175  
 agt ttt aca cct cat gtg ctc aca gta aat gcc ggt gag gat gtg aca  
 576  
 Ser Phe Thr Pro His Val Leu Thr Val Asn Ala Gly Glu Asp Val Thr  
 180 185 190  
 atg aag ata atg aca ttc tct caa caa ggc tcg cgt gct att tgt att  
 624  
 Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg Ala Ile Cys Ile  
 195 200 205  
 ctt tca gcg aac ggt ccc ata tcc aat gtt aca ctt cgt caa tct atg  
 672  
 Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu Arg Gln Ser Met  
 210 215 220  
 aca tct ggt ggt act ctc act tat gag ggt cat ttt gag att ctt tct  
 720  
 Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly His Phe Glu Ile Leu Ser  
 225 230 235 240  
 ttg acg ggt tcg ttt ata cca agc gag agt gga gga acc cga agc aga  
 768  
 Leu Thr Gly Ser Phe Ile Pro Ser Glu Ser Gly Gly Thr Arg Ser Arg  
 245 250 255  
 gct ggt ggg atg agt gtc tct ctt gca gga caa gat ggt cgt gtc ttt  
 816  
 Ala Gly Gly Met Ser Val Ser Leu Ala Gly Gln Asp Gly Arg Val Phe  
 260 265 270  
 ggt ggt gga ctt gct ggt ctc ttt att gcc gct ggt cct gtt cag gta  
 864  
 Gly Gly Gly Leu Ala Gly Leu Phe Ile Ala Ala Gly Pro Val Gln Val  
 275 280 285



atg gta ggg agt ttt ata gcg ggt cag gag gaa tcg cag cag cag cag  
 912  
 Met Val Gly Ser Phe Ile Ala Gly Gln Glu Glu Ser Gln Gln Gln Gln  
 290 295 300  
 cag cag ata aag aag caa aga agg gaa aga ctc ggg atc ccg aca aca  
 960  
 Gln Gln Ile Lys Lys Gln Arg Arg Glu Arg Leu Gly Ile Pro Thr Thr  
 305 310 315 320  
 aca caa gct tct aat atc tca ttc ggt ggc tca gcg gaa gat cct aag  
 1008  
 Thr Gln Ala Ser Asn Ile Ser Phe Gly Gly Ser Ala Glu Asp Pro Lys  
 325 330 335  
 gct aga tac ggg ctc aac aag cct gtt gtt att cag cca cca ccg gtg  
 1056  
 Ala Arg Tyr Gly Leu Asn Lys Pro Val Val Ile Gln Pro Pro Pro Val  
 340 345 350  
 tct gca cca cct gtg tcc ttt tcg cat gaa cca agt act aac acc gtc  
 1104  
 Ser Ala Pro Pro Val Ser Phe Ser His Glu Pro Ser Thr Asn Thr Val  
 355 360 365  
 cat ggt tac tat gca aat aac aca gct aac cat atc aag gat ctc ttc  
 1152  
 His Gly Tyr Tyr Ala Asn Asn Thr Ala Asn His Ile Lys Asp Leu Phe  
 370 375 380  
 tct tcc ctc cct gga gaa gat agg gaa gaa gat gag gat gat tta gaa  
 1200  
 Ser Ser Leu Pro Gly Glu Asp Arg Glu Glu Asp Glu Asp Asp Leu Glu  
 385 390 395 400  
 ggt gaa gat gat gaa gaa ttc gga ggc cat agc gaa tct gac acc gag  
 1248  
 Gly Glu Asp Asp Glu Glu Phe Gly Gly His Ser Glu Ser Asp Thr Glu  
 405 410 415  
 gtt cca agc tga tgatcgatgg aaagaatccg acatatatgt gttatgaatc  
 1300  
 Val Pro Ser  
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 1360  
 ttcagattgt tagttgttaa agtcttaaac agagatatatt cactaaaagt tagggtttac  
 1420  
 tagaggatgt aatcttttagg gttctttgac ttgtgtcttt cttttaatcc tcagatgggt  
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 1540  
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 1556



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370

Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn Ile Pro Thr Ser Phe  
1 5 10 15

Gly Leu Lys Gln His Glu Thr Pro Leu Pro Pro Pro Gly Tyr Pro Pro  
20 25 30

Arg Ser Glu Asn Pro Asn Leu Phe Pro Val Gly Gln Ser Ser Thr Ser  
35 40 45

Ser Ala Ala Ala Ala Val Lys Pro Ser Glu Asn Val Ala Pro Pro Phe  
50 55 60

Ser Leu Thr Met Pro Val Glu Asn Ser Ser Ser Glu Leu Lys Lys Lys  
65 70 75 80

Arg Gly Arg Pro Arg Lys Tyr Asn Pro Asp Gly Ser Leu Ala Val Thr  
85 90 95

Leu Ser Pro Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe  
100 105 110

Gly Ser Arg Lys Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly  
115 120 125

Arg Gly Arg Gly Gln Gly Gln Gly Ser Arg Glu Pro Asn Asn Asn Asn  
130 135 140

Asn Asp Asn Asn Trp Leu Lys Asn Pro Gln Met Phe Glu Phe Asn Asn  
145 150 155 160

Asn Thr Pro Thr Ser Gly Gly Gly Gly Pro Ala Glu Ile Val Ser Pro  
165 170 175

Ser Phe Thr Pro His Val Leu Thr Val Asn Ala Gly Glu Asp Val Thr  
180 185 190

Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg Ala Ile Cys Ile  
195 200 205

Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu Arg Gln Ser Met  
210 215 220

Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly His Phe Glu Ile Leu Ser  
225 230 235 240



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290 295 300

Gln Gln Ile Lys Lys Gln Arg Arg Glu Arg Leu Gly Ile Pro Thr Thr  
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Thr Gln Ala Ser Asn Ile Ser Phe Gly Gly Ser Ala Glu Asp Pro Lys  
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 180 185 190  
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 Glu Glu Leu Asp Glu Thr Glu Ser Thr Val Asp Gly Pro Leu Leu Lys  
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676



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Trp Ile Gln Val Glu Gly Glu Arg Phe Arg Phe Pro Gly Gly Gly Thr  
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Ile Pro Leu Thr Asp Gly Ala Ile Arg Thr Ala Ile Asp Thr Gly Cys



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Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Ile Met Gly Ser Arg Arg						
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Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro Pro Ile						
	325			330		335
Asn Trp Lys Lys Tyr Trp Lys Gly Trp Glu Arg Ser Gln Glu Asp Leu						
	340			345		350
Lys Gln Glu Gln Asp Ser Ile Glu Asp Ala Ala Arg Ser Leu Cys Trp						
	355			360		365
Lys Lys Val Thr Glu Lys Gly Asp Leu Ser Ile Trp Gln Lys Pro Ile						
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Pro Arg Ile Ile Gly Gly Thr Ile Pro Asp Ile Asn Ala Glu Lys Phe						
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Pro Gly Arg Gly Asn Pro Glu Asn Glu Asp Val Leu Val Ala Asp Val 705 710 715 720		
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Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn  
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 336  
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 384  
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768

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816

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864

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912

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960

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1008

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1104

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1152

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1248

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675 680 685

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930 935 940

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 Val Asn Leu Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala  
 325 330 335  
 atg cgg aag gag ccg aag ttg ata ata tct ttg tta atg aaa ggg gca  
 1112  
 Met Arg Lys Glu Pro Lys Leu Ile Ile Ser Leu Leu Met Lys Gly Ala  
 340 345 350  
 aat att tta gac aca aca ttg gat ggt aga acc gct tta gtg att gta  
 1160  
 Asn Ile Leu Asp Thr Thr Leu Asp Gly Arg Thr Ala Leu Val Ile Val  
 355 360 365  
 aaa cga ctc act aaa gcg gat gac tac aaa act agt acg gag gac ggt  
 1208  
 Lys Arg Leu Thr Lys Ala Asp Asp Tyr Lys Thr Ser Thr Glu Asp Gly  
 370 375 380 385  
 acg cct tct ctg aaa ggc gga tta tgc ata gag gta ctt gag cat gaa  
 1256  
 Thr Pro Ser Leu Lys Gly Gly Leu Cys Ile Glu Val Leu Glu His Glu  
 390 395 400



caa aaa cta gaa tat ttg tcg cct ata gag gct tca ctt tct ctt cca  
 1304  
 Gln Lys Leu Glu Tyr Leu Ser Pro Ile Glu Ala Ser Leu Ser Leu Pro  
 405 410 415  
 gta act cca gag gag ttg agg atg agg ttg ctc tat tat gaa aac cga  
 1352  
 Val Thr Pro Glu Glu Leu Arg Met Arg Leu Leu Tyr Tyr Glu Asn Arg  
 420 425 430  
 gtt gca ctt gct cga ctt ctc ttt cca gtg gaa act gaa act gta cag  
 1400  
 Val Ala Leu Ala Arg Leu Leu Phe Pro Val Glu Thr Glu Thr Val Gln  
 435 440 445  
 ggt att gcc aaa ttg gag gaa aca tgc gag ttt aca gct tct agt ctc  
 1448  
 Gly Ile Ala Lys Leu Glu Glu Thr Cys Glu Phe Thr Ala Ser Ser Leu  
 450 455 460 465  
 gag cct gat cat cac att ggt gaa aag cgg aca tca cta gac cta aat  
 1496  
 Glu Pro Asp His His Ile Gly Glu Lys Arg Thr Ser Leu Asp Leu Asn  
 470 475 480  
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 1544  
 Met Ala Pro Phe Gln Ile His Glu Lys His Leu Ser Arg Leu Arg Ala  
 485 490 495  
 ctt tgt aaa acc gtg gaa ctg ggg aaa cgc tac ttc aaa cga tgt tcg  
 1592  
 Leu Cys Lys Thr Val Glu Leu Gly Lys Arg Tyr Phe Lys Arg Cys Ser  
 500 505 510  
 ctt gat cac ttt atg gat act gag gac ttg aat cat ctt gct agc gta  
 1640  
 Leu Asp His Phe Met Asp Thr Glu Asp Leu Asn His Leu Ala Ser Val  
 515 520 525  
 gaa gaa gat act cct gag aaa cgg cta caa aag aag caa agg tac atg  
 1688  
 Glu Glu Asp Thr Pro Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met  
 530 535 540 545  
 gaa cta caa gag act ctg atg aag acc ttt agt gag gac aag gag gaa  
 1736  
 Glu Leu Gln Glu Thr Leu Met Lys Thr Phe Ser Glu Asp Lys Glu Glu  
 550 555 560  
 tgt gga aag tct tcc aca cgg aaa cca acc tct gcg gtg agg tct aat  
 1784  
 Cys Gly Lys Ser Ser Thr Pro Lys Pro Thr Ser Ala Val Arg Ser Asn  
 565 570 575  
 aga aaa ctc tct cac cgg cgc cta aaa gtg gac aaa cgg gat ttt ttg  
 1832  
 Arg Lys Leu Ser His Arg Arg Leu Lys Val Asp Lys Arg Asp Phe Leu  
 580 585 590



aaa cga cct tac ggg aac ggg gat taa ggaatgggaa atcatattcc  
1879

Lys Arg Pro Tyr Gly Asn Gly Asp  
595 600

atttcactcc cacaactaaa aatgatgtat gtcctatatc atgatgtttc gtgagtttca  
1939

aataaattga aacgtacata tatcagtttt tcatctacgt gactgcgttg tatagttttc  
1999

gttcttcact tagcatcatg tgtattctag ctccaagtgc gtttcaaaca aatatagtta  
2059

tttttagcca attatatata cggt  
2083

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382

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20 25 30

Ser Leu Asp Tyr Pro Thr Glu Phe Leu Thr Pro Pro Glu Val Ser Ala  
35 40 45

Leu Lys Leu Leu Ser Asn Cys Leu Glu Ser Val Phe Asp Ser Pro Glu  
50 55 60

Thr Phe Tyr Ser Asp Ala Lys Leu Val Leu Ala Gly Gly Arg Glu Val  
65 70 75 80

Ser Phe His Arg Cys Ile Leu Ser Ala Arg Ile Pro Val Phe Lys Ser  
85 90 95

Ala Leu Ala Thr Val Lys Glu Gln Lys Ser Ser Thr Thr Val Lys Leu  
100 105 110

Gln Leu Lys Glu Ile Ala Arg Asp Tyr Glu Val Gly Phe Asp Ser Val  
115 120 125

Val Ala Val Leu Ala Tyr Val Tyr Ser Gly Arg Val Arg Ser Pro Pro  
130 135 140

Lys Gly Ala Ser Ala Cys Val Asp Asp Asp Cys Cys His Val Ala Cys  
145 150 155 160



Arg Ser Lys Val Asp Phe Met Val Glu Val Leu Tyr Leu Ser Phe Val  
165 170 175

Phe Gln Ile Gln Glu Leu Val Thr Leu Tyr Glu Arg Gln Phe Leu Glu  
180 185 190

Ile Val Asp Lys Val Val Val Glu Asp Ile Leu Val Ile Phe Lys Leu  
195 200 205

Asp Thr Leu Cys Gly Thr Thr Tyr Lys Lys Leu Leu Asp Arg Cys Ile  
210 215 220

Glu Ile Ile Val Lys Ser Asp Ile Glu Leu Val Ser Leu Glu Lys Ser  
225 230 235 240

Leu Pro Gln His Ile Phe Lys Gln Ile Ile Asp Ile Arg Glu Ala Leu  
245 250 255

Cys Leu Glu Pro Pro Lys Leu Glu Arg His Val Lys Asn Ile Tyr Lys  
260 265 270

Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Met Leu Leu Leu Glu  
275 280 285

Gly His Thr Asn Leu Asp Glu Ala Tyr Ala Leu His Phe Ala Ile Ala  
290 295 300

His Cys Ala Val Lys Thr Ala Tyr Asp Leu Leu Glu Leu Glu Leu Ala  
305 310 315 320

Asp Val Asn Leu Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala  
325 330 335

Ala Met Arg Lys Glu Pro Lys Leu Ile Ile Ser Leu Leu Met Lys Gly  
340 345 350

Ala Asn Ile Leu Asp Thr Thr Leu Asp Gly Arg Thr Ala Leu Val Ile  
355 360 365

Val Lys Arg Leu Thr Lys Ala Asp Asp Tyr Lys Thr Ser Thr Glu Asp  
370 375 380

Gly Thr Pro Ser Leu Lys Gly Gly Leu Cys Ile Glu Val Leu Glu His  
385 390 395 400

Glu Gln Lys Leu Glu Tyr Leu Ser Pro Ile Glu Ala Ser Leu Ser Leu



714



cat tgg aga cct gca gaa gac gag aag cta aga gaa ctc gtc gag caa  
 104  
 His Trp Arg Pro Ala Glu Asp Glu Lys Leu Arg Glu Leu Val Glu Gln  
           10                  15                  20

ttt ggt cct cat aat tgg aac gcc ata gct cag aag ctc tct ggt cga  
 152  
 Phe Gly Pro His Asn Trp Asn Ala Ile Ala Gln Lys Leu Ser Gly Arg  
           25                  30                  35

tct ggt aag agt tgt aga ttg aga tgg ttt aat caa ttg gat cct agg  
 200  
 Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg  
           40                  45                  50

att aac cga aac cct ttc acg gag gaa gaa gaa gaa agg ctt tta gcg  
 248  
 Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu Glu Glu Arg Leu Leu Ala  
           55                  60                  65                  70

cct cat cgg atc cat ggg aac aga tgg tct gtg atc gct aga ttt ttt  
 296  
 Pro His Arg Ile His Gly Asn Arg Trp Ser Val Ile Ala Arg Phe Phe  
                   75                  80                  85

ccc ggt cga act gat aac gct gtt aaa aac cat tgg cac gtc atc atg  
 344  
 Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Trp His Val Ile Met  
           90                  95                  100

gct cgt cgt ggc cga gaa cgg tcc aag ctc cgt cca cga ggc ctt ggc  
 392  
 Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg Pro Arg Gly Leu Gly  
           105                  110                  115

cat gat ggc acg gtg gct gcg act ggg atg att ggt aat tat aaa gac  
 440  
 His Asp Gly Thr Val Ala Ala Thr Gly Met Ile Gly Asn Tyr Lys Asp  
           120                  125                  130

tgc gat aag gag aga aga ttg gca acc aca acc gct atc aat ttt cct  
 488  
 Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr Ala Ile Asn Phe Pro  
           135                  140                  145                  150

tat caa ttc tct cat att aat cat ttt caa gtc ctc aaa gag tcc ttg  
 536  
 Tyr Gln Phe Ser His Ile Asn His Phe Gln Val Leu Lys Glu Ser Leu  
                   155                  160                  165

acc gga aag atc ggg ttc aga aat agt act act cca ata caa gaa gga  
 584  
 Thr Gly Lys Ile Gly Phe Arg Asn Ser Thr Thr Pro Ile Gln Glu Gly  
           170                  175                  180

gca ata gac caa act aaa cga ccg atg gag ttc tac aat ttt ctc caa  
 632  
 Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe Tyr Asn Phe Leu Gln  
           185                  190                  195



gta aac acg gat tcg aag ata cac gaa ttg ata gat aat tca aga aaa  
 680  
 Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile Asp Asn Ser Arg Lys  
 200 205 210

gac gaa gaa gaa gat gtc gat caa aac aac cga att cgt aac gag aat  
 728  
 Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg Ile Arg Asn Glu Asn  
 215 220 225 230

tgt gtt cca ttt ttc gac ttt ttg tct gtt gga aac tct gcc tct cag  
 776  
 Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn Ser Ala Ser Gln  
 235 240 245

ggt tta tgt taa tttgtccgta ccacatgtac tataagggtg accatatgtt  
 828  
 Gly Leu Cys

aactaaagat aatgtagaaa gtactaatca attagagctc ctgtttgagc caaatgtgaa  
 888

aattagttaa gacatcccaa acattttctt gtataacaca tataagggtg tactttttatc  
 948

aggtctaatt ttctattttt attttaagga tgtttaatca gaccataac cattcgataa  
 1008

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 1020

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Arg Glu Leu Val Glu Gln Phe Gly Pro His Asn Trp Asn Ala Ile Ala  
 20 25 30

Gln Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe  
 35 40 45

Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu  
 50 55 60

Glu Glu Arg Leu Leu Ala Pro His Arg Ile His Gly Asn Arg Trp Ser  
 65 70 75 80

Val Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn  
 85 90 95

His Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu



100 105 110  
 Arg Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met  
 115 120 125  
 Ile Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr  
 130 135 140  
 Thr Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln  
 145 150 155 160  
 Val Leu Lys Glu Ser Leu Thr Gly Lys Ile Gly Phe Arg Asn Ser Thr  
 165 170 175  
 Thr Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu  
 180 185 190  
 Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu  
 195 200 205  
 Ile Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn  
 210 215 220  
 Arg Ile Arg Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val  
 225 230 235 240  
 Gly Asn Ser Ala Ser Gln Gly Leu Cys  
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atg gag ggt tcg tcc aaa ggg ctg cga aaa ggt gct tgg act act gaa  
 106  
 Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu  
 1 5 10 15

gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa  
 154  
 Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys  
 20 25 30

tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt  
 202  
 Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser  
 35 40 45



tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga  
 250  
 Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
 50 55 60

aaa ctt agc tct gat gaa gtc gat ctt ctt ctt cgc ctt cat agg ctt  
 298  
 Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu  
 65 70 75 80

cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc  
 346  
 Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
 85 90 95

gca aat gac gtc aag aat tac tgg aac act cat ctg agt aag aaa cat  
 394  
 Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
 100 105 110

gaa ccg tgt tgt aag ata aag atg aaa aag aga gac att acg ccc att  
 442  
 Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile  
 115 120 125

cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga  
 490  
 Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg  
 130 135 140

tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa  
 538  
 Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys  
 145 150 155 160

gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt  
 586  
 Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys  
 165 170 175

gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg  
 634  
 Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val  
 180 185 190

aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta agg  
 682  
 Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Arg  
 195 200 205

aaa gcc aag agg tag atattttggt tcctgaagcg acgacaacag aaaaggggga  
 737  
 Lys Ala Lys Arg  
 210

caccttggt tttgacgttg atcaactttg gagtcttttc gatggagaga ctgtgaaatt  
 797

tgattagtgt ttcgaacatt tgtttgcgtt tgtgtatagg tttgctttca ccttttaatt  
 857



tgtgtgtttt gataaataag ctaatagttt ttagcatttt aatgaaatat ttcaagtttc  
917

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925

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20 25 30

Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser  
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
50 55 60

Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu  
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
100 105 110

Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile  
115 120 125

Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg  
130 135 140

Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys  
145 150 155 160

Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys  
165 170 175

Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val  
180 185 190

Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Arg  
195 200 205



Lys Ala Lys Arg  
210

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49

Met Asn Gln Ile Lys Asn Lys Thr Leu Pro Glu Met Thr Thr  
1 5 10

gag caa gct ttg ttg tct atg gaa gct tta cct tta ggt ttc aga ttc  
97

Glu Gln Ala Leu Leu Ser Met Glu Ala Leu Pro Leu Gly Phe Arg Phe  
15 20 25 30

aga cca acg gat gaa gaa ctc atc aat cat tac cta agg tta aaa atc  
145

Arg Pro Thr Asp Glu Glu Leu Ile Asn His Tyr Leu Arg Leu Lys Ile  
35 40 45

aac ggc cgt gat tta gag gtt aga gtc atc cct gag atc gat gtt tgc  
193

Asn Gly Arg Asp Leu Glu Val Arg Val Ile Pro Glu Ile Asp Val Cys  
50 55 60

aag tgg gaa cca tgg gac tta cct ggg cta tcg gtg ata aag aca gat  
241

Lys Trp Glu Pro Trp Asp Leu Pro Gly Leu Ser Val Ile Lys Thr Asp  
65 70 75

gat caa gaa tgg ttc ttt ttt tgt cct cgt gat cga aag tat ccg agt  
289

Asp Gln Glu Trp Phe Phe Phe Cys Pro Arg Asp Arg Lys Tyr Pro Ser  
80 85 90

ggt cat cgt tct aat aga gct act gat att ggt tac tgg aaa gct act  
337

Gly His Arg Ser Asn Arg Ala Thr Asp Ile Gly Tyr Trp Lys Ala Thr  
95 100 105 110

ggg aaa gat cga act att aag tct aag aag atg att att ggt atg aag  
385

Gly Lys Asp Arg Thr Ile Lys Ser Lys Lys Met Ile Ile Gly Met Lys  
115 120 125

aag act ctt gtt ttc tat cgt gga aga gct cct aga gga gag cgt act  
433

Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Arg Gly Glu Arg Thr  
130 135 140

aat tgg att atg cat gag tat cgt gct aca gac aag gaa cta gat ggt  
481

Asn Trp Ile Met His Glu Tyr Arg Ala Thr Asp Lys Glu Leu Asp Gly  
145 150 155

act gga cct ggt cag aat ccg tat gtt ttg tgt cgc ttg ttc cac aag  
529



Thr Gly Pro Gly Gln Asn Pro Tyr Val Leu Cys Arg Leu Phe His Lys  
 160 165 170  
 cct agt gat agt tgt gat cct gca cac tgt gag gaa ata gag aaa gtt  
 577  
 Pro Ser Asp Ser Cys Asp Pro Ala His Cys Glu Glu Ile Glu Lys Val  
 175 180 185 190  
 aat ttt act cca acc acc acc act aga tgc tct cct gat gac aca tct  
 625  
 Asn Phe Thr Pro Thr Thr Thr Thr Arg Cys Ser Pro Asp Asp Thr Ser  
 195 200 205  
 tct gaa atg gtc caa gaa aca gct aca tct ggt gta cat gct cta gat  
 673  
 Ser Glu Met Val Gln Glu Thr Ala Thr Ser Gly Val His Ala Leu Asp  
 210 215 220  
 aga tca gat gac act gag agg tgt tta agt gac aag ggc aat aat gat  
 721  
 Arg Ser Asp Asp Thr Glu Arg Cys Leu Ser Asp Lys Gly Asn Asn Asp  
 225 230 235  
 gtg aaa cct gat gtt tca gtg ata aac aat act tct gtc aat cac gct  
 769  
 Val Lys Pro Asp Val Ser Val Ile Asn Asn Thr Ser Val Asn His Ala  
 240 245 250  
 gaa act tct cgt gcc aaa gac cgt aat ttg ggc aag acg tta gta gag  
 817  
 Glu Thr Ser Arg Ala Lys Asp Arg Asn Leu Gly Lys Thr Leu Val Glu  
 255 260 265 270  
 gaa aat cca ctt cta agg gac gtt cca act ctt cat gga ccc atc ttg  
 865  
 Glu Asn Pro Leu Leu Arg Asp Val Pro Thr Leu His Gly Pro Ile Leu  
 275 280 285  
 agt gag aaa tca tat tat cca gga cag tca agc atc ggt ttt gct aca  
 913  
 Ser Glu Lys Ser Tyr Tyr Pro Gly Gln Ser Ser Ile Gly Phe Ala Thr  
 290 295 300  
 tct cac atg gat tct atg tat tct agt gat ttt gga aac tgt gat tat  
 961  
 Ser His Met Asp Ser Met Tyr Ser Ser Asp Phe Gly Asn Cys Asp Tyr  
 305 310 315  
 ggg cta cat ttt caa gat ggt gcc tct gaa caa gat gca tct tta aca  
 1009  
 Gly Leu His Phe Gln Asp Gly Ala Ser Glu Gln Asp Ala Ser Leu Thr  
 320 325 330  
 gat gtc ttg gat gaa gta ttc cat aac cat aat gaa tcc tct aat gac  
 1057  
 Asp Val Leu Asp Glu Val Phe His Asn His Asn Glu Ser Ser Asn Asp  
 335 340 345 350  
 agg aaa gac ttt gta ctt ccg aat atg atg cat tgg cct ggt aat aca  
 1105  
 Arg Lys Asp Phe Val Leu Pro Asn Met Met His Trp Pro Gly Asn Thr



355 360 365  
 aga ctg ttg tct act gag tac cca ttt ctc aaa gat tct gtt gct ttt  
 1153  
 Arg Leu Leu Ser Thr Glu Tyr Pro Phe Leu Lys Asp Ser Val Ala Phe  
 370 375 380  
 gtt gac ggc agt gct gaa gtt tcc ggc tca cag caa ttt gtt cct gac  
 1201  
 Val Asp Gly Ser Ala Glu Val Ser Gly Ser Gln Gln Phe Val Pro Asp  
 385 390 395  
 att tta gct tct aga tgg gtc agt gaa cag aac gtt gat agc aag gag  
 1249  
 Ile Leu Ala Ser Arg Trp Val Ser Glu Gln Asn Val Asp Ser Lys Glu  
 400 405 410  
 gca gta gag att cta tct tca acc ggg tcc tct cgg acc ttg acg cca  
 1297  
 Ala Val Glu Ile Leu Ser Ser Thr Gly Ser Ser Arg Thr Leu Thr Pro  
 415 420 425 430  
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 1345  
 Leu His Asn Asn Val Phe Gly Gln Tyr Ala Ser Ser Ser Tyr Ala Ala  
 435 440 445  
 atc gat cca ttt aac tat aat gtc aat cag cct gaa cag tca tcc ttt  
 1393  
 Ile Asp Pro Phe Asn Tyr Asn Val Asn Gln Pro Glu Gln Ser Ser Phe  
 450 455 460  
 gag caa agc cat gtt gac cgc aac att agt ccc agt aac att ttt gag  
 1441  
 Glu Gln Ser His Val Asp Arg Asn Ile Ser Pro Ser Asn Ile Phe Glu  
 465 470 475  
 ttc aag gct agg tct cga gag aat cag aga gat ctg gac tct gtt gtg  
 1489  
 Phe Lys Ala Arg Ser Arg Glu Asn Gln Arg Asp Leu Asp Ser Val Val  
 480 485 490  
 gac caa ggc act gct cct aga aga att cgg ctg cag atc gaa cag cca  
 1537  
 Asp Gln Gly Thr Ala Pro Arg Arg Ile Arg Leu Gln Ile Glu Gln Pro  
 495 500 505 510  
 ttg acg cca gtt acc aac aag aaa gag aga gat gcg gac aac tat gaa  
 1585  
 Leu Thr Pro Val Thr Asn Lys Lys Glu Arg Asp Ala Asp Asn Tyr Glu  
 515 520 525  
 gaa gaa gat gaa gta caa tct gcc atg tcc aag gtc gta gag gaa gaa  
 1633  
 Glu Glu Asp Glu Val Gln Ser Ala Met Ser Lys Val Val Glu Glu Glu  
 530 535 540  
 ccg gct aat tta agt gct cag ggg act gct cag agg aga atc cgc ctg  
 1681  
 Pro Ala Asn Leu Ser Ala Gln Gly Thr Ala Gln Arg Arg Ile Arg Leu  
 545 550 555



cag acg aga ttg agg aag cct ctc ata acc cta aac aat aca aaa aga  
1729

Gln Thr Arg Leu Arg Lys Pro Leu Ile Thr Leu Asn Asn Thr Lys Arg  
560 565 570

aac tca aat ggc aga gaa gga gaa gca agc cat agg aag tgt gaa atg  
1777

Asn Ser Asn Gly Arg Glu Gly Glu Ala Ser His Arg Lys Cys Glu Met  
575 580 585 590

cag gaa aaa gaa gat ata tca tca tca tca tca tgg cag aaa cag aag  
1825

Gln Glu Lys Glu Asp Ile Ser Ser Ser Ser Ser Trp Gln Lys Gln Lys  
595 600 605

aag agc ttg gtg cag ttt agt agt gtg gtg ata ata gtg gcg gtg ata  
1873

Lys Ser Leu Val Gln Phe Ser Ser Val Val Ile Ile Val Ala Val Ile  
610 615 620

gtt gtt tta gta gaa ata tgg aaa gag tca aga gat gcg aaa tgt agc  
1921

Val Val Leu Val Glu Ile Trp Lys Glu Ser Arg Asp Ala Lys Cys Ser  
625 630 635

ttc ttg ttt cat caa tta gat tcc ttc aaa ggc atg ttt act tga  
1966

Phe Leu Phe His Gln Leu Asp Ser Phe Lys Gly Met Phe Thr  
640 645 650

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1989

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Thr Asp Glu Glu Leu Ile Asn His Tyr Leu Arg Leu Lys Ile Asn Gly  
35 40 45

Arg Asp Leu Glu Val Arg Val Ile Pro Glu Ile Asp Val Cys Lys Trp  
50 55 60

Glu Pro Trp Asp Leu Pro Gly Leu Ser Val Ile Lys Thr Asp Asp Gln  
65 70 75 80

Glu Trp Phe Phe Phe Cys Pro Arg Asp Arg Lys Tyr Pro Ser Gly His  
85 90 95



Arg Ser Asn Arg Ala Thr Asp Ile Gly Tyr Trp Lys Ala Thr Gly Lys  
 100 105 110

Asp Arg Thr Ile Lys Ser Lys Lys Met Ile Ile Gly Met Lys Lys Thr  
 115 120 125

Leu Val Phe Tyr Arg Gly Arg Ala Pro Arg Gly Glu Arg Thr Asn Trp  
 130 135 140

Ile Met His Glu Tyr Arg Ala Thr Asp Lys Glu Leu Asp Gly Thr Gly  
 145 150 155 160

Pro Gly Gln Asn Pro Tyr Val Leu Cys Arg Leu Phe His Lys Pro Ser  
 165 170 175

Asp Ser Cys Asp Pro Ala His Cys Glu Glu Ile Glu Lys Val Asn Phe  
 180 185 190

Thr Pro Thr Thr Thr Thr Arg Cys Ser Pro Asp Asp Thr Ser Ser Glu  
 195 200 205

Met Val Gln Glu Thr Ala Thr Ser Gly Val His Ala Leu Asp Arg Ser  
 210 215 220

Asp Asp Thr Glu Arg Cys Leu Ser Asp Lys Gly Asn Asn Asp Val Lys  
 225 230 235 240

Pro Asp Val Ser Val Ile Asn Asn Thr Ser Val Asn His Ala Glu Thr  
 245 250 255

Ser Arg Ala Lys Asp Arg Asn Leu Gly Lys Thr Leu Val Glu Glu Asn  
 260 265 270

Pro Leu Leu Arg Asp Val Pro Thr Leu His Gly Pro Ile Leu Ser Glu  
 275 280 285

Lys Ser Tyr Tyr Pro Gly Gln Ser Ser Ile Gly Phe Ala Thr Ser His  
 290 295 300

Met Asp Ser Met Tyr Ser Ser Asp Phe Gly Asn Cys Asp Tyr Gly Leu  
 305 310 315 320

His Phe Gln Asp Gly Ala Ser Glu Gln Asp Ala Ser Leu Thr Asp Val  
 325 330 335



Leu Asp Glu Val Phe His Asn His Asn Glu Ser Ser Asn Asp Arg Lys  
 340 345 350

Asp Phe Val Leu Pro Asn Met Met His Trp Pro Gly Asn Thr Arg Leu  
 355 360 365

Leu Ser Thr Glu Tyr Pro Phe Leu Lys Asp Ser Val Ala Phe Val Asp  
 370 375 380

Gly Ser Ala Glu Val Ser Gly Ser Gln Gln Phe Val Pro Asp Ile Leu  
 385 390 395 400

Ala Ser Arg Trp Val Ser Glu Gln Asn Val Asp Ser Lys Glu Ala Val  
 405 410 415

Glu Ile Leu Ser Ser Thr Gly Ser Ser Arg Thr Leu Thr Pro Leu His  
 420 425 430

Asn Asn Val Phe Gly Gln Tyr Ala Ser Ser Ser Tyr Ala Ala Ile Asp  
 435 440 445

Pro Phe Asn Tyr Asn Val Asn Gln Pro Glu Gln Ser Ser Phe Glu Gln  
 450 455 460

Ser His Val Asp Arg Asn Ile Ser Pro Ser Asn Ile Phe Glu Phe Lys  
 465 470 475 480

Ala Arg Ser Arg Glu Asn Gln Arg Asp Leu Asp Ser Val Val Asp Gln  
 485 490 495

Gly Thr Ala Pro Arg Arg Ile Arg Leu Gln Ile Glu Gln Pro Leu Thr  
 500 505 510

Pro Val Thr Asn Lys Lys Glu Arg Asp Ala Asp Asn Tyr Glu Glu Glu  
 515 520 525

Asp Glu Val Gln Ser Ala Met Ser Lys Val Val Glu Glu Glu Pro Ala  
 530 535 540

Asn Leu Ser Ala Gln Gly Thr Ala Gln Arg Arg Ile Arg Leu Gln Thr  
 545 550 555 560

Arg Leu Arg Lys Pro Leu Ile Thr Leu Asn Asn Thr Lys Arg Asn Ser  
 565 570 575

Asn Gly Arg Glu Gly Glu Ala Ser His Arg Lys Cys Glu Met Gln Glu



580 585 590  
 Lys Glu Asp Ile Ser Ser Ser Ser Ser Trp Gln Lys Gln Lys Lys Ser  
 595 600 605  
 Leu Val Gln Phe Ser Ser Val Val Ile Ile Val Ala Val Ile Val Val  
 610 615 620  
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 1 5 10 15  
 aac gac aac gaa aac aac aac aac aac aac aat ggt gga act gac  
 96  
 Asn Asp Asn Glu Asn Asn Asn Asn Asn Asn Asn Gly Gly Thr Asp  
 20 25 30  
 aac act aat gct gga aat gat tct gga gat caa gat ttc gac agt ggg  
 144  
 Asn Thr Asn Ala Gly Asn Asp Ser Gly Asp Gln Asp Phe Asp Ser Gly  
 35 40 45  
 aat acc tca agt ggc aat cat gga gaa ggg ttg gga aac aat caa gct  
 192  
 Asn Thr Ser Ser Gly Asn His Gly Glu Gly Leu Gly Asn Asn Gln Ala  
 50 55 60  
 cct cgt cat aag aag aaa aaa tac aat cgt cac acc caa ctt cag att  
 240  
 Pro Arg His Lys Lys Lys Lys Tyr Asn Arg His Thr Gln Leu Gln Ile  
 65 70 75 80  
 tcg gag atg gaa gct ttc ttc aga gag tgt cct cac cca gat gac aaa  
 288  
 Ser Glu Met Glu Ala Phe Phe Arg Glu Cys Pro His Pro Asp Asp Lys  
 85 90 95  
 caa agg tac gac ctt agc gct caa ttg gga ttg gac cct gtt cag atc  
 336  
 Gln Arg Tyr Asp Leu Ser Ala Gln Leu Gly Leu Asp Pro Val Gln Ile  
 100 105 110  
 aaa ttc tgg ttc cag aac aaa cgc act caa aac aag aat caa caa gaa  
 384  
 Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln Asn Lys Asn Gln Gln Glu



115	120	125
cgc ttt gag aac tca gaa ctt	cgg aat ctg aac aac cac ctt	agg tct
432		
Arg Phe Glu Asn Ser Glu Leu	Arg Asn Leu Asn Asn His Leu	Arg Ser
130	135	140
gaa aat cag cgg tta cga gaa gct att cat caa gcc tta tgc cct aag		
480		
Glu Asn Gln Arg Leu Arg Glu Ala Ile His Gln Ala Leu Cys Pro Lys		
145	150	155 160
tgt gga ggc caa act gca att ggc gaa atg acc ttc gaa gag cac cat		
528		
Cys Gly Gly Gln Thr Ala Ile Gly Glu Met Thr Phe Glu Glu His His		
	165 170	175
ctt cgc atc ctc aac gct cgt ttg act gaa gag atc aag caa ctt tcc		
576		
Leu Arg Ile Leu Asn Ala Arg Leu Thr Glu Glu Ile Lys Gln Leu Ser		
	180 185	190
gtg aca gcg gaa aag ata tca agg ctt acg ggg ata cca gta agg agc		
624		
Val Thr Ala Glu Lys Ile Ser Arg Leu Thr Gly Ile Pro Val Arg Ser		
	195 200	205
cat ccc cgt gtg tct cct cct aat cct cct cca aat ttc gag ttc ggg		
672		
His Pro Arg Val Ser Pro Pro Asn Pro Pro Pro Asn Phe Glu Phe Gly		
	210 215	220
atg gga tct aag gga aat gtc gga aac cac tcg agg gaa acc act gga		
720		
Met Gly Ser Lys Gly Asn Val Gly Asn His Ser Arg Glu Thr Thr Gly		
225	230	235 240
cct gca gat gct aat acc aag ccg atc atc atg gag ttg gca ttt gga		
768		
Pro Ala Asp Ala Asn Thr Lys Pro Ile Ile Met Glu Leu Ala Phe Gly		
	245	250 255
gcc atg gag gag ctc ttg gtg atg gct caa gtg gct gaa cca ctg tgg		
816		
Ala Met Glu Glu Leu Leu Val Met Ala Gln Val Ala Glu Pro Leu Trp		
	260 265	270
atg gga gga ttt aat ggc act agc tta gct ttg aac ttg gat gaa tac		
864		
Met Gly Gly Phe Asn Gly Thr Ser Leu Ala Leu Asn Leu Asp Glu Tyr		
	275 280	285
gaa aag acg ttt cgc acg ggt ctc ggt cct aga ctt ggc ggg ttt cga		
912		
Glu Lys Thr Phe Arg Thr Gly Leu Gly Pro Arg Leu Gly Gly Phe Arg		
	290 295	300
acc gag gca tcc agg gaa act gca ctc gtg gca atg tgt cct act ggc		
960		
Thr Glu Ala Ser Arg Glu Thr Ala Leu Val Ala Met Cys Pro Thr Gly		
305	310	315 320



att gtt gaa atg ctc atg caa gag aat ctg tgg tca aca atg ttt gcc  
1008

Ile Val Glu Met Leu Met Gln Glu Asn Leu Trp Ser Thr Met Phe Ala  
325 330 335

gga att gtt ggt aga gcc agg act cat gaa cag ata atg gct gat gct  
1056

Gly Ile Val Gly Arg Ala Arg Thr His Glu Gln Ile Met Ala Asp Ala  
340 345 350

gct gga aac ttc aat gga aat ctc caa ata atg agt gct gag tac caa  
1104

Ala Gly Asn Phe Asn Gly Asn Leu Gln Ile Met Ser Ala Glu Tyr Gln  
355 360 365

gtg ctt tcc ccg cta gtc aca acc cgc gaa agc tac ttc gtc cgc tac  
1152

Val Leu Ser Pro Leu Val Thr Thr Arg Glu Ser Tyr Phe Val Arg Tyr  
370 375 380

tgt aag caa caa gga gag ggt ttg tgg gcg gtg gtc gat att tcc atc  
1200

Cys Lys Gln Gln Gly Glu Gly Leu Trp Ala Val Val Asp Ile Ser Ile  
385 390 395 400

gac cat ctc ctc cca aac atc aac cta aaa tgt cgc cgc cga ccc tct  
1248

Asp His Leu Leu Pro Asn Ile Asn Leu Lys Cys Arg Arg Arg Pro Ser  
405 410 415

gga tgt ctg att caa gaa atg cat agt ggt tac tcc aag gtt aca tgg  
1296

Gly Cys Leu Ile Gln Glu Met His Ser Gly Tyr Ser Lys Val Thr Trp  
420 425 430

gtg gaa cat gtg gaa gta gat gat gca gga agt tac agc atc ttt gag  
1344

Val Glu His Val Glu Val Asp Asp Ala Gly Ser Tyr Ser Ile Phe Glu  
435 440 445

aaa tta atc tgt act ggt caa gct ttt gct gct aac cgc tgg gtt ggt  
1392

Lys Leu Ile Cys Thr Gly Gln Ala Phe Ala Ala Asn Arg Trp Val Gly  
450 455 460

aca ttg gta cgc cag tgt gag cgg ata tct agc atc ttg tcg aca gat  
1440

Thr Leu Val Arg Gln Cys Glu Arg Ile Ser Ser Ile Leu Ser Thr Asp  
465 470 475 480

ttt caa tct gtc gat tcc ggt gat cac ata acg cta act aac cat gga  
1488

Phe Gln Ser Val Asp Ser Gly Asp His Ile Thr Leu Thr Asn His Gly  
485 490 495

aag atg agc atg ctg aag ata gct gag cgg att gcg aga acc ttc ttt  
1536

Lys Met Ser Met Leu Lys Ile Ala Glu Arg Ile Ala Arg Thr Phe Phe  
500 505 510



gct gga atg acc aat gcg acg ggg tct aca ata ttt tct ggt gtt gaa  
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 Ala Gly Met Thr Asn Ala Thr Gly Ser Thr Ile Phe Ser Gly Val Glu  
 515 520 525

gga gaa gat atc aga gtg atg aca atg aag agc gtg aat gat cca gga  
 1632  
 Gly Glu Asp Ile Arg Val Met Thr Met Lys Ser Val Asn Asp Pro Gly  
 530 535 540

aag cct ccc ggt gtc att att tgt gca gcc act tcc ttt tgg ctt cct  
 1680  
 Lys Pro Pro Gly Val Ile Ile Cys Ala Ala Thr Ser Phe Trp Leu Pro  
 545 550 555 560

gct cct cct aac act gtc ttt gac ttc ctc aga gag gct act cac cga  
 1728  
 Ala Pro Pro Asn Thr Val Phe Asp Phe Leu Arg Glu Ala Thr His Arg  
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cac aat tgg gat gtt ctc tgc aac gga gag atg atg cac aag ata gca  
 1776  
 His Asn Trp Asp Val Leu Cys Asn Gly Glu Met Met His Lys Ile Ala  
 580 585 590

gag att acg aat ggg ata gac aaa agg aac tgt gca agt tta ctc cgg  
 1824  
 Glu Ile Thr Asn Gly Ile Asp Lys Arg Asn Cys Ala Ser Leu Leu Arg  
 595 600 605

cat gga cac act agc aag agc aag atg atg ata gtt caa gag act tct  
 1872  
 His Gly His Thr Ser Lys Ser Lys Met Met Ile Val Gln Glu Thr Ser  
 610 615 620

act gac cca aca gct tca ttt gtg ctt tat gcg cct gtt gat atg aca  
 1920  
 Thr Asp Pro Thr Ala Ser Phe Val Leu Tyr Ala Pro Val Asp Met Thr  
 625 630 635 640

tca atg gat att act ctc cat gga ggt ggt gat cct gac ttt gtg gtg  
 1968  
 Ser Met Asp Ile Thr Leu His Gly Gly Gly Asp Pro Asp Phe Val Val  
 645 650 655

atc ctg cct tct ggt ttt gct att ttt cca gat ggt acg ggt aag cct  
 2016  
 Ile Leu Pro Ser Gly Phe Ala Ile Phe Pro Asp Gly Thr Gly Lys Pro  
 660 665 670

gga gga aaa gaa gga gga tca ctt ttg acc att tcc ttc caa atg ctg  
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 Gly Gly Lys Glu Gly Gly Ser Leu Leu Thr Ile Ser Phe Gln Met Leu  
 675 680 685

gtt gag tca ggt cct gag gct agg ctg agt gtt agc tct gtt gca act  
 2112  
 Val Glu Ser Gly Pro Glu Ala Arg Leu Ser Val Ser Ser Val Ala Thr  
 690 695 700



act gag aat ctg att cgt aca acc gtg cgg agg atc aaa gat ttg ttt

2160

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cct tgt cag act gct tga

2178

Pro Cys Gln Thr Ala  
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Asn Thr Asn Ala Gly Asn Asp Ser Gly Asp Gln Asp Phe Asp Ser Gly  
35 40 45

Asn Thr Ser Ser Gly Asn His Gly Glu Gly Leu Gly Asn Asn Gln Ala  
50 55 60

Pro Arg His Lys Lys Lys Lys Tyr Asn Arg His Thr Gln Leu Gln Ile  
65 70 75 80

Ser Glu Met Glu Ala Phe Phe Arg Glu Cys Pro His Pro Asp Asp Lys  
85 90 95

Gln Arg Tyr Asp Leu Ser Ala Gln Leu Gly Leu Asp Pro Val Gln Ile  
100 105 110

Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln Asn Lys Asn Gln Gln Glu  
115 120 125

Arg Phe Glu Asn Ser Glu Leu Arg Asn Leu Asn Asn His Leu Arg Ser  
130 135 140

Glu Asn Gln Arg Leu Arg Glu Ala Ile His Gln Ala Leu Cys Pro Lys  
145 150 155 160

Cys Gly Gly Gln Thr Ala Ile Gly Glu Met Thr Phe Glu Glu His His  
165 170 175

Leu Arg Ile Leu Asn Ala Arg Leu Thr Glu Glu Ile Lys Gln Leu Ser  
180 185 190



Val Thr Ala Glu Lys Ile Ser Arg Leu Thr Gly Ile Pro Val Arg Ser  
 195 200 205

His Pro Arg Val Ser Pro Pro Asn Pro Pro Pro Asn Phe Glu Phe Gly  
 210 215 220

Met Gly Ser Lys Gly Asn Val Gly Asn His Ser Arg Glu Thr Thr Gly  
 225 230 235 240

Pro Ala Asp Ala Asn Thr Lys Pro Ile Ile Met Glu Leu Ala Phe Gly  
 245 250 255

Ala Met Glu Glu Leu Leu Val Met Ala Gln Val Ala Glu Pro Leu Trp  
 260 265 270

Met Gly Gly Phe Asn Gly Thr Ser Leu Ala Leu Asn Leu Asp Glu Tyr  
 275 280 285

Glu Lys Thr Phe Arg Thr Gly Leu Gly Pro Arg Leu Gly Gly Phe Arg  
 290 295 300

Thr Glu Ala Ser Arg Glu Thr Ala Leu Val Ala Met Cys Pro Thr Gly  
 305 310 315 320

Ile Val Glu Met Leu Met Gln Glu Asn Leu Trp Ser Thr Met Phe Ala  
 325 330 335

Gly Ile Val Gly Arg Ala Arg Thr His Glu Gln Ile Met Ala Asp Ala  
 340 345 350

Ala Gly Asn Phe Asn Gly Asn Leu Gln Ile Met Ser Ala Glu Tyr Gln  
 355 360 365

Val Leu Ser Pro Leu Val Thr Thr Arg Glu Ser Tyr Phe Val Arg Tyr  
 370 375 380

Cys Lys Gln Gln Gly Glu Gly Leu Trp Ala Val Val Asp Ile Ser Ile  
 385 390 395 400

Asp His Leu Leu Pro Asn Ile Asn Leu Lys Cys Arg Arg Arg Pro Ser  
 405 410 415

Gly Cys Leu Ile Gln Glu Met His Ser Gly Tyr Ser Lys Val Thr Trp  
 420 425 430



Val Glu His Val Glu Val Asp Asp Ala Gly Ser Tyr Ser Ile Phe Glu  
435 440 445

Lys Leu Ile Cys Thr Gly Gln Ala Phe Ala Ala Asn Arg Trp Val Gly  
450 455 460

Thr Leu Val Arg Gln Cys Glu Arg Ile Ser Ser Ile Leu Ser Thr Asp  
465 470 475 480

Phe Gln Ser Val Asp Ser Gly Asp His Ile Thr Leu Thr Asn His Gly  
485 490 495

Lys Met Ser Met Leu Lys Ile Ala Glu Arg Ile Ala Arg Thr Phe Phe  
500 505 510

Ala Gly Met Thr Asn Ala Thr Gly Ser Thr Ile Phe Ser Gly Val Glu  
515 520 525

Gly Glu Asp Ile Arg Val Met Thr Met Lys Ser Val Asn Asp Pro Gly  
530 535 540

Lys Pro Pro Gly Val Ile Ile Cys Ala Ala Thr Ser Phe Trp Leu Pro  
545 550 555 560

Ala Pro Pro Asn Thr Val Phe Asp Phe Leu Arg Glu Ala Thr His Arg  
565 570 575

His Asn Trp Asp Val Leu Cys Asn Gly Glu Met Met His Lys Ile Ala  
580 585 590

Glu Ile Thr Asn Gly Ile Asp Lys Arg Asn Cys Ala Ser Leu Leu Arg  
595 600 605

His Gly His Thr Ser Lys Ser Lys Met Met Ile Val Gln Glu Thr Ser  
610 615 620

Thr Asp Pro Thr Ala Ser Phe Val Leu Tyr Ala Pro Val Asp Met Thr  
625 630 635 640

Ser Met Asp Ile Thr Leu His Gly Gly Gly Asp Pro Asp Phe Val Val  
645 650 655

Ile Leu Pro Ser Gly Phe Ala Ile Phe Pro Asp Gly Thr Gly Lys Pro  
660 665 670

Gly Gly Lys Glu Gly Gly Ser Leu Leu Thr Ile Ser Phe Gln Met Leu



675	680	685
Val Glu Ser Gly Pro Glu Ala Arg Leu Ser Val Ser Ser Val Ala Thr		
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 35 40 45  
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 192  
 Gly Pro Leu Val Glu Val Pro Arg Tyr Gly Glu Arg Val Phe Tyr Phe  
 50 55 60  
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 65 70 75 80  
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 288  
 Val Asp Gln Glu Ile Pro Val Phe Asn Leu Pro Pro Lys Ile Leu Cys  
 85 90 95  
 cgt gtt ctt agt gtt acg tta aaa gca gaa cat gag acc gat gag gtt  
 336  
 Arg Val Leu Ser Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val  
 100 105 110  
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 384  
 Tyr Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr  
 115 120 125  
 agt ctt gac cca cct tta gta gaa cca gct aaa cca acg gtt gat tct  
 432



Ser Leu Asp Pro Pro Leu Val Glu Pro Ala Lys Pro Thr Val Asp Ser  
 130 135 140  
 ttt gtg aag att cta aca gct tca gat aca agc aca cat ggt gga ttc  
 480  
 Phe Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe  
 145 150 155 160  
 tct gtt ctt cgt aaa cac gcc act gag tgt tta cct tca ctt gat atg  
 528  
 Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met  
 165 170 175  
 aca caa cct aca ccg act caa gaa ctt gta gct aga gat ctt cac ggc  
 576  
 Thr Gln Pro Thr Pro Thr Gln Glu Leu Val Ala Arg Asp Leu His Gly  
 180 185 190  
 tat gaa tgg agg ttt aag cat ata ttt aga ggg caa ccg agg agg cat  
 624  
 Tyr Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His  
 195 200 205  
 tta ctt aca acc ggt tgg agt aca ttt gta acc tcg aaa aga ctt gta  
 672  
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 210 215 220  
 gct gga gat gca ttt gtg ttc ttg agg ggt gaa acc ggg gat tta cgg  
 720  
 Ala Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Thr Gly Asp Leu Arg  
 225 230 235 240  
 gtt ggt gtg agg cgt tta gct aag cag caa agc acg atg ccc gca tcc  
 768  
 Val Gly Val Arg Arg Leu Ala Lys Gln Gln Ser Thr Met Pro Ala Ser  
 245 250 255  
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 816  
 Val Ile Ser Ser Gln Ser Met Arg Leu Gly Val Leu Ala Thr Ala Ser  
 260 265 270  
 cat gct gtt acc aca aca act ata ttt gtt gtc ttc tat aaa cca agg  
 864  
 His Ala Val Thr Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg  
 275 280 285  
 ata agc cag ttt ata att agt gtg aac aag tat atg atg gcg atg aag  
 912  
 Ile Ser Gln Phe Ile Ile Ser Val Asn Lys Tyr Met Met Ala Met Lys  
 290 295 300  
 aac ggg ttt tct ctc ggt atg cgg tat agg atg aga ttc gaa gga gaa  
 960  
 Asn Gly Phe Ser Leu Gly Met Arg Tyr Arg Met Arg Phe Glu Gly Glu  
 305 310 315 320  
 gag tct cct gag aga ata ttt aca ggt acc att att ggc agt gga gat  
 1008  
 Glu Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Ile Gly Ser Gly Asp



	325		330		335
cta tct tct caa tgg cca gct tcc aaa tgg agg tca ttg cag atc caa					
1056					
Leu Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Ile Gln					
	340		345		350
tgg gac gag cca tct tct ata cag aga cca aac aag gtc tca ccg tgg					
1104					
Trp Asp Glu Pro Ser Ser Ile Gln Arg Pro Asn Lys Val Ser Pro Trp					
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gag atc gag cct ttc tca cca tcc gcg ctt aca cca acc cct act caa					
1152					
Glu Ile Glu Pro Phe Ser Pro Ser Ala Leu Thr Pro Thr Pro Thr Gln					
	370		375		380
caa caa tca aag tcc aaa cgg tcc aga cca atc tca gaa atc aca ggg					
1200					
Gln Gln Ser Lys Ser Lys Arg Ser Arg Pro Ile Ser Glu Ile Thr Gly					
	385		390		400
agt cct gta gct tct agt ttc ttg agt agt ttc tcg cag agc cac gag					
1248					
Ser Pro Val Ala Ser Ser Phe Leu Ser Ser Phe Ser Gln Ser His Glu					
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tct aat cca tcg gtc aaa ctg ttg ttt caa gat cca gca acc gag aga					
1296					
Ser Asn Pro Ser Val Lys Leu Leu Phe Gln Asp Pro Ala Thr Glu Arg					
	420		425		430
aac tca aac aaa tca gtg ttt tca agt gga tta caa tgc aag ata acc					
1344					
Asn Ser Asn Lys Ser Val Phe Ser Ser Gly Leu Gln Cys Lys Ile Thr					
	435		440		445
gag gct ccg gtc aca agt agt tgt agg tta ttc gga ttc gat ctc acg					
1392					
Glu Ala Pro Val Thr Ser Ser Cys Arg Leu Phe Gly Phe Asp Leu Thr					
	450		455		460
agc aag cct gct tct gct aca att cct cat gac aag cag cta ata agt					
1440					
Ser Lys Pro Ala Ser Ala Thr Ile Pro His Asp Lys Gln Leu Ile Ser					
	465		470		475
gtg gat tca aat ata tct gat tct acc acc aag tgt caa gat cct aac					
1488					
Val Asp Ser Asn Ile Ser Asp Ser Thr Thr Lys Cys Gln Asp Pro Asn					
	485		490		495
tct tca aac tca cca aaa gag cag aaa caa caa aca tcc aca aga agc					
1536					
Ser Ser Asn Ser Pro Lys Glu Gln Lys Gln Gln Thr Ser Thr Arg Ser					
	500		505		510
cga atc aag gtg caa atg caa gga aca gcg gtt gga cgc gcg gtt gat					
1584					
Arg Ile Lys Val Gln Met Gln Gly Thr Ala Val Gly Arg Ala Val Asp					
	515		520		525



tta aca ttg ttg aga tca tac gat gaa cta ata aaa gag cta gag aaa  
1632

Leu Thr Leu Leu Arg Ser Tyr Asp Glu Leu Ile Lys Glu Leu Glu Lys  
530 535 540

atg ttt gag att gaa gga gaa ctt agt cct aaa gac aaa tgg gct atc  
1680

Met Phe Glu Ile Glu Gly Glu Leu Ser Pro Lys Asp Lys Trp Ala Ile  
545 550 555 560

gtg ttt aca gac gat gaa gga gat agg atg ctt gta gga gat gat cca  
1728

Val Phe Thr Asp Asp Glu Gly Asp Arg Met Leu Val Gly Asp Asp Pro  
565 570 575

tgg aat gag ttc tgt aaa atg gca aag aag tta ttc ata tat ccg agt  
1776

Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Leu Phe Ile Tyr Pro Ser  
580 585 590

gat gag gtc aag aaa atg agg tcg aag tcg ttg ttg ggt gat aaa ggt  
1824

Asp Glu Val Lys Lys Met Arg Ser Lys Ser Leu Leu Gly Asp Lys Gly  
595 600 605

acg atc gta aat ctt gaa tca gat cag agg aca gtt cac gtt taa  
1869

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610 615 620

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392

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1 5 10 15

Gln Ile Leu Gln Leu Trp Leu Lys Leu Ile Ala Val Gly Trp Asn Leu  
20 25 30

Gly Ser Asn Asp Asp Glu Leu Tyr Thr Glu Leu Trp Lys Ala Cys Ala  
35 40 45

Gly Pro Leu Val Glu Val Pro Arg Tyr Gly Glu Arg Val Phe Tyr Phe  
50 55 60

Pro Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Val  
65 70 75 80

Val Asp Gln Glu Ile Pro Val Phe Asn Leu Pro Pro Lys Ile Leu Cys  
85 90 95

Arg Val Leu Ser Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val  
100 105 110



Tyr Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr  
 115 120 125

Ser Leu Asp Pro Pro Leu Val Glu Pro Ala Lys Pro Thr Val Asp Ser  
 130 135 140

Phe Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe  
 145 150 155 160

Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met  
 165 170 175

Thr Gln Pro Thr Pro Thr Gln Glu Leu Val Ala Arg Asp Leu His Gly  
 180 185 190

Tyr Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His  
 195 200 205

Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys Arg Leu Val  
 210 215 220

Ala Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Thr Gly Asp Leu Arg  
 225 230 235 240

Val Gly Val Arg Arg Leu Ala Lys Gln Gln Ser Thr Met Pro Ala Ser  
 245 250 255

Val Ile Ser Ser Gln Ser Met Arg Leu Gly Val Leu Ala Thr Ala Ser  
 260 265 270

His Ala Val Thr Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg  
 275 280 285

Ile Ser Gln Phe Ile Ile Ser Val Asn Lys Tyr Met Met Ala Met Lys  
 290 295 300

Asn Gly Phe Ser Leu Gly Met Arg Tyr Arg Met Arg Phe Glu Gly Glu  
 305 310 315 320

Glu Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Ile Gly Ser Gly Asp  
 325 330 335

Leu Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Ile Gln  
 340 345 350



Trp Asp Glu Pro Ser Ser Ile Gln Arg Pro Asn Lys Val Ser Pro Trp  
 355 360 365

Glu Ile Glu Pro Phe Ser Pro Ser Ala Leu Thr Pro Thr Pro Thr Gln  
 370 375 380

Gln Gln Ser Lys Ser Lys Arg Ser Arg Pro Ile Ser Glu Ile Thr Gly  
 385 390 395 400

Ser Pro Val Ala Ser Ser Phe Leu Ser Ser Phe Ser Gln Ser His Glu  
 405 410 415

Ser Asn Pro Ser Val Lys Leu Leu Phe Gln Asp Pro Ala Thr Glu Arg  
 420 425 430

Asn Ser Asn Lys Ser Val Phe Ser Ser Gly Leu Gln Cys Lys Ile Thr  
 435 440 445

Glu Ala Pro Val Thr Ser Ser Cys Arg Leu Phe Gly Phe Asp Leu Thr  
 450 455 460

Ser Lys Pro Ala Ser Ala Thr Ile Pro His Asp Lys Gln Leu Ile Ser  
 465 470 475 480

Val Asp Ser Asn Ile Ser Asp Ser Thr Thr Lys Cys Gln Asp Pro Asn  
 485 490 495

Ser Ser Asn Ser Pro Lys Glu Gln Lys Gln Gln Thr Ser Thr Arg Ser  
 500 505 510

Arg Ile Lys Val Gln Met Gln Gly Thr Ala Val Gly Arg Ala Val Asp  
 515 520 525

Leu Thr Leu Leu Arg Ser Tyr Asp Glu Leu Ile Lys Glu Leu Glu Lys  
 530 535 540

Met Phe Glu Ile Glu Gly Glu Leu Ser Pro Lys Asp Lys Trp Ala Ile  
 545 550 555 560

Val Phe Thr Asp Asp Glu Gly Asp Arg Met Leu Val Gly Asp Asp Pro  
 565 570 575

Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Leu Phe Ile Tyr Pro Ser  
 580 585 590



Asp Glu Val Lys Lys Met Arg Ser Lys Ser Leu Leu Gly Asp Lys Gly  
 595 600 605

Thr Ile Val Asn Leu Glu Ser Asp Gln Arg Thr Val His Val  
 610 615 620

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 cca aag agt acc tct gat aac gac ttg gga atc acc ggt agc cga gaa  
 96  
 Pro Lys Ser Thr Ser Asp Asn Asp Leu Gly Ile Thr Gly Ser Arg Glu  
 20 25 30  
 gat gac ttt gag acc aag tca ggt acc gaa gtc act act gag aat cct  
 144  
 Asp Asp Phe Glu Thr Lys Ser Gly Thr Glu Val Thr Thr Glu Asn Pro  
 35 40 45  
 tct ggt gaa gag ctt caa gat cct agc caa cgt ccc aac aaa aag aag  
 192  
 Ser Gly Glu Glu Leu Gln Asp Pro Ser Gln Arg Pro Asn Lys Lys Lys  
 50 55 60  
 cgt tac cat cgc cac acg caa cgc caa att caa gag ctc gaa tca ttc  
 240  
 Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe  
 65 70 75 80  
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 288  
 Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser  
 85 90 95  
 cgt gat ctc aat tta gag cct ctt caa gtt aag ttt tgg ttc caa aac  
 336  
 Arg Asp Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn  
 100 105 110  
 aaa cgc aca cag atg aag gca caa agt gag agg cat gag aac cag att  
 384  
 Lys Arg Thr Gln Met Lys Ala Gln Ser Glu Arg His Glu Asn Gln Ile  
 115 120 125  
 cta aag tca gac aat gac aag ctc aga gca gag aac aat aga tac aaa  
 432  
 Leu Lys Ser Asp Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys  
 130 135 140  
 gaa gct cta agc aat gct aca tgc cct aac tgt ggc ggt cca gct gct  
 480  
 Glu Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala  
 145 150 155 160



att gga gaa atg tct ttt gac gaa caa cat ctc agg atc gaa aat gct  
 528  
 Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala  
 165 170 175

cgg ctc cgc gaa gag att gat agg atc tct gct att gct gcg aaa tac  
 576  
 Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr  
 180 185 190

gtt ggg aag ccg tta gga tcg tct ttc gct cca cta gcg atc cac gcg  
 624  
 Val Gly Lys Pro Leu Gly Ser Ser Phe Ala Pro Leu Ala Ile His Ala  
 195 200 205

cct tct cgt tcg ctt gat ctt gaa gtt gga aac ttt ggg aac cag aca  
 672  
 Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly Asn Gln Thr  
 210 215 220

ggc ttt gta gga gaa atg tat gga aca ggg gac att ttg agg tca gtt  
 720  
 Gly Phe Val Gly Glu Met Tyr Gly Thr Gly Asp Ile Leu Arg Ser Val  
 225 230 235 240

tcg att cct tct gag act gat aag cct ata atc gtg gag cta gcg gtt  
 768  
 Ser Ile Pro Ser Glu Thr Asp Lys Pro Ile Ile Val Glu Leu Ala Val  
 245 250 255

gca gct atg gag gaa ctc gtg aga atg gct caa act gga gat cct tta  
 816  
 Ala Ala Met Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu  
 260 265 270

tgg ctt tca acc gat aat tca gtc gag att ctc aac gaa gaa gag tat  
 864  
 Trp Leu Ser Thr Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr  
 275 280 285

ttc aga acg ttt ccg aga gga att gga cca aag cca tta gga tta aga  
 912  
 Phe Arg Thr Phe Pro Arg Gly Ile Gly Pro Lys Pro Leu Gly Leu Arg  
 290 295 300

tca gag gcg tca aga caa tct gca gtt gtt ata atg aat cac atc aat  
 960  
 Ser Glu Ala Ser Arg Gln Ser Ala Val Val Ile Met Asn His Ile Asn  
 305 310 315 320

ctc gtt gag att ctc atg gat gtg aat caa tgg tct tgt gtt ttc tct  
 1008  
 Leu Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Cys Val Phe Ser  
 325 330 335

ggg att gtg tca aga gcc ttg aca ctt gaa gtt ctt tca act gga gtt  
 1056  
 Gly Ile Val Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val  
 340 345 350



gct ggg aac tac aac ggt gct tta caa gtg atg aca gct gag ttt caa  
1104

Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln  
355 360 365

gtt cca tca ccc cta gtc cca acg cgt gag aac tac ttt gtg aga tac  
1152

Val Pro Ser Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr  
370 375 380

tgc aaa caa cac agt gac ggc tct tgg gct gtg gtt gat gtc tct ttg  
1200

Cys Lys Gln His Ser Asp Gly Ser Trp Ala Val Val Asp Val Ser Leu  
385 390 395 400

gac agc ctt aga cca agt act cca atc tta aga act aga aga agg cct  
1248

Asp Ser Leu Arg Pro Ser Thr Pro Ile Leu Arg Thr Arg Arg Arg Pro  
405 410 415

tca ggt tgt ctg att caa gaa ttg cct aat ggt tat tct aag gtt aca  
1296

Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys Val Thr  
420 425 430

tgg ata gag cat atg gag gta gat gat aga tca gtt cac aac atg tat  
1344

Trp Ile Glu His Met Glu Val Asp Asp Arg Ser Val His Asn Met Tyr  
435 440 445

aaa ccg ttg gtt cag tcc ggt tta gct ttc ggt gcg aaa cgt tgg gtg  
1392

Lys Pro Leu Val Gln Ser Gly Leu Ala Phe Gly Ala Lys Arg Trp Val  
450 455 460

gct aca ctc gaa cga caa tgc gag cgg ctt gct agc tcc atg gcc agc  
1440

Ala Thr Leu Glu Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser  
465 470 475 480

aac att cct ggt gat ctt tcc gtg ata acg agt cct gaa gga agg aag  
1488

Asn Ile Pro Gly Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys  
485 490 495

agt atg ttg aag cta gct gag aga atg gtt atg agt ttc tgc agt ggt  
1536

Ser Met Leu Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Ser Gly  
500 505 510

gtt ggc gcg tcg act gca cac gct tgg aca aca atg tcg aca aca gga  
1584

Val Gly Ala Ser Thr Ala His Ala Trp Thr Thr Met Ser Thr Thr Gly  
515 520 525

tcc gat gat gtt cgg gtc atg acc cgc aag agt atg gat gat cca gga  
1632

Ser Asp Asp Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly  
530 535 540



aga cct ccg ggt att gtt ctt agt gca gct act tca ttc tgg atc cca  
 1680  
 Arg Pro Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro  
 545 550 555 560

gtt gct ccc aaa cgt gtt ttt gat ttc ctc cgt gac gaa aat tca aga  
 1728  
 Val Ala Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg  
 565 570 575

aaa gag tgg gat att ctg tca aat gga ggt atg gtt cag gaa atg gct  
 1776  
 Lys Glu Trp Asp Ile Leu Ser Asn Gly Gly Met Val Gln Glu Met Ala  
 580 585 590

cat ata gcc aat ggt cat gaa cct gga aac tgt gtc tcc ttg ctc cga  
 1824  
 His Ile Ala Asn Gly His Glu Pro Gly Asn Cys Val Ser Leu Leu Arg  
 595 600 605

gtc aat agt gga aac tcg agc cag agc aac atg ttg att cta caa gag  
 1872  
 Val Asn Ser Gly Asn Ser Ser Gln Ser Asn Met Leu Ile Leu Gln Glu  
 610 615 620

agc tgt aca gat gca tca gga tcg tat gtg att tac gcg cca gtg gat  
 1920  
 Ser Cys Thr Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp  
 625 630 635 640

ata gtg gcg atg aat gtg gtt cta agc ggt gga gat cct gat tac gtg  
 1968  
 Ile Val Ala Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val  
 645 650 655

gcg ttg ttg ccg tct ggt ttt gct att tta ccg gat ggt tcg gtt gga  
 2016  
 Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Val Gly  
 660 665 670

gga gga gat ggg aat cag cat cag gaa atg gtt tct act act tct tct  
 2064  
 Gly Gly Asp Gly Asn Gln His Gln Glu Met Val Ser Thr Thr Ser Ser  
 675 680 685

ggg agt tgt ggt ggt tcg ctt tta acc gtt gcg ttt cag att ctt gtt  
 2112  
 Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val  
 690 695 700

gac tct gtt cct aca gct aaa ctc tca ctt ggc tcg gtg gct acg gtt  
 2160  
 Asp Ser Val Pro Thr Ala Lys Leu Ser Leu Gly Ser Val Ala Thr Val  
 705 710 715 720

aat agt ctg atc aaa tgt acg gtg gag agg att aaa gct gct gtt tct  
 2208  
 Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys Ala Ala Val Ser  
 725 730 735



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 2232  
 Cys Asp Val Gly Gly Gly Ala  
 740

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 20 25 30

Asp Asp Phe Glu Thr Lys Ser Gly Thr Glu Val Thr Thr Glu Asn Pro  
 35 40 45

Ser Gly Glu Glu Leu Gln Asp Pro Ser Gln Arg Pro Asn Lys Lys Lys  
 50 55 60

Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe  
 65 70 75 80

Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser  
 85 90 95

Arg Asp Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn  
 100 105 110

Lys Arg Thr Gln Met Lys Ala Gln Ser Glu Arg His Glu Asn Gln Ile  
 115 120 125

Leu Lys Ser Asp Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys  
 130 135 140

Glu Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala  
 145 150 155 160

Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala  
 165 170 175

Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr  
 180 185 190

Val Gly Lys Pro Leu Gly Ser Ser Phe Ala Pro Leu Ala Ile His Ala  
 195 200 205



Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly Asn Gln Thr  
 210 215 220

Gly Phe Val Gly Glu Met Tyr Gly Thr Gly Asp Ile Leu Arg Ser Val  
 225 230 235 240

Ser Ile Pro Ser Glu Thr Asp Lys Pro Ile Ile Val Glu Leu Ala Val  
 245 250 255

Ala Ala Met Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu  
 260 265 270

Trp Leu Ser Thr Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr  
 275 280 285

Phe Arg Thr Phe Pro Arg Gly Ile Gly Pro Lys Pro Leu Gly Leu Arg  
 290 295 300

Ser Glu Ala Ser Arg Gln Ser Ala Val Val Ile Met Asn His Ile Asn  
 305 310 315 320

Leu Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Cys Val Phe Ser  
 325 330 335

Gly Ile Val Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val  
 340 345 350

Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln  
 355 360 365

Val Pro Ser Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr  
 370 375 380

Cys Lys Gln His Ser Asp Gly Ser Trp Ala Val Val Asp Val Ser Leu  
 385 390 395 400

Asp Ser Leu Arg Pro Ser Thr Pro Ile Leu Arg Thr Arg Arg Arg Pro  
 405 410 415

Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys Val Thr  
 420 425 430

Trp Ile Glu His Met Glu Val Asp Asp Arg Ser Val His Asn Met Tyr  
 435 440 445

Lys Pro Leu Val Gln Ser Gly Leu Ala Phe Gly Ala Lys Arg Trp Val



450                      455                      460  
 Ala Thr Leu Glu Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser  
 465                      470                      475                      480  
 Asn Ile Pro Gly Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys  
                     485                      490                      495  
 Ser Met Leu Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Ser Gly  
                     500                      505                      510  
 Val Gly Ala Ser Thr Ala His Ala Trp Thr Thr Met Ser Thr Thr Gly  
                     515                      520                      525  
 Ser Asp Asp Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly  
                     530                      535                      540  
 Arg Pro Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro  
 545                      550                      555                      560  
 Val Ala Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg  
                     565                      570                      575  
 Lys Glu Trp Asp Ile Leu Ser Asn Gly Gly Met Val Gln Glu Met Ala  
                     580                      585                      590  
 His Ile Ala Asn Gly His Glu Pro Gly Asn Cys Val Ser Leu Leu Arg  
                     595                      600                      605  
 Val Asn Ser Gly Asn Ser Ser Gln Ser Asn Met Leu Ile Leu Gln Glu  
                     610                      615                      620  
 Ser Cys Thr Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp  
 625                      630                      635                      640  
 Ile Val Ala Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val  
                     645                      650                      655  
 Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Val Gly  
                     660                      665                      670  
 Gly Gly Asp Gly Asn Gln His Gln Glu Met Val Ser Thr Thr Ser Ser  
                     675                      680                      685  
 Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val  
                     690                      695                      700



Asp Ser Val Pro Thr Ala, Lys Leu Ser Leu Gly Ser Val Ala Thr Val  
705 710 715 720

Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys Ala Ala Val Ser  
725 730 735

Cys Asp Val Gly Gly Gly Ala  
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114  
Met Met Met Asp Glu Phe Met  
1 5

gat ctt aga cca gtg aag tac aca gag cac aag aot gtt atc aga aag  
162  
Asp Leu Arg Pro Val Lys Tyr Thr Glu His Lys Thr Val Ile Arg Lys  
10 15 20

tac act aaa aag tcg tct atg gag agg aag acc agt gtt cgt gac tcg  
210  
Tyr Thr Lys Lys Ser Ser Met Glu Arg Lys Thr Ser Val Arg Asp Ser  
25 30 35

gcc agg ttg gtt cgg gtc tca atg acg gat cgt gac gcc act gat tca  
258  
Ala Arg Leu Val Arg Val Ser Met Thr Asp Arg Asp Ala Thr Asp Ser  
40 45 50 55

tca agc gac gag gaa gag ttt ctg ttc cct cga aga cgt gtc aag aga  
306  
Ser Ser Asp Glu Glu Glu Phe Leu Phe Pro Arg Arg Arg Val Lys Arg  
60 65 70

ttg att aac gag atc aga gtc gag cct agc agc tct tcc acc ggc gac  
354  
Leu Ile Asn Glu Ile Arg Val Glu Pro Ser Ser Ser Ser Thr Gly Asp  
75 80 85

gtc tct gct tct ccg acg aag gac cgg aaa aga atc aac gtt gat tct  
402  
Val Ser Ala Ser Pro Thr Lys Asp Arg Lys Arg Ile Asn Val Asp Ser  
90 95 100

acg gtt caa aag ccc tct gtt tcc ggc caa aac cag aag aag tac cgc  
450  
Thr Val Gln Lys Pro Ser Val Ser Gly Gln Asn Gln Lys Lys Tyr Arg  
105 110 115



ggc gtg aga cag cga cca tgg gga aaa tgg gcg gcg gag att cgt gat  
 498  
 Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp  
 120 125 130 135  
 cct gag caa cgc cgg aga atc tgg ctc ggt act ttt gca acg gcg gag  
 546  
 Pro Glu Gln Arg Arg Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu  
 140 145 150  
 gaa gct gcc atc gtc tac gac aac gca gca atc aaa ctt cgt ggc cct  
 594  
 Glu Ala Ala Ile Val Tyr Asp Asn Ala Ala Ile Lys Leu Arg Gly Pro  
 155 160 165  
 gat gct ctt acc aac ttc acc gta caa cca gaa cca gaa ccg gta caa  
 642  
 Asp Ala Leu Thr Asn Phe Thr Val Gln Pro Glu Pro Glu Pro Val Gln  
 170 175 180  
 gaa caa gaa caa gaa ccg gag agc aac atg tcg gtt tcg ata tca gaa  
 690  
 Glu Gln Glu Gln Glu Pro Glu Ser Asn Met Ser Val Ser Ile Ser Glu  
 185 190 195  
 tca atg gac gat tct caa cat cta tca tct ccg aca tcg gtt ctc aac  
 738  
 Ser Met Asp Asp Ser Gln His Leu Ser Ser Pro Thr Ser Val Leu Asn  
 200 205 210 215  
 tac caa aca tat gtc tcg gag gaa cca atc gat agt ctt atc aaa ccg  
 786  
 Tyr Gln Thr Tyr Val Ser Glu Glu Pro Ile Asp Ser Leu Ile Lys Pro  
 220 225 230  
 gtt aaa caa gag ttt ctt gaa cca gaa caa gag cca ata agc tgg cat  
 834  
 Val Lys Gln Glu Phe Leu Glu Pro Glu Gln Glu Pro Ile Ser Trp His  
 235 240 245  
 ctt gga gaa ggt aat act aat act aat gat gat tca ttt cca ttg gac  
 882  
 Leu Gly Glu Gly Asn Thr Asn Thr Asn Asp Asp Ser Phe Pro Leu Asp  
 250 255 260  
 att aca ttt ctc gac aac tat ttc aat gaa tca tta cca gac atc tcc  
 930  
 Ile Thr Phe Leu Asp Asn Tyr Phe Asn Glu Ser Leu Pro Asp Ile Ser  
 265 270 275  
 atc ttc gat caa cct atg tct cct att caa cca aca gag aat gat ttc  
 978  
 Ile Phe Asp Gln Pro Met Ser Pro Ile Gln Pro Thr Glu Asn Asp Phe  
 280 285 290 295  
 ttc aac gac ctt atg tta ttc gat agc aac gca gaa gaa tac tac tcc  
 1026  
 Phe Asn Asp Leu Met Leu Phe Asp Ser Asn Ala Glu Glu Tyr Tyr Ser  
 300 305 310



tcc gag atc aaa gag att ggt tca tcg ttc aac gat ctt gat gat tct  
 1074  
 Ser Glu Ile Lys Glu Ile Gly Ser Ser Phe Asn Asp Leu Asp Asp Ser  
           315                          320                          325

ttg ata tcc gat ctc tta ctt gtg tga ttttttgcc attaaccaaa  
 1121  
 Leu Ile Ser Asp Leu Leu Leu Val  
           330                          335

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 1136

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His Lys Thr Val Ile Arg Lys Tyr Thr Lys Lys Ser Ser Met Glu Arg  
           20                          25                          30

Lys Thr Ser Val Arg Asp Ser Ala Arg Leu Val Arg Val Ser Met Thr  
           35                          40                          45

Asp Arg Asp Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Phe Leu Phe  
           50                          55                          60

Pro Arg Arg Arg Val Lys Arg Leu Ile Asn Glu Ile Arg Val Glu Pro  
   65                          70                          75                          80

Ser Ser Ser Ser Thr Gly Asp Val Ser Ala Ser Pro Thr Lys Asp Arg  
                           85                          90                          95

Lys Arg Ile Asn Val Asp Ser Thr Val Gln Lys Pro Ser Val Ser Gly  
           100                          105                          110

Gln Asn Gln Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys  
           115                          120                          125

Trp Ala Ala Glu Ile Arg Asp Pro Glu Gln Arg Arg Arg Ile Trp Leu  
           130                          135                          140

Gly Thr Phe Ala Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn Ala  
   145                          150                          155                          160

Ala Ile Lys Leu Arg Gly Pro Asp Ala Leu Thr Asn Phe Thr Val Gln  
           165                          170                          175



Pro Glu Pro Glu Pro Val Gln Glu Gln Glu Gln Glu Pro Glu Ser Asn  
 180 185 190

Met Ser Val Ser Ile Ser Glu Ser Met Asp Asp Ser Gln His Leu Ser  
 195 200 205

Ser Pro Thr Ser Val Leu Asn Tyr Gln Thr Tyr Val Ser Glu Glu Pro  
 210 215 220

Ile Asp Ser Leu Ile Lys Pro Val Lys Gln Glu Phe Leu Glu Pro Glu  
 225 230 235 240

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Glu Ser Leu Pro Asp Ile Ser Ile Phe Asp Gln Pro Met Ser Pro Ile  
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Gln Pro Thr Glu Asn Asp Phe Phe Asn Asp Leu Met Leu Phe Asp Ser  
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Lys His Leu Gln Lys Arg Gly Pro Thr Glu Glu Ala Glu Gly Gly Asp  
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2174

Asp Ala Thr Thr Ser Ser Arg Asp His Val Thr Glu Arg Arg Ile Ala  
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2222

Val Glu Thr Leu Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala His Gln  
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Arg His Cys Val Gln Val Arg Glu Lys Ser Leu Asn Ser Leu Lys Ile  
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Glu Asn Leu Pro Pro Pro Pro Pro Leu Pro Lys Phe Ser Pro Ser  
100 105 110

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115 120 125

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130 135 140

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165 170 175

Arg Lys Arg Leu Glu Lys Thr Thr Pro Glu Ile Val Ser Ala Ser Pro  
180 185 190

Ala Asn Ser Met Ala Trp Asp Tyr Phe Phe Met Val Glu Asn Met Pro  
195 200 205

Gly Pro Asn Leu Asp Asp Arg Glu Val Arg Asn Gly Tyr Glu Asn Gln  
210 215 220

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225 230 235 240

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245 250 255



Val Glu Glu Met Glu Pro Lys Thr Pro Glu Lys Val Glu Glu Glu Glu  
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 Thr Trp Asn Lys Ser Leu Arg Gly Ile Ser Asn Gly Glu Gly Gly Lys  
 385 390 395 400  
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Phe Asp Thr Leu Val Thr His Gln Lys Gln Tyr Ile Asn Ser Leu Asn  
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Asn Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser Ser Leu Lys Glu  
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Lys Val Ser Ser Pro Pro Arg Pro Gln Arg Pro Pro Ile Gln Ala Leu  
595 600 605

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610 615 620

Lys Ser Ala Ile Ser Ser Phe Ala Ala Val Ile Lys Thr Ile Leu Leu  
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His Leu Gln Lys Arg Gly Pro Thr Glu Glu Ala Glu Gly Gly Asp Asp  
675 680 685

Ala Thr Thr Ser Ser Arg Asp His Val Thr Glu Arg Arg Ile Ala Val  
690 695 700

Glu Thr Leu Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala His Gln Arg  
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His Cys Val Gln Val Arg Glu Lys Ser Leu Asn Ser Leu Lys Ile Arg  
725 730 735



Leu Pro Glu Ile Phe Arg Ala Leu Ser Asp Tyr Ala His Ala Cys Ala  
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Asp Cys Ser Asp Leu Phe Phe Val Asp Gln Met Ser Leu Glu Pro Ala  
 35 40 45

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Ile Pro Ser Pro Cys Tyr Gly Glu Ser Asp Thr Gly Ser Val Lys Ile  
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 299

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Pro Ser Pro Cys Tyr Gly Glu Ser Asp Thr Gly Ser Val Lys Ile Asn  
50 55 60

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85 90 95

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115 120 125

Lys Lys Met Ile Gln Pro Glu Met Thr Asp Glu Arg Lys Arg Lys Arg  
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145 150 155 160

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180 185 190

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600

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648  
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35 40 45

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85 90 95

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 1661  
 aactcatttt tcgttcttat tctttgtttt ccaacggaat ttggcgacac aacgatttat  
 1721  
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 1740  
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 402  
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1 5 10 15

Gln Leu Lys Ser Phe Trp Ser Lys Gly Met Glu Gly Asp Leu Asn Val  
20 25 30

Lys Asn His Glu Phe Pro Ile Ser Arg Ile Lys Arg Ile Met Lys Phe  
35 40 45

Asp Pro Asp Val Ser Met Ile Ala Ala Glu Ala Pro Asn Leu Leu Ser  
50 55 60

Lys Ala Cys Glu Met Phe Val Met Asp Leu Thr Met Arg Ser Trp Leu  
65 70 75 80

His Ala Gln Glu Ser Asn Arg Leu Thr Ile Arg Lys Ser Asp Val Asp  
85 90 95

Ala Val Val Ser Gln Thr Val Ile Phe Asp Phe Leu Arg Asp Asp Val  
100 105 110

Pro Lys Asp Glu Gly Glu Pro Val Val Ala Ala Ala Asp Pro Val Asp  
115 120 125

Asp Val Ala Asp His Val Ala Val Pro Asp Leu Asn Asn Glu Glu Leu  
130 135 140

Pro Pro Gly Thr Val Ile Gly Thr Pro Val Cys Tyr Gly Leu Gly Ile  
145 150 155 160

His Ala Pro His Pro Gln Met Pro Gly Ala Trp Thr Glu Glu Asp Ala  
165 170 175

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180 185

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1 5 10 15  
tct tcc caa ctg ccg ccg cca cca ttg tat tat caa tca atg ccg ttg  
96  
Ser Ser Gln Leu Pro Pro Pro Pro Leu Tyr Tyr Gln Ser Met Pro Leu  
20 25 30



ccg tca tat tca ctg ccg ctg ccg tac tca ccg cag atg cgg aat tat  
 144  
 Pro Ser Tyr Ser Leu Pro Leu Pro Tyr Ser Pro Gln Met Arg Asn Tyr  
 35 40 45

tgg att gcg cag atg gga aac gca act gat gtt aag cat cat gcg ttt  
 192  
 Trp Ile Ala Gln Met Gly Asn Ala Thr Asp Val Lys His His Ala Phe  
 50 55 60

cca cta acc agg ata aag aaa atc atg aag tcc aac ccg gaa gtg aac  
 240  
 Pro Leu Thr Arg Ile Lys Lys Ile Met Lys Ser Asn Pro Glu Val Asn  
 65 70 75 80

atg gtc act gca gag gct ccg gtc ctt ata tcg aag gcc tgt gag atg  
 288  
 Met Val Thr Ala Glu Ala Pro Val Leu Ile Ser Lys Ala Cys Glu Met  
 85 90 95

ctc att ctt gat ctc aca atg cga tcg tgg ctt cat acc gtg gag ggc  
 336  
 Leu Ile Leu Asp Leu Thr Met Arg Ser Trp Leu His Thr Val Glu Gly  
 100 105 110

ggt cgc caa act ctc aag aga tcc gat acg ctc acg aga tcc gat atc  
 384  
 Gly Arg Gln Thr Leu Lys Arg Ser Asp Thr Leu Thr Arg Ser Asp Ile  
 115 120 125

tcc gcc gca acg act cgt agt ttc aaa ttt acc ttc ctt ggc gac gtt  
 432  
 Ser Ala Ala Thr Thr Arg Ser Phe Lys Phe Thr Phe Leu Gly Asp Val  
 130 135 140

gtc cca aga gac cct tcc gtc gtt acc gat gat ccc gtg cta cat ccg  
 480  
 Val Pro Arg Asp Pro Ser Val Val Thr Asp Asp Pro Val Leu His Pro  
 145 150 155 160

gac ggt gaa gta ctt cct ccg gga acg gtg ata gga tat ccg gtg ttt  
 528  
 Asp Gly Glu Val Leu Pro Pro Gly Thr Val Ile Gly Tyr Pro Val Phe  
 165 170 175

gat tgt aat ggt gtg tac gcg tca ccg cca cag atg cag gag tgg ccg  
 576  
 Asp Cys Asn Gly Val Tyr Ala Ser Pro Pro Gln Met Gln Glu Trp Pro  
 180 185 190

gcg gtg cct ggt gac gga gag gag gca gct ggg gaa att gga gga agc  
 624  
 Ala Val Pro Gly Asp Gly Glu Glu Ala Ala Gly Glu Ile Gly Gly Ser  
 195 200 205

agc ggc ggt aat tga  
 639  
 Ser Gly Gly Asn  
 210



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Met Glu Glu Asn Asn Gly Asn Asn Asn His Tyr Leu Pro Gln Pro Ser  
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20 25 30

Pro Ser Tyr Ser Leu Pro Leu Pro Tyr Ser Pro Gln Met Arg Asn Tyr  
35 40 45

Trp Ile Ala Gln Met Gly Asn Ala Thr Asp Val Lys His His Ala Phe  
50 55 60

Pro Leu Thr Arg Ile Lys Lys Ile Met Lys Ser Asn Pro Glu Val Asn  
65 70 75 80

Met Val Thr Ala Glu Ala Pro Val Leu Ile Ser Lys Ala Cys Glu Met  
85 90 95

Leu Ile Leu Asp Leu Thr Met Arg Ser Trp Leu His Thr Val Glu Gly  
100 105 110

Gly Arg Gln Thr Leu Lys Arg Ser Asp Thr Leu Thr Arg Ser Asp Ile  
115 120 125

Ser Ala Ala Thr Thr Arg Ser Phe Lys Phe Thr Phe Leu Gly Asp Val  
130 135 140

Val Pro Arg Asp Pro Ser Val Val Thr Asp Asp Pro Val Leu His Pro  
145 150 155 160

Asp Gly Glu Val Leu Pro Pro Gly Thr Val Ile Gly Tyr Pro Val Phe  
165 170 175

Asp Cys Asn Gly Val Tyr Ala Ser Pro Pro Gln Met Gln Glu Trp Pro  
180 185 190

Ala Val Pro Gly Asp Gly Glu Glu Ala Ala Gly Glu Ile Gly Gly Ser  
195 200 205

Ser Gly Gly Asn  
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 1 5 10 15  
 aat ctt aac aac gag tca aaa gaa aca tct gag aac agt gat gac caa  
 96  
 Asn Leu Asn Asn Glu Ser Lys Glu Thr Ser Glu Asn Ser Asp Asp Gln  
 20 25 30  
 cac agc gag atc aca aca att aca tcg gaa gaa gag aaa aca act gaa  
 144  
 His Ser Glu Ile Thr Thr Ile Thr Ser Glu Glu Glu Lys Thr Thr Glu  
 35 40 45  
 ctg aag aaa cca gac aag att ctt cca tgt ccg aga tgc aac agc gca  
 192  
 Leu Lys Lys Pro Asp Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Ala  
 50 55 60  
 gac acc aaa ttc tgt tac tac aac aac tac aac gtt aac cag cca cgt  
 240  
 Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg  
 65 70 75 80  
 cac ttc tgt aga aaa tgc cag agg tat tgg acc gct ggt gga tcc atg  
 288  
 His Phe Cys Arg Lys Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met  
 85 90 95  
 agg atc gtc ccg gtt ggc tca ggc cgt cgc aag aac aag gga tgg gtt  
 336  
 Arg Ile Val Pro Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Val  
 100 105 110  
 tct tca gac cag tac ctg cac atc act tcc gag gat act gac aat tac  
 384  
 Ser Ser Asp Gln Tyr Leu His Ile Thr Ser Glu Asp Thr Asp Asn Tyr  
 115 120 125  
 aat agc tcc tca aca aag att cta agc ttc gag tct tcg gac tct ttg  
 432  
 Asn Ser Ser Ser Thr Lys Ile Leu Ser Phe Glu Ser Ser Asp Ser Leu  
 130 135 140  
 gta act gag agg cct aag cat caa tca aac gaa gtg aag ata aac gct  
 480  
 Val Thr Glu Arg Pro Lys His Gln Ser Asn Glu Val Lys Ile Asn Ala  
 145 150 155 160  
 gaa cct gtt tca caa gaa ccc aac aac ttc caa ggg tta ctt cct ccc  
 528  
 Glu Pro Val Ser Gln Glu Pro Asn Asn Phe Gln Gly Leu Leu Pro Pro  
 165 170 175  
 caa gca tcc cct gtt tcg cct cct tgg cct tac caa tac cct cca aac  
 576  
 Gln Ala Ser Pro Val Ser Pro Pro Trp Pro Tyr Gln Tyr Pro Pro Asn  
 180 185 190



cct agt ttc tac cac atg ccc gtc tac tgg ggc tgc gcg ata ccg gtt  
624

Pro Ser Phe Tyr His Met Pro Val Tyr Trp Gly Cys Ala Ile Pro Val  
195 200 205

tgg tct acc ctc gac act tct aca tgt ctt ggg aaa agg aca aga gac  
672

Trp Ser Thr Leu Asp Thr Ser Thr Cys Leu Gly Lys Arg Thr Arg Asp  
210 215 220

gaa act tct cat gaa act gtt aaa gag agt aaa aat gct ttt gag aga  
720

Glu Thr Ser His Glu Thr Val Lys Glu Ser Lys Asn Ala Phe Glu Arg  
225 230 235 240

aca agc ttg ctt ttg gaa tct cag agc atc aaa aat gaa aca agt atg  
768

Thr Ser Leu Leu Leu Glu Ser Gln Ser Ile Lys Asn Glu Thr Ser Met  
245 250 255

gct aca aat aac cat gtg tgg tat cca gta ccg atg acc cgc gag aag  
816

Ala Thr Asn Asn His Val Trp Tyr Pro Val Pro Met Thr Arg Glu Lys  
260 265 270

aca caa gaa ttc agc ttt ttc agt aat gga gct gaa aca aag agc agc  
864

Thr Gln Glu Phe Ser Phe Phe Ser Asn Gly Ala Glu Thr Lys Ser Ser  
275 280 285

aac aac aga ttc gtc cct gaa acg tat ctt aac ctg caa gca aac cct  
912

Asn Asn Arg Phe Val Pro Glu Thr Tyr Leu Asn Leu Gln Ala Asn Pro  
290 295 300

gca gcc atg gca aga tct atg aac ttc aga gag agc ata taa  
954

Ala Ala Met Ala Arg Ser Met Asn Phe Arg Glu Ser Ile  
305 310 315

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406

Met Asn Asn Gln Ser Val Thr Asp Asn Thr Ser Leu Lys Leu Ser Ser  
1 5 10 15

Asn Leu Asn Asn Glu Ser Lys Glu Thr Ser Glu Asn Ser Asp Asp Gln  
20 25 30

His Ser Glu Ile Thr Thr Ile Thr Ser Glu Glu Glu Lys Thr Thr Glu  
35 40 45

Leu Lys Lys Pro Asp Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Ala  
50 55 60



Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg  
65 70 75 80

His Phe Cys Arg Lys Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met  
85 90 95

Arg Ile Val Pro Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Val  
100 105 110

Ser Ser Asp Gln Tyr Leu His Ile Thr Ser Glu Asp Thr Asp Asn Tyr  
115 120 125

Asn Ser Ser Ser Thr Lys Ile Leu Ser Phe Glu Ser Ser Asp Ser Leu  
130 135 140

Val Thr Glu Arg Pro Lys His Gln Ser Asn Glu Val Lys Ile Asn Ala  
145 150 155 160

Glu Pro Val Ser Gln Glu Pro Asn Asn Phe Gln Gly Leu Leu Pro Pro  
165 170 175

Gln Ala Ser Pro Val Ser Pro Pro Trp Pro Tyr Gln Tyr Pro Pro Asn  
180 185 190

Pro Ser Phe Tyr His Met Pro Val Tyr Trp Gly Cys Ala Ile Pro Val  
195 200 205

Trp Ser Thr Leu Asp Thr Ser Thr Cys Leu Gly Lys Arg Thr Arg Asp  
210 215 220

Glu Thr Ser His Glu Thr Val Lys Glu Ser Lys Asn Ala Phe Glu Arg  
225 230 235 240

Thr Ser Leu Leu Leu Glu Ser Gln Ser Ile Lys Asn Glu Thr Ser Met  
245 250 255

Ala Thr Asn Asn His Val Trp Tyr Pro Val Pro Met Thr Arg Glu Lys  
260 265 270

Thr Gln Glu Phe Ser Phe Phe Ser Asn Gly Ala Glu Thr Lys Ser Ser  
275 280 285

Asn Asn Arg Phe Val Pro Glu Thr Tyr Leu Asn Leu Gln Ala Asn Pro  
290 295 300

Ala Ala Met Ala Arg Ser Met Asn Phe Arg Glu Ser Ile



305

310

315

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 49

Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu  
 1 5 10 15

ggc gaa aac aac aat cct ttt tct tcc tta gat gac aaa aca tta atg  
 97

Gly Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met  
 20 25 30

atg atg gct cct tct tta atc ttt tct ggc gat gta ggt cca tct tct  
 145

Met Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser  
 35 40 45

tct tct tgt act cca gca ggt tat cat cta tct gct cag ctg gag aac  
 193

Ser Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn  
 50 55 60

ttt cga gga ggt gga gga gag atg gga gga tta gtg agt aat aat agc  
 241

Phe Arg Gly Gly Gly Gly Glu Met Gly Gly Leu Val Ser Asn Asn Ser  
 65 70 75

aat aat agt gat cat aat aag aat tgc aac aaa gga aaa ggg aag aga  
 289

Asn Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg  
 80 85 90 95

act ttg gca atg cag agg ata gct ttt cat aca agg agt gat gat gat  
 337

Thr Leu Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp  
 100 105 110

gtt ctt gat gat ggt tat cgt tgg cga aag tac ggt cag aaa tct gtc  
 385

Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val  
 115 120 125

aag aac aat gct cat ccc agg agc tat tat aga tgt aca tac cac aca  
 433

Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr  
 130 135 140

tgc aac gtg aag aaa caa gtg caa aga ctg gca aaa gat cca aac gtt  
 481

Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val  
 145 150 155

gtc gta aca acc tac gaa ggt gtt cat aat cat cct tgt gag aag ctc  
 529

Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu  
 160 165 170 175



atg gag act ctt agc cct ctc ctt agg caa ctt cag ttc ctc tca aga  
577

Met Glu Thr Leu Ser Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Arg  
180 185 190

gtt tct gat ctg taa ttattgaatg ttaattagt gtgtaataca ttaattatgc  
632

Val Ser Asp Leu  
195

tttaatctct ccattgaccc tcaatc  
658

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408

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1 5 10 15

Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met Met  
20 25 30

Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser Ser  
35 40 45

Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn Phe  
50 55 60

Arg Gly Gly Gly Gly Glu Met Gly Gly Leu Val Ser Asn Asn Ser Asn  
65 70 75 80

Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg Thr  
85 90 95

Leu Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val  
100 105 110

Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys  
115 120 125

Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys  
130 135 140

Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val  
145 150 155 160

Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met  
165 170 175



Glu Thr Leu Ser Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Arg Val  
 180 185 190

Ser Asp Leu  
 195

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 <221> CDS <222> (92)..(844) <223> G1939

<400> 409  
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 60

aaaagaaaac actaaacca gatcgaaaac c atg tct att aac aac aac aac  
 112

Met Ser Ile Asn Asn Asn Asn  
 1 5

aac aac aac aac aat aac aac gat ggt ctt atg atc tca tca aac gga  
 160

Asn Asn Asn Asn Asn Asn Asn Asp Gly Leu Met Ile Ser Ser Asn Gly  
 10 15 20

gct tta atc gaa caa caa cca tca gtc gtt gtg aag aaa cca ccg gcg  
 208

Ala Leu Ile Glu Gln Gln Pro Ser Val Val Val Lys Lys Pro Pro Ala  
 25 30 35

aaa gat cga cat agc aaa gtc gat gga aga ggg aga aga atc cgt atg  
 256

Lys Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met  
 40 45 50 55

ccg att ata tgt gct gct cgt gtt ttt cag cta acg aga gag ctt ggt  
 304

Pro Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly  
 60 65 70

cat aag tca gat ggc caa aca att gaa tgg tta ctt cgt caa gca gag  
 352

His Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu  
 75 80 85

cct tct att ata gct gca aca gga act ggt aca act cca gcg agt ttc  
 400

Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe  
 90 95 100

tca act gct tct gtc tct atc cgt gga gcc acc aat tct act tct tta  
 448

Ser Thr Ala Ser Val Ser Ile Arg Gly Ala Thr Asn Ser Thr Ser Leu  
 105 110 115

gat cat aaa ccc act tct tta ctt ggt ggt acg tca ccg ttt ata ctt  
 496

Asp His Lys Pro Thr Ser Leu Leu Gly Gly Thr Ser Pro Phe Ile Leu  
 120 125 130 135



ggg aaa cgt gtt aga gct gat gag gat agt aat aat agt cat aat cat  
544

Gly Lys Arg Val Arg Ala Asp Glu Asp Ser Asn Asn Ser His Asn His  
140 145 150

agt tct gtt ggt aaa gat gag acc ttt acg aca aca cca gct ggg ttt  
592

Ser Ser Val Gly Lys Asp Glu Thr Phe Thr Thr Thr Pro Ala Gly Phe  
155 160 165

tgg gct gtt ccg gcg agg ccg gat ttt gga caa gtt tgg agt ttt gct  
640

Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp Ser Phe Ala  
170 175 180

gga gct cca caa gag atg ttt tta caa caa caa cat cat cat cag caa  
688

Gly Ala Pro Gln Glu Met Phe Leu Gln Gln Gln His His His Gln Gln  
185 190 195

cca ttg ttt gtt cat cag caa cag caa caa caa gct gca atg ggt gaa  
736

Pro Leu Phe Val His Gln Gln Gln Gln Gln Gln Ala Ala Met Gly Glu  
200 205 210 215

gct tct gct gct aga gtt ggg aat tat ctt ccg ggt cat ctt aat ttg  
784

Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His Leu Asn Leu  
220 225 230

ctt gct tct tta tcc ggt gga tct ccc ggg tcg gat cga aga gag gaa  
832

Leu Ala Ser Leu Ser Gly Gly Ser Pro Gly Ser Asp Arg Arg Glu Glu  
235 240 245

gat cca cgt taa tgggttaagc ccttttaggt ttgagggcaa aatttggtat  
884

Asp Pro Arg  
250

atatatttat tatcttctct tctctattgt tgcattggt tctctatgtg tgtgttttag  
944

tggtgttaga gattgatttg gtttcagaat ctctgcaagt gatttgagag ttttcgtag  
1004

ctttaagtaa gttaaagacg gttgtttttg attaggggta aattaggggt taagaatctg  
1064

ttgttttttt ggaggagat cgatttctta tcggatccaa gattactttt aggaaaaaag  
1124

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1172

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410

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1 5 10 15



Leu Met Ile Ser Ser Asn Gly Ala Leu Ile Glu Gln Gln Pro Ser Val  
 20 25 30

Val Val Lys Lys Pro Pro Ala Lys Asp Arg His Ser Lys Val Asp Gly  
 35 40 45

Arg Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe  
 50 55 60

Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu  
 65 70 75 80

Trp Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr  
 85 90 95

Gly Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Val Ser Ile Arg Gly  
 100 105 110

Ala Thr Asn Ser Thr Ser Leu Asp His Lys Pro Thr Ser Leu Leu Gly  
 115 120 125

Gly Thr Ser Pro Phe Ile Leu Gly Lys Arg Val Arg Ala Asp Glu Asp  
 130 135 140

Ser Asn Asn Ser His Asn His Ser Ser Val Gly Lys Asp Glu Thr Phe  
 145 150 155 160

Thr Thr Thr Pro Ala Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe  
 165 170 175

Gly Gln Val Trp Ser Phe Ala Gly Ala Pro Gln Glu Met Phe Leu Gln  
 180 185 190

Gln Gln His His His Gln Gln Pro Leu Phe Val His Gln Gln Gln Gln  
 195 200 205

Gln Gln Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly Asn Tyr  
 210 215 220

Leu Pro Gly His Leu Asn Leu Leu Ala Ser Leu Ser Gly Gly Ser Pro  
 225 230 235 240

Gly Ser Asp Arg Arg Glu Glu Asp Pro Arg  
 245 250



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 <221> CDS <222> (1)..(513) <223> G1974

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 1 5 10 15  
 agc tgt ctg atg ttg tta tca gga att gga gaa cac gac gga aga aag  
 96  
 Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys  
 20 25 30  
 aaa cgt gtt ttc cga tgc aag act tgt gag aga gac ttc gat tcg ttc  
 144  
 Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe  
 35 40 45  
 caa gct tta gga ggc cac cgt gca agc cac tcg aaa cta acc aac agt  
 192  
 Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser  
 50 55 60  
 gac gat aaa tca ctt cct gga tca cca aag aag aag cct aaa act acg  
 240  
 Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr  
 65 70 75 80  
 act acg acg acg gct cat act tgt ccg att tgt ggc ttg gag ttt ccg  
 288  
 Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro  
 85 90 95  
 atg gga caa gct. ctt ggt ggt cac atg agg aaa cat agg aac gag aaa  
 336  
 Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys  
 100 105 110  
 gaa cga gaa aag gct tct aac gta ttg gtt acg cat tct ttc atg ccg  
 384  
 Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro  
 115 120 125  
 gag acg aca acg gtg acg act ttg aag aaa tcg agt agt ggg aag aga  
 432  
 Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg  
 130 135 140  
 gtg gcg tgt ttg gat ttc gac tta act tcg gtg gag agc ttt gtc aac  
 480  
 Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn  
 145 150 155 160  
 acg gaa ttg gag ttg gga aga acg atg tac tga  
 513  
 Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr  
 165 170



<210> 412 <211> 170 <212> PRT <213> Arabidopsis thaliana <400>  
412

Met Val Ala Glu Ser Asp Asn Arg Asp Leu Thr Val Asp Thr Ala Ala  
1 5 10 15

Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys  
20 25 30

Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe  
35 40 45

Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser  
50 55 60

Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr  
65 70 75 80

Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro  
85 90 95

Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys  
100 105 110

Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro  
115 120 125

Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg  
130 135 140

Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn  
145 150 155 160

Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr  
165 170

<210> 413 <211> 1536 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (42)..(1487) <223> G2105

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56

Met Glu Asp His Gln  
1 5

aac cat cca cag tac ggt ata gaa caa cca tct tct caa ttc tcc tct  
104

Asn His Pro Gln Tyr Gly Ile Glu Gln Pro Ser Ser Gln Phe Ser Ser  
10 15 20



gat ctc ttc ggc ttc aac ctc gtt tca gcg ccg gac cag cac cat cgt  
 152  
 Asp Leu Phe Gly Phe Asn Leu Val Ser Ala Pro Asp Gln His His Arg  
 25 30 35  
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 200  
 Leu His Phe Thr Asp His Glu Ile Ser Leu Leu Pro Arg Gly Ile Gln  
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 Gly Leu Thr Val Ala Gly Asn Asn Ser Asn Thr Ile Thr Thr Ile Gln  
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 70 75 80 85  
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 344  
 Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Met Leu Leu Glu Val Arg  
 90 95 100  
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 392  
 Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn Gln Lys Gly Pro Leu  
 105 110 115  
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 Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu His Gly Tyr Thr Arg  
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 Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr  
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 Lys Lys Thr Lys Glu Gly Lys Ser Gly Arg Arg Gln Asp Gly Lys Asn  
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 Tyr Arg Phe Phe Arg Gln Leu Glu Ala Ile Tyr Gly Glu Ser Lys Asp  
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 632  
 Ser Val Ser Cys Tyr Asn Asn Thr Gln Phe Ile Met Thr Asn Ala Leu  
 185 190 195  
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 680  
 His Ser Asn Phe Arg Ala Ser Asn Ile His Asn Ile Val Pro His His  
 200 205 210



cag aat ccc ttg atg acc aat acc aat act caa agt caa agc ctt agc  
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 Gln Asn Pro Leu Met Thr Asn Thr Asn Thr Gln Ser Gln Ser Leu Ser  
 215 220 225

att tct aac aat ttc aac tcc tcc tcc gat ttg gat cta act tct tcc  
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 Ile Ser Asn Asn Phe Asn Ser Ser Ser Asp Leu Asp Leu Thr Ser Ser  
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 Ser Glu Gly Asn Glu Thr Thr Lys Arg Glu Gly Met His Trp Lys Glu  
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aag atc aag gaa ttc att ggt gtt cat atg gag agg ttg ata gag aag  
 872  
 Lys Ile Lys Glu Phe Ile Gly Val His Met Glu Arg Leu Ile Glu Lys  
 265 270 275

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 280 285 290

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 295 300 305

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 310 315 320 325

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 330 335 340

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 1112  
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 345 350 355

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 Gly Asn Gly Ser Asp Lys Met Met Ala Asp Asn Glu Phe Ala Asp Glu  
 360 365 370

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 1208  
 Gly Asn Lys Gly Lys Met Asp Lys Lys Gln Met Asn Lys Lys Arg Lys  
 375 380 385

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 Glu Lys Trp Ser Ser His Gly Gly Asn His Pro Arg Thr Lys Glu Asn  
 390 395 400 405



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 Met Met Ile Tyr Asn Asn Gln Glu Thr Lys Ile Asn Asp Phe Cys Arg  
 410 415 420

gat gat gac caa tgc cat cat gaa ggt tac tca cct tca aac tcc aag  
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 425 430 435

aac gca gga act ccg agc tgc agc aat gcc atg gca gct agt aca aag  
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 Cys Phe Pro Leu Leu Glu Gly Glu Gly Asp Gln Asn Leu Trp Glu Gly  
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 35 40 45

Pro Arg Gly Ile Gln Gly Leu Thr Val Ala Gly Asn Asn Ser Asn Thr  
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Ile Thr Thr Ile Gln Ser Gly Gly Cys Val Gly Gly Phe Ser Gly Phe  
 65 70 75 80

Thr Asp Gly Gly Gly Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Met  
 85 90 95

Leu Leu Glu Val Arg Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn  
 100 105 110

Gln Lys Gly Pro Leu Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu



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 His Gly Tyr Thr Arg Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn  
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 Leu Tyr Lys Tyr Tyr Lys Lys Thr Lys Glu Gly Lys Ser Gly Arg Arg  
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 Gln Asp Gly Lys Asn Tyr Arg Phe Phe Arg Gln Leu Glu Ala Ile Tyr  
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 Gly Glu Ser Lys Asp Ser Val Ser Cys Tyr Asn Asn Thr Gln Phe Ile  
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 Met Thr Asn Ala Leu His Ser Asn Phe Arg Ala Ser Asn Ile His Asn  
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 Ile Val Pro His His Gln Asn Pro Leu Met Thr Asn Thr Asn Thr Gln  
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 Ser Gln Ser Leu Ser Ile Ser Asn Asn Phe Asn Ser Ser Ser Asp Leu  
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 Asp Leu Thr Ser Ser Ser Glu Gly Asn Glu Thr Thr Lys Arg Glu Gly  
                     245                      250                      255  
 Met His Trp Lys Glu Lys Ile Lys Glu Phe Ile Gly Val His Met Glu  
                     260                      265                      270  
 Arg Leu Ile Glu Lys Gln Asp Phe Trp Leu Glu Lys Leu Met Lys Ile  
                     275                      280                      285  
 Val Glu Asp Lys Glu His Gln Arg Met Leu Arg Glu Glu Glu Trp Arg  
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 Arg Ile Glu Ala Glu Arg Ile Asp Lys Glu Arg Ser Phe Trp Thr Lys  
     305                      310                      315                      320  
 Glu Arg Glu Arg Ile Glu Ala Arg Asp Val Ala Val Ile Asn Ala Leu  
                     325                      330                      335  
 Gln Tyr Leu Thr Gly Arg Ala Leu Ile Arg Pro Asp Ser Ser Ser Pro  
                     340                      345                      350  
 Thr Glu Arg Ile Asn Gly Asn Gly Ser Asp Lys Met Met Ala Asp Asn  
                     355                      360                      365



Glu Phe Ala Asp Glu Gly Asn Lys Gly Lys Met Asp Lys Lys Gln Met  
 370 375 380

Asn Lys Lys Arg Lys Glu Lys Trp Ser Ser His Gly Gly Asn His Pro  
 385 390 395 400

Arg Thr Lys Glu Asn Met Met Ile Tyr Asn Asn Gln Glu Thr Lys Ile  
 405 410 415

Asn Asp Phe Cys Arg Asp Asp Asp Gln Cys His His Glu Gly Tyr Ser  
 420 425 430

Pro Ser Asn Ser Lys Asn Ala Gly Thr Pro Ser Cys Ser Asn Ala Met  
 435 440 445

Ala Ala Ser Thr Lys Cys Phe Pro Leu Leu Glu Gly Glu Gly Asp Gln  
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 agg caa gtt aca tac acg aag aga aaa aat ggg att ttg aag aaa gcc  
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 Arg Gln Val Thr Tyr Thr Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala  
 20 25 30  
 aaa gag tta tcg att ttg tgt gat att gat att gtc ctt ctt atg ttt  
 144  
 Lys Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe  
 35 40 45  
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 192  
 Ser Pro Thr Gly Arg Ala Thr Ala Phe His Gly Glu His Arg Tyr Asn  
 50 55 60  
 tat caa aat cat tct tat gca ttg aag aaa act ttt aag aaa ctg gat  
 240  
 Tyr Gln Asn His Ser Tyr Ala Leu Lys Lys Thr Phe Lys Lys Leu Asp



65	70	75	80
cat gat gta aat ata cat gac ttt tta gga gca agg aat caa act att			
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His Asp Val Asn Ile His Asp Phe Leu Gly Ala Arg Asn Gln Thr Ile			
	85	90	95
gag gta tgg atc gac cat ctt cgg ttc atg aat ttt ctt gga tac ttt			
336			
Glu Val Trp Ile Asp His Leu Arg Phe Met Asn Phe Leu Gly Tyr Phe			
	100	105	110
tta atc tct ttg agt caa att gct aaa gtc tgt gtt aac att acc aca			
384			
Leu Ile Ser Leu Ser Gln Ile Ala Lys Val Cys Val Asn Ile Thr Thr			
	115	120	125
cga cag ggt cta agt aac caa gta gcc att tac caa gct cag cta atg			
432			
Arg Gln Gly Leu Ser Asn Gln Val Ala Ile Tyr Gln Ala Gln Leu Met			
	130	135	140
gag tgt cat agg agg ttg agt tgt tgg acg aac atc gat aga ata gaa			
480			
Glu Cys His Arg Arg Leu Ser Cys Trp Thr Asn Ile Asp Arg Ile Glu			
	145	150	155
aac act gag cac ctc gat tta ttg gaa gaa tca ttg agg aaa tcc att			
528			
Asn Thr Glu His Leu Asp Leu Leu Glu Glu Ser Leu Arg Lys Ser Ile			
	165	170	175
gaa aga atc cag att cac aag gaa cat tac aga aag aac caa ctc ttg			
576			
Glu Arg Ile Gln Ile His Lys Glu His Tyr Arg Lys Asn Gln Leu Leu			
	180	185	190
cca ata gaa tgt gca aca aca cag ttt cac agc ggg ata cag ttg cct			
624			
Pro Ile Glu Cys Ala Thr Thr Gln Phe His Ser Gly Ile Gln Leu Pro			
	195	200	205
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672			
Met Ala Met Gly Gly Asn Ser Ser Met Gln Glu Ala His Ser Met Ser			
	210	215	220
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720			
Trp Leu Pro Asp Asn Asp His Gln Gln Thr Ile Leu Pro Gly Asp Ser			
	225	230	235
agt ttt ctt ccc cat aga gag atg gat ggt tcg att ccc gtt tac tca			
768			
Ser Phe Leu Pro His Arg Glu Met Asp Gly Ser Ile Pro Val Tyr Ser			
	245	250	255
agc tgc ttc ttt gag tct acg aaa cca gaa gat cag ata tgc agc aac			
816			
Ser Cys Phe Phe Glu Ser Thr Lys Pro Glu Asp Gln Ile Cys Ser Asn			
	260	265	270



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 Pro Gly Gln Gln Phe Glu Gln Leu Glu Gln Gln Gly Asn Gly Cys Leu  
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ggg tta caa caa ctt gga gag gaa tat tca tat cct aca ccg ttt ggt  
 912  
 Gly Leu Gln Gln Leu Gly Glu Glu Tyr Ser Tyr Pro Thr Pro Phe Gly  
           290                          295                          300

act act ttg gga atg gaa gaa gat caa gag aaa aag ata aaa tct gaa  
 960  
 Thr Thr Leu Gly Met Glu Glu Asp Gln Glu Lys Lys Ile Lys Ser Glu  
           305                          310                          315                          320

atg gaa ttg aac aac ttg caa caa cag caa cag caa caa caa caa  
 1008  
 Met Glu Leu Asn Asn Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln  
                           325                          330                          335

caa caa caa gat cct tca atg tat gat ccc atg gct aat aat aat ggt  
 1056  
 Gln Gln Gln Asp Pro Ser Met Tyr Asp Pro Met Ala Asn Asn Asn Gly  
                           340                          345                          350

ggc tgc ttt cag att cct cat gat cag tcc atg ttt gtc aat gat cat  
 1104  
 Gly Cys Phe Gln Ile Pro His Asp Gln Ser Met Phe Val Asn Asp His  
           355                          360                          365

cat cat cat cat cac cac cat cat caa aat tgg gtt cca gat tca atg  
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 His His His His His His His His Gln Asn Trp Val Pro Asp Ser Met  
           370                          375                          380

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 1200  
 Phe Gly Gln Thr Ser Tyr Asn Gln Val Cys Val Phe Thr Pro Pro Leu  
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 Glu Leu Ser Arg

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Lys Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe  
           35                          40                          45



Ser Pro Thr Gly Arg Ala Thr Ala Phe His Gly Glu His Arg Tyr Asn  
 50 55 60

Tyr Gln Asn His Ser Tyr Ala Leu Lys Lys Thr Phe Lys Lys Leu Asp  
 65 70 75 80

His Asp Val Asn Ile His Asp Phe Leu Gly Ala Arg Asn Gln Thr Ile  
 85 90 95

Glu Val Trp Ile Asp His Leu Arg Phe Met Asn Phe Leu Gly Tyr Phe  
 100 105 110

Leu Ile Ser Leu Ser Gln Ile Ala Lys Val Cys Val Asn Ile Thr Thr  
 115 120 125

Arg Gln Gly Leu Ser Asn Gln Val Ala Ile Tyr Gln Ala Gln Leu Met  
 130 135 140

Glu Cys His Arg Arg Leu Ser Cys Trp Thr Asn Ile Asp Arg Ile Glu  
 145 150 155 160

Asn Thr Glu His Leu Asp Leu Leu Glu Glu Ser Leu Arg Lys Ser Ile  
 165 170 175

Glu Arg Ile Gln Ile His Lys Glu His Tyr Arg Lys Asn Gln Leu Leu  
 180 185 190

Pro Ile Glu Cys Ala Thr Thr Gln Phe His Ser Gly Ile Gln Leu Pro  
 195 200 205

Met Ala Met Gly Gly Asn Ser Ser Met Gln Glu Ala His Ser Met Ser  
 210 215 220

Trp Leu Pro Asp Asn Asp His Gln Gln Thr Ile Leu Pro Gly Asp Ser  
 225 230 235 240

Ser Phe Leu Pro His Arg Glu Met Asp Gly Ser Ile Pro Val Tyr Ser  
 245 250 255

Ser Cys Phe Phe Glu Ser Thr Lys Pro Glu Asp Gln Ile Cys Ser Asn  
 260 265 270

Pro Gly Gln Gln Phe Glu Gln Leu Glu Gln Gln Gly Asn Gly Cys Leu  
 275 280 285



Gly Leu Gln Gln Leu Gly Glu Glu Tyr Ser Tyr Pro Thr Pro Phe Gly  
 290 295 300

Thr Thr Leu Gly Met Glu Glu Asp Gln Glu Lys Lys Ile Lys Ser Glu  
 305 310 315 320

Met Glu Leu Asn Asn Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln  
 325 330 335

Gln Gln Gln Asp Pro Ser Met Tyr Asp Pro Met Ala Asn Asn Asn Gly  
 340 345 350

Gly Cys Phe Gln Ile Pro His Asp Gln Ser Met Phe Val Asn Asp His  
 355 360 365

His His His His His His His His Gln Asn Trp Val Pro Asp Ser Met  
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Arg Arg Val Lys Phe Thr Glu Asn Arg Thr Val Thr Asn Val Ala Ala  
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aca cca tct aac ggg tct ccg aga ctg gtc cgt atc act gtt act gat  
 151

Thr Pro Ser Asn Gly Ser Pro Arg Leu Val Arg Ile Thr Val Thr Asp  
 25 30 35

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 199

Pro Phe Ala Thr Asp Ser Ser Ser Asp Asp Asp Asp Asn Asn Asn Val  
 40 45 50

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 247

Thr Val Val Pro Arg Val Lys Arg Tyr Val Lys Glu Ile Arg Phe Cys  
 55 60 65



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 295  
 Gln Gly Glu Ser Ser Ser Ser Thr Ala Ala Arg Lys Gly Lys His Lys  
 70 75 80 85  
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 Glu Glu Glu Ser Val Val Val Glu Asp Asp Val Ser Thr Ser Val Lys  
 90 95 100  
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 391  
 Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala  
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 439  
 Ala Glu Ile Arg Asp Pro Ser Ser Arg Thr Arg Ile Trp Leu Gly Thr  
 120 125 130  
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 487  
 Phe Val Thr Ala Glu Glu Ala Ala Ile Ala Tyr Asp Arg Ala Ala Ile  
 135 140 145  
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 535  
 His Leu Lys Gly Pro Lys Ala Leu Thr Asn Phe Leu Thr Pro Pro Thr  
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 Pro Thr Pro Val Ile Asp Leu Gln Thr Val Ser Ala Cys Asp Tyr Gly  
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 679  
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 727  
 Pro Glu Arg Lys Ser Thr Val Ile Lys Glu Glu Glu Glu Ser Ser Ala  
 215 220 225  
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 230 235 240 245  
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 Gly Glu Cys Phe Trp Asp Thr Glu Ile Ala Pro Asp Leu Leu Phe Leu  
 250 255 260



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871

Asp Glu Glu Thr Lys Ile Gln Ser Thr Leu Leu Pro Asn Thr Glu Val  
265 270 275

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919

Ser Lys Gln Gly Glu Asn Glu Thr Glu Asp Phe Glu Phe Gly Leu Ile  
280 285 290

gat gat ttc gag tct tct cca tgg gat gtg gat cat ttc ttc gac cat  
967

Asp Asp Phe Glu Ser Ser Pro Trp Asp Val Asp His Phe Phe Asp His  
295 300 305

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35 40 45

Asp Asn Asn Asn Val Thr Val Val Pro Arg Val Lys Arg Tyr Val Lys  
50 55 60

Glu Ile Arg Phe Cys Gln Gly Glu Ser Ser Ser Ser Thr Ala Ala Arg  
65 70 75 80

Lys Gly Lys His Lys Glu Glu Glu Ser Val Val Val Glu Asp Asp Val  
85 90 95

Ser Thr Ser Val Lys Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro  
100 105 110

Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Ser Arg Thr Arg  
115 120 125

Ile Trp Leu Gly Thr Phe Val Thr Ala Glu Glu Ala Ala Ile Ala Tyr  
130 135 140

Asp Arg Ala Ala Ile His Leu Lys Gly Pro Lys Ala Leu Thr Asn Phe



145                      150                      155                      160  
 Leu Thr Pro Pro Thr Pro Thr Pro Val Ile Asp Leu Gln Thr Val Ser  
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 Ala Cys Asp Tyr Gly Arg Asp Ser Arg Gln Ser Leu His Ser Pro Thr  
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 Ser Val Leu Arg Phe Asn Val Asn Glu Glu Thr Glu His Glu Ile Glu  
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 Ala Ile Glu Leu Ser Pro Glu Arg Lys Ser Thr Val Ile Lys Glu Glu  
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 Asp Leu Ser Leu Ala Gly Glu Cys Phe Trp Asp Thr Glu Ile Ala Pro  
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 Asp Leu Leu Phe Leu Asp Glu Glu Thr Lys Ile Gln Ser Thr Leu Leu  
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 Pro Asn Thr Glu Val Ser Lys Gln Gly Glu Asn Glu Thr Glu Asp Phe  
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 174  
                                  Met Glu Lys Pro Val Phe Ala Pro  
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 tgg cgt tcc gac caa gtt ttc cgg cca ccg gag aca cca tta gag ccg  
 222  
 Trp Arg Ser Asp Gln Val Phe Arg Pro Pro Glu Thr Pro Leu Glu Pro



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270		
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aaa gct ctc act cct tct cag caa ctc ctc tca aaa gcc tca atc gaa		
318		
Lys Ala Leu Thr Pro Ser Gln Gln Leu Leu Ser Lys Ala Ser Ile Glu		
	45	50 55
aac acc acc gtc att ctc gaa gaa ccc atc gcc gcc ggc gag acc gaa		
366		
Asn Thr Thr Val Ile Leu Glu Glu Pro Ile Ala Ala Gly Glu Thr Glu		
	60	65 70
acg gag gac aac agc ttc gtc tcc gga aac cct ttc tcc ttc gct tgc		
414		
Thr Glu Asp Asn Ser Phe Val Ser Gly Asn Pro Phe Ser Phe Ala Cys		
	75	80 85
tca gaa act tct cag atg gtc atg gat cgt atc tta tct cag tct cag		
462		
Ser Glu Thr Ser Gln Met Val Met Asp Arg Ile Leu Ser Gln Ser Gln		
	90	95 100
gaa gtg tcg cca cga aca tct ggt cgg ctt tct cat agc agc ggt cct		
510		
Glu Val Ser Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Gly Pro		
105	110	115 120
ctc aat ggt tct tta acc gac agt cct ccg att tcg ccg cat caa gtc		
558		
Leu Asn Gly Ser Leu Thr Asp Ser Pro Pro Ile Ser Pro His Gln Val		
	125	130 135
gac gac att aag caa ttt tgc cga tca aac aac aat ttc aac tct caa		
606		
Asp Asp Ile Lys Gln Phe Cys Arg Ser Asn Asn Asn Phe Asn Ser Gln		
	140	145 150
tac cgt tca acg gga aca act ccg gga cct atc act gca aca act aca		
654		
Tyr Arg Ser Thr Gly Thr Thr Pro Gly Pro Ile Thr Ala Thr Thr Thr		
	155	160 165
cag tcc aag aca gtt gga cgg tgg ttg aaa gac agg agg gag aaa aag		
702		
Gln Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg Glu Lys Lys		
	170	175 180
aag gaa gag atg aga gca cac aat gct cag ata cat gct gct gta tca		
750		
Lys Glu Glu Met Arg Ala His Asn Ala Gln Ile His Ala Ala Val Ser		
185	190	195 200
gta gct ggt gtg gca gcc gcg gtg gct gct atc gcg gct gca act gct		
798		
Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala Ala Thr Ala		
	205	210 215



gct tcg tcg agt gct gga aaa gat gag aat atg gct aag acg gat atg  
 846  
 Ala Ser Ser Ser Ala Gly Lys Asp Glu Asn Met Ala Lys Thr Asp Met  
 220 225 230

gct gtg gct tct gct gca aca ctt gtg gct gct caa tgt gtg gaa gct  
 894  
 Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Gln Cys Val Glu Ala  
 235 240 245

gct gaa gtt atg gga gct gag agg gat cat tta gct tcc gtt gtt agt  
 942  
 Ala Glu Val Met Gly Ala Glu Arg Asp His Leu Ala Ser Val Val Ser  
 250 255 260

tct gct gtt aat gtt cga tct gcg gga gat atc atg aca tta acc gct  
 990  
 Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr Leu Thr Ala  
 265 270 275 280

gga gca gcc aca gcg tta aga gga gtg gct aca ttg aag gct aga gct  
 1038  
 Gly Ala Ala Thr Ala Leu Arg Gly Val Ala Thr Leu Lys Ala Arg Ala  
 285 290 295

atg aag gag gtg tgg cac att gca tca gtt att coa atg gat aaa gga  
 1086  
 Met Lys Glu Val Trp His Ile Ala Ser Val Ile Pro Met Asp Lys Gly  
 300 305 310

atc aat ctc gga ggt tgc agc aat gtt aat ggt aac ggg agc tat gtc  
 1134  
 Ile Asn Leu Gly Gly Cys Ser Asn Val Asn Gly Asn Gly Ser Tyr Val  
 315 320 325

agc tca agc agc agt cat agt ggc gaa ttt cta gtt gag gat aat ttc  
 1182  
 Ser Ser Ser Ser Ser His Ser Gly Glu Phe Leu Val Glu Asp Asn Phe  
 330 335 340

ttg gga cat tgc aat aga gaa tgg ctt gct cga ggt ggc caa ctt ctt  
 1230  
 Leu Gly His Cys Asn Arg Glu Trp Leu Ala Arg Gly Gly Gln Leu Leu  
 345 350 355 360

aaa cgc acc cgc aaa ggt gat ctt cat tgg aaa ata gtt tca gtt tac  
 1278  
 Lys Arg Thr Arg Lys Gly Asp Leu His Trp Lys Ile Val Ser Val Tyr  
 365 370 375

ata aac agg cta aat caa gtt ata ttg aag atg aag agc agg cat gta  
 1326  
 Ile Asn Arg Leu Asn Gln Val Ile Leu Lys Met Lys Ser Arg His Val  
 380 385 390

gga ggg acc ttc acg aag aag aac aaa aat gtt gtg att gat gtg atc  
 1374  
 Gly Gly Thr Phe Thr Lys Lys Asn Lys Asn Val Val Ile Asp Val Ile  
 395 400 405



aaa aac gtt caa gct tgg cca ggc cgc cat ttg ctg gaa gga gga gag  
1422

Lys Asn Val Gln Ala Trp Pro Gly Arg His Leu Leu Glu Gly Gly Glu  
410 415 420

gat ttg aga tac ttt ggg tta aag acg gtt ccg cga ggg att gta gaa  
1470

Asp Leu Arg Tyr Phe Gly Leu Lys Thr Val Pro Arg Gly Ile Val Glu  
425 430 435 440

ttt cag tgc aag agc cag aga gag tat gaa atg tgg aca caa ggt gtc  
1518

Phe Gln Cys Lys Ser Gln Arg Glu Tyr Glu Met Trp Thr Gln Gly Val  
445 450 455

tca agg ctt att gct gtt gct gcc gag agg aat aac aga tat agg ata  
1566

Ser Arg Leu Ile Ala Val Ala Ala Glu Arg Asn Asn Arg Tyr Arg Ile  
460 465 470

tga agggagtagt agttttaaga gttcagagct actttttgag gggtagatgc  
1619

taacttatgg ggccaaatta taacttggag aaagttaagg gtgttttctt tagagtaatg  
1679

tctttttgta aggtatatag gattaaatgt ggcctctata agggtagcta gtgaaacaaa  
1739

tcttggtggtt tgtatatata ttttttttgg ggaaaaagtt taatatcaaa tttttaattt  
1799

aaaa  
1803

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Met Glu Lys Pro Val Phe Ala Pro Trp Arg Ser Asp Gln Val Phe Arg  
1 5 10 15

Pro Pro Glu Thr Pro Leu Glu Pro Met Glu Phe Leu Ser Arg Ser Trp  
20 25 30

Ser Val Ser Ala His Glu Val Ser Lys Ala Leu Thr Pro Ser Gln Gln  
35 40 45

Leu Leu Ser Lys Ala Ser Ile Glu Asn Thr Thr Val Ile Leu Glu Glu  
50 55 60

Pro Ile Ala Ala Gly Glu Thr Glu Thr Glu Asp Asn Ser Phe Val Ser  
65 70 75 80

Gly Asn Pro Phe Ser Phe Ala Cys Ser Glu Thr Ser Gln Met Val Met  
85 90 95



Asp Arg Ile Leu Ser Gln Ser Gln Glu Val Ser Pro Arg Thr Ser Gly  
 100 105 110

Arg Leu Ser His Ser Ser Gly Pro Leu Asn Gly Ser Leu Thr Asp Ser  
 115 120 125

Pro Pro Ile Ser Pro His Gln Val Asp Asp Ile Lys Gln Phe Cys Arg  
 130 135 140

Ser Asn Asn Asn Phe Asn Ser Gln Tyr Arg Ser Thr Gly Thr Thr Pro  
 145 150 155 160

Gly Pro Ile Thr Ala Thr Thr Thr Gln Ser Lys Thr Val Gly Arg Trp  
 165 170 175

Leu Lys Asp Arg Arg Glu Lys Lys Lys Glu Glu Met Arg Ala His Asn  
 180 185 190

Ala Gln Ile His Ala Ala Val Ser Val Ala Gly Val Ala Ala Ala Val  
 195 200 205

Ala Ala Ile Ala Ala Ala Thr Ala Ala Ser Ser Ser Ala Gly Lys Asp  
 210 215 220

Glu Asn Met Ala Lys Thr Asp Met Ala Val Ala Ser Ala Ala Thr Leu  
 225 230 235 240

Val Ala Ala Gln Cys Val Glu Ala Ala Glu Val Met Gly Ala Glu Arg  
 245 250 255

Asp His Leu Ala Ser Val Val Ser Ser Ala Val Asn Val Arg Ser Ala  
 260 265 270

Gly Asp Ile Met Thr Leu Thr Ala Gly Ala Ala Thr Ala Leu Arg Gly  
 275 280 285

Val Ala Thr Leu Lys Ala Arg Ala Met Lys Glu Val Trp His Ile Ala  
 290 295 300

Ser Val Ile Pro Met Asp Lys Gly Ile Asn Leu Gly Gly Cys Ser Asn  
 305 310 315 320

Val Asn Gly Asn Gly Ser Tyr Val Ser Ser Ser Ser Ser His Ser Gly  
 325 330 335



Glu Phe Leu Val Glu Asp Asn Phe Leu Gly His Cys Asn Arg Glu Trp  
340 345 350

Leu Ala Arg Gly Gly Gln Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu  
355 360 365

His Trp Lys Ile Val Ser Val Tyr Ile Asn Arg Leu Asn Gln Val Ile  
370 375 380

Leu Lys Met Lys Ser Arg His Val Gly Gly Thr Phe Thr Lys Lys Asn  
385 390 395 400

Lys Asn Val Val Ile Asp Val Ile Lys Asn Val Gln Ala Trp Pro Gly  
405 410 415

Arg His Leu Leu Glu Gly Gly Glu Asp Leu Arg Tyr Phe Gly Leu Lys  
420 425 430

Thr Val Pro Arg Gly Ile Val Glu Phe Gln Cys Lys Ser Gln Arg Glu  
435 440 445

Tyr Glu Met Trp Thr Gln Gly Val Ser Arg Leu Ile Ala Val Ala Ala  
450 455 460

Glu Arg Asn Asn Arg Tyr Arg Ile  
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1 5 10 15  
cct cct ccg ccg cca cct att ttc cac cgt gcg agc tct acg ggg acg  
96  
Pro Pro Pro Pro Pro Pro Ile Phe His Arg Ala Ser Ser Thr Gly Thr  
20 25 30  
agt ttt ccg atc tta gcc gtc gcg gtg atc gga atc tta gcc aca gca  
144  
Ser Phe Pro Ile Leu Ala Val Ala Val Ile Gly Ile Leu Ala Thr Ala  
35 40 45  
ttt tta ctt gta agc tat tat gtt ttt gtt atc aaa tgt tgt ctc aac  
192  
Phe Leu Leu Val Ser Tyr Tyr Val Phe Val Ile Lys Cys Cys Leu Asn  
50 55 60



tgg cac cga atc gac att ctt ggt cga ttc tcg tta tct cga agg cga  
 240  
 Trp His Arg Ile Asp Ile Leu Gly Arg Phe Ser Leu Ser Arg Arg Arg  
 65 70 75 80  
 cgc aac gac caa gat cct tta atg gtt tac tct cca gag ctt aga agc  
 288  
 Arg Asn Asp Gln Asp Pro Leu Met Val Tyr Ser Pro Glu Leu Arg Ser  
 85 90 95  
 cgc ggt ctt gat gaa tcc gtc att aga gca atc cca atc ttt aag ttc  
 336  
 Arg Gly Leu Asp Glu Ser Val Ile Arg Ala Ile Pro Ile Phe Lys Phe  
 100 105 110  
 aag aag aga tac gac caa aac gac ggc gtt ttt aca gga gaa gga gaa  
 384  
 Lys Lys Arg Tyr Asp Gln Asn Asp Gly Val Phe Thr Gly Glu Gly Glu  
 115 120 125  
 gaa gaa gaa gag aag aga tct caa gaa tgc tct gtt tgt ttg agt gag  
 432  
 Glu Glu Glu Glu Lys Arg Ser Gln Glu Cys Ser Val Cys Leu Ser Glu  
 130 135 140  
 ttt caa gat gag gag aag ctg agg att atc cca aat tgt tct cat ttg  
 480  
 Phe Gln Asp Glu Glu Lys Leu Arg Ile Ile Pro Asn Cys Ser His Leu  
 145 150 155 160  
 ttt cat atc gac tgt atc gat gtg tgg ctt cag aac aac gcc aat tgt  
 528  
 Phe His Ile Asp Cys Ile Asp Val Trp Leu Gln Asn Asn Ala Asn Cys  
 165 170 175  
 cct ttg tgt aga act agg gtt tct tgt gac aca agt ttt cct ccg gat  
 576  
 Pro Leu Cys Arg Thr Arg Val Ser Cys Asp Thr Ser Phe Pro Pro Asp  
 180 185 190  
 cgg gtt tct gcg ccg agc act tct ccc gag aat ctg gtc atg tta aga  
 624  
 Arg Val Ser Ala Pro Ser Thr Ser Pro Glu Asn Leu Val Met Leu Arg  
 195 200 205  
 ggt gag aac gag tat gtg gtc att gag ctg ggc agt agc atc ggt agt  
 672  
 Gly Glu Asn Glu Tyr Val Val Ile Glu Leu Gly Ser Ser Ile Gly Ser  
 210 215 220  
 gac aga gat agt cca aga cac gga agg tta ctt acg gga caa gaa agg  
 720  
 Asp Arg Asp Ser Pro Arg His Gly Arg Leu Leu Thr Gly Gln Glu Arg  
 225 230 235 240  
 tca aat tca ggt tat cta ctg aac gaa aac acc caa aat tcg atc agt  
 768  
 Ser Asn Ser Gly Tyr Leu Leu Asn Glu Asn Thr Gln Asn Ser Ile Ser  
 245 250 255



cca tct ccg aag aag ctt gac cgc gga ggg ctt cca aga aaa ttc cga  
 816  
 Pro Ser Pro Lys Lys Leu Asp Arg Gly Gly Leu Pro Arg Lys Phe Arg  
                   260                                  265                                  270

aag ctt cac aag atg acg agt atg gga gac gaa tgc atc gac ata aga  
 864  
 Lys Leu His Lys Met Thr Ser Met Gly Asp Glu Cys Ile Asp Ile Arg  
                   275                                  280                                  285

aga ggt aaa gac gaa cag ttc ggt agt att cag ccc att aga aga tca  
 912  
 Arg Gly Lys Asp Glu Gln Phe Gly Ser Ile Gln Pro Ile Arg Arg Ser  
                   290                                  295                                  300

atc tca atg gat tca tcg gcg gat aga cag ctt tac ttg gcg gtt caa  
 960  
 Ile Ser Met Asp Ser Ser Ala Asp Arg Gln Leu Tyr Leu Ala Val Gln  
                                   310                                  315                                  320

gag gcg att cgg aaa aac cgc gaa gtt ctg gtg gtt gga gac gga gga  
 1008  
 Glu Ala Ile Arg Lys Asn Arg Glu Val Leu Val Val Gly Asp Gly Gly  
                                   325                                  330                                  335

gga tgt agc agt agt agt ggc aat gtt agt aat tcc aaa gtg aag aga  
 1056  
 Gly Cys Ser Ser Ser Ser Gly Asn Val Ser Asn Ser Lys Val Lys Arg  
                                   340                                  345                                  350

tct ttc ttc tct ttt ggg agc agt aga cgt tct aga agt tcc tct aaa  
 1104  
 Ser Phe Phe Ser Phe Gly Ser Ser Arg Arg Ser Arg Ser Ser Ser Lys  
                   355                                  360                                  365

ttg cca ctt tat ttt gaa ccc taa  
 1128  
 Leu Pro Leu Tyr Phe Glu Pro  
                   370                                  375

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 1                                  5                                  10                                  15

Pro Pro Pro Pro Pro Pro Ile Phe His Arg Ala Ser Ser Thr Gly Thr  
                   20                                  25                                  30

Ser Phe Pro Ile Leu Ala Val Ala Val Ile Gly Ile Leu Ala Thr Ala  
                   35                                  40                                  45

Phe Leu Leu Val Ser Tyr Tyr Val Phe Val Ile Lys Cys Cys Leu Asn  
                   50                                  55                                  60

Trp His Arg Ile Asp Ile Leu Gly Arg Phe Ser Leu Ser Arg Arg Arg



65	70	75	80
Arg Asn Asp Gln Asp Pro Leu Met Val Tyr Ser Pro Glu Leu Arg Ser	85	90	95
Arg Gly Leu Asp Glu Ser Val Ile Arg Ala Ile Pro Ile Phe Lys Phe	100	105	110
Lys Lys Arg Tyr Asp Gln Asn Asp Gly Val Phe Thr Gly Glu Gly Glu	115	120	125
Glu Glu Glu Glu Lys Arg Ser Gln Glu Cys Ser Val Cys Leu Ser Glu	130	135	140
Phe Gln Asp Glu Glu Lys Leu Arg Ile Ile Pro Asn Cys Ser His Leu	145	150	155
Phe His Ile Asp Cys Ile Asp Val Trp Leu Gln Asn Asn Ala Asn Cys	165	170	175
Pro Leu Cys Arg Thr Arg Val Ser Cys Asp Thr Ser Phe Pro Pro Asp	180	185	190
Arg Val Ser Ala Pro Ser Thr Ser Pro Glu Asn Leu Val Met Leu Arg	195	200	205
Gly Glu Asn Glu Tyr Val Val Ile Glu Leu Gly Ser Ser Ile Gly Ser	210	215	220
Asp Arg Asp Ser Pro Arg His Gly Arg Leu Leu Thr Gly Gln Glu Arg	225	230	235
Ser Asn Ser Gly Tyr Leu Leu Asn Glu Asn Thr Gln Asn Ser Ile Ser	245	250	255
Pro Ser Pro Lys Lys Leu Asp Arg Gly Gly Leu Pro Arg Lys Phe Arg	260	265	270
Lys Leu His Lys Met Thr Ser Met Gly Asp Glu Cys Ile Asp Ile Arg	275	280	285
Arg Gly Lys Asp Glu Gln Phe Gly Ser Ile Gln Pro Ile Arg Arg Ser	290	295	300
Ile Ser Met Asp Ser Ser Ala Asp Arg Gln Leu Tyr Leu Ala Val Gln	305	310	315
			320



Glu Ala Ile Arg Lys Asn Arg Glu Val Leu Val Val Gly Asp Gly Gly  
 325 330 335

Gly Cys Ser Ser Ser Ser Gly Asn Val Ser Asn Ser Lys Val Lys Arg  
 340 345 350

Ser Phe Phe Ser Phe Gly Ser Ser Arg Arg Ser Arg Ser Ser Ser Lys  
 355 360 365

Leu Pro Leu Tyr Phe Glu Pro  
 370 375

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 1 5 10 15

cct tca tca ctt cca caa gaa cca ccg tta tct ctc cgc tcc agc gca  
 96  
 Pro Ser Ser Leu Pro Gln Glu Pro Pro Leu Ser Leu Arg Ser Ser Ala  
 20 25 30

aac ttc gat cta aac agc aaa atc agt cca agt att ctc ctc ata atc  
 144  
 Asn Phe Asp Leu Asn Ser Lys Ile Ser Pro Ser Ile Leu Leu Ile Ile  
 35 40 45

ata atc ctc tca atc atc ttc ttc atc tcc ggt ctc ctt cat ctc tta  
 192  
 Ile Ile Leu Ser Ile Ile Phe Phe Ile Ser Gly Leu Leu His Leu Leu  
 50 55 60

gtc aga ttc ctc ctc aca cca tcg agc aga gac aga gaa gat tac ttc  
 240  
 Val Arg Phe Leu Leu Thr Pro Ser Ser Arg Asp Arg Glu Asp Tyr Phe  
 65 70 75 80

gac aac gtc act gct ctt caa ggc cag ctt caa cag ctt ttt cat ctc  
 288  
 Asp Asn Val Thr Ala Leu Gln Gly Gln Leu Gln Gln Leu Phe His Leu  
 85 90 95

cat gat tct gga gtt gac caa tcc ttc atc gac acg tta cct gtt ttc  
 336  
 His Asp Ser Gly Val Asp Gln Ser Phe Ile Asp Thr Leu Pro Val Phe  
 100 105 110

cat tac aaa tcc ata atc ggt ctc aag aac tat cct ttt gat tgt gca  
 384  
 His Tyr Lys Ser Ile Ile Gly Leu Lys Asn Tyr Pro Phe Asp Cys Ala  
 115 120 125



gtt tgt ctt tgt gag ttc gaa aca gag gat aag ctc agg ctc tta cct  
 432  
 Val Cys Leu Cys Glu Phe Glu Thr Glu Asp Lys Leu Arg Leu Leu Pro  
 130 135 140

aaa tgc agc cac gcc ttt cac atg gat tgt atc gat act tgg ctt cta  
 480  
 Lys Cys Ser His Ala Phe His Met Asp Cys Ile Asp Thr Trp Leu Leu  
 145 150 155 160

tct cac tct act tgt cct ttg tgt aga tcc agt ctc ctc tct gat ctc  
 528  
 Ser His Ser Thr Cys Pro Leu Cys Arg Ser Ser Leu Leu Ser Asp Leu  
 165 170 175

tct tcg cac caa gat cct cgt tct tct ttc ctc ctt gtg ctc gag tct  
 576  
 Ser Ser His Gln Asp Pro Arg Ser Ser Phe Leu Leu Val Leu Glu Ser  
 180 185 190

gcg agt gat cat agc tcg aga gag att gga gga gat aga gac agt gca  
 624  
 Ala Ser Asp His Ser Ser Arg Glu Ile Gly Gly Asp Arg Asp Ser Ala  
 195 200 205

gct tgt gtg gct gca aat gat gat att gat gtg tct agt gct cat ctt  
 672  
 Ala Cys Val Ala Ala Asn Asp Asp Ile Asp Val Ser Ser Ala His Leu  
 210 215 220

ggt ttg gtc gga aac aat gat ctt gga tca acc agg ata gat tcg ggt  
 720  
 Gly Leu Val Gly Asn Asn Asp Leu Gly Ser Thr Arg Ile Asp Ser Gly  
 225 230 235 240

cac gga gat cag tac ctg gat ggt gaa ttg ggt ggt tcg gtt gga aag  
 768  
 His Gly Asp Gln Tyr Leu Asp Gly Glu Leu Gly Gly Ser Val Gly Lys  
 245 250 255

gtt gtt cct ttt tca gtt aag cta ggg aag ttt agg aat ata gat att  
 816  
 Val Val Pro Phe Ser Val Lys Leu Gly Lys Phe Arg Asn Ile Asp Ile  
 260 265 270

ggt gaa gga act agt agc aac aac aac att ggt aat agt agt agt tta  
 864  
 Gly Glu Gly Thr Ser Ser Asn Asn Asn Ile Gly Asn Ser Ser Ser Leu  
 275 280 285

gat gag agg agg tgt ttc tca atg gga tca tat gag tat ata atg gat  
 912  
 Asp Glu Arg Arg Cys Phe Ser Met Gly Ser Tyr Glu Tyr Ile Met Asp  
 290 295 300

gaa gaa acg act ctt aag gtt cat gtt tca acc aag aaa caa tca agc  
 960  
 Glu Glu Thr Thr Leu Lys Val His Val Ser Thr Lys Lys Gln Ser Ser  
 305 310 315 320



aag aac cgt ggc ttg ccc ggt cat agg aca gcg atg tcc gaa tgc ggg  
1008

Lys Asn Arg Gly Leu Pro Gly His Arg Thr Ala Met Ser Glu Cys Gly  
325 330 335

ttt gat cca aca ggg aga ttg aaa ttc agt ggg agt gga tcg atg agg  
1056

Phe Asp Pro Thr Gly Arg Leu Lys Phe Ser Gly Ser Gly Ser Met Arg  
340 345 350

ata gtg gaa gaa gcg gcc gag aag aat gta gtg gaa aga gag agc ttt  
1104

Ile Val Glu Glu Ala Ala Glu Lys Asn Val Val Glu Arg Glu Ser Phe  
355 360 365

tcg gta tcg aaa ata tgg cta agg ggg aag gag aag cat agt aaa  
1152

Ser Val Ser Lys Ile Trp Leu Arg Gly Lys Lys Glu Lys His Ser Lys  
370 375 380

gtt caa gga aaa gag gat agt tca ttg gtt tct tcg tct tcg gga aga  
1200

Val Gln Gly Lys Glu Asp Ser Ser Leu Val Ser Ser Ser Ser Gly Arg  
385 390 395 400

gca ttc tct ttc agg tta tcg aac cag cgg aac cat ccc gat gcg atg  
1248

Ala Phe Ser Phe Arg Leu Ser Asn Gln Arg Asn His Pro Asp Ala Met  
405 410 415

atc gaa agt ggt tgc gaa gaa gat aat caa aag tgc gaa aac tcg gag  
1296

Ile Glu Ser Gly Cys Glu Glu Asp Asn Gln Lys Cys Glu Asn Ser Glu  
420 425 430

tct ttg gag act aaa aca cca tct ttt gct agg agg act atg ctt tgg  
1344

Ser Leu Glu Thr Lys Thr Pro Ser Phe Ala Arg Arg Thr Met Leu Trp  
435 440 445

ctt gca ggg aga caa aac aag gtt gtt cat tct tct tct tca act aat  
1392

Leu Ala Gly Arg Gln Asn Lys Val Val His Ser Ser Ser Ser Thr Asn  
450 455 460

gtc tag

1398

Val

465

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424

Met Lys Trp Val Phe Pro Glu Ile Lys Thr Thr Gln Asn Phe Leu Ser  
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Pro Ser Ser Leu Pro Gln Glu Pro Pro Leu Ser Leu Arg Ser Ser Ala  
20 25 30



Asn Phe Asp Leu Asn Ser Lys Ile Ser Pro Ser Ile Leu Leu Ile Ile  
 35 40 45  
 Ile Ile Leu Ser Ile Ile Phe Phe Ile Ser Gly Leu Leu His Leu Leu  
 50 55 60  
 Val Arg Phe Leu Leu Thr Pro Ser Ser Arg Asp Arg Glu Asp Tyr Phe  
 65 70 75 80  
 Asp Asn Val Thr Ala Leu Gln Gly Gln Leu Gln Gln Leu Phe His Leu  
 85 90 95  
 His Asp Ser Gly Val Asp Gln Ser Phe Ile Asp Thr Leu Pro Val Phe  
 100 105 110  
 His Tyr Lys Ser Ile Ile Gly Leu Lys Asn Tyr Pro Phe Asp Cys Ala  
 115 120 125  
 Val Cys Leu Cys Glu Phe Glu Thr Glu Asp Lys Leu Arg Leu Leu Pro  
 130 135 140  
 Lys Cys Ser His Ala Phe His Met Asp Cys Ile Asp Thr Trp Leu Leu  
 145 150 155 160  
 Ser His Ser Thr Cys Pro Leu Cys Arg Ser Ser Leu Leu Ser Asp Leu  
 165 170 175  
 Ser Ser His Gln Asp Pro Arg Ser Ser Phe Leu Leu Val Leu Glu Ser  
 180 185 190  
 Ala Ser Asp His Ser Ser Arg Glu Ile Gly Gly Asp Arg Asp Ser Ala  
 195 200 205  
 Ala Cys Val Ala Ala Asn Asp Asp Ile Asp Val Ser Ser Ala His Leu  
 210 215 220  
 Gly Leu Val Gly Asn Asn Asp Leu Gly Ser Thr Arg Ile Asp Ser Gly  
 225 230 235 240  
 His Gly Asp Gln Tyr Leu Asp Gly Glu Leu Gly Gly Ser Val Gly Lys  
 245 250 255  
 Val Val Pro Phe Ser Val Lys Leu Gly Lys Phe Arg Asn Ile Asp Ile  
 260 265 270



Gly'Glu Gly Thr Ser Ser Asn Asn Asn Ile Gly Asn Ser Ser Ser Leu  
 275 280 285

Asp Glu Arg Arg Cys Phe Ser Met Gly Ser Tyr Glu Tyr Ile Met Asp  
 290 295 300

Glu Glu Thr Thr Leu Lys Val His Val Ser Thr Lys Lys Gln Ser Ser  
 305 310 315 320

Lys Asn Arg Gly Leu Pro Gly His Arg Thr Ala Met Ser Glu Cys Gly  
 325 330 335

Phe Asp Pro Thr Gly Arg Leu Lys Phe Ser Gly Ser Gly Ser Met Arg  
 340 345 350

Ile Val Glu Glu Ala Ala Glu Lys Asn Val Val Glu Arg Glu Ser Phe  
 355 360 365

Ser Val Ser Lys Ile Trp Leu Arg Gly Lys Lys Glu Lys His Ser Lys  
 370 375 380

Val Gln Gly Lys Glu Asp Ser Ser Leu Val Ser Ser Ser Ser Gly Arg  
 385 390 395 400

Ala Phe Ser Phe Arg Leu Ser Asn Gln Arg Asn His Pro Asp Ala Met  
 405 410 415

Ile Glu Ser Gly Cys Glu Glu Asp Asn Gln Lys Cys Glu Asn Ser Glu  
 420 425 430

Ser Leu Glu Thr Lys Thr Pro Ser Phe Ala Arg Arg Thr Met Leu Trp  
 435 440 445

Leu Ala Gly Arg Gln Asn Lys Val Val His Ser Ser Ser Ser Thr Asn  
 450 455 460

Val  
 465

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 60

acttaaagct ttaccagaaa atg gag ggt cag aga aca caa cgc cgg ggt tac  
 113



Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr  
 1 5 10  
 ttg aaa gac aag gct aca gtc tcc aac ctt gtt gaa gaa gaa atg gag  
 161  
 Leu Lys Asp Lys Ala Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu  
 15 20 25  
 aat ggc atg gat gga gaa gag gag gat gga gga gac gaa gac aaa agg  
 209  
 Asn Gly Met Asp Gly Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg  
 30 35 40  
 aag aag gtg atg gaa aga gtt aga ggt cct agc act gac cgt gtt cca  
 257  
 Lys Lys Val Met Glu Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro  
 45 50 55  
 tcg cga ctg tgc cag gtc gat agg tgc act gtt aat ttg act gag gcc  
 305  
 Ser Arg Leu Cys Gln Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala  
 60 65 70 75  
 aag cag tat tac cgc aga cac aga gta tgt gaa gta cat gca aag gca  
 353  
 Lys Gln Tyr Tyr Arg Arg His Arg Val Cys Glu Val His Ala Lys Ala  
 80 85 90  
 tct gct gcg act gtt gca ggg gtc agg caa cgc ttt tgt caa caa tgc  
 401  
 Ser Ala Ala Thr Val Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys  
 95 100 105  
 agc agg ttt cat gag cta cca gag ttt gat gaa gct aaa aga agc tgc  
 449  
 Ser Arg Phe His Glu Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys  
 110 115 120  
 agg agg cgc tta gct gga cac aat gag agg agg agg aag atc tct ggt  
 497  
 Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly  
 125 130 135  
 gac agt ttt gga gaa ggg tca ggc cgg aga ggg ttt agc ggt caa ctg  
 545  
 Asp Ser Phe Gly Glu Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu  
 140 145 150 155  
 atc cag act caa gaa aga aac agg gta gac agg aaa ctt cct atg acc  
 593  
 Ile Gln Thr Gln Glu Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr  
 160 165 170  
 aac tca tca ttc aag cga cca cag atc aga taa accctccgc tctctctctt  
 646  
 Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg  
 175 180  
 ctgtcatcta catatgctct atctacactc ttattagaca aataatggca tctaacaatg  
 706



tcaagaaaag ttggtcatgg tattaaatcc tacacggata tataactata aacctctagt  
766

cccctctatg ctgtcctgta atgaatatct atccggaaat gtattcgcat agtcttgcgt  
826

ctaataatgt ttattgattt tgta  
850

<210> 426 <211> 181 <212> PRT <213> Arabidopsis thaliana <400>  
426

Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr Leu Lys Asp Lys Ala  
1 5 10 15

Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu Asn Gly Met Asp Gly  
20 25 30

Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg Lys Lys Val Met Glu  
35 40 45

Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro Ser Arg Leu Cys Gln  
50 55 60

Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala Lys Gln Tyr Tyr Arg  
65 70 75 80

Arg His Arg Val Cys Glu Val His Ala Lys Ala Ser Ala Ala Thr Val  
85 90 95

Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Glu  
100 105 110

Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys Arg Arg Arg Leu Ala  
115 120 125

Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly Asp Ser Phe Gly Glu  
130 135 140

Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu Ile Gln Thr Gln Glu  
145 150 155 160

Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr Asn Ser Ser Phe Lys  
165 170 175

Arg Pro Gln Ile Arg  
180



<210> 427 <211> 762 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(630) <223> G2421

<400> 427

atg gag ggt tgc tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa  
 48  
 Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu  
 1 5 10 15

gaa gat agt ctc ttg agg cag tgt att ggt aag tat gga gaa ggc aaa  
 96  
 Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys  
 20 25 30

tgg cat caa gtt cct tta aga gct ggg cta aat cgg tgc agg aaa agt  
 144  
 Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser  
 35 40 45

tgt aga cta aga tgg tta aac tat ttg aag cca agt atc aag aga gga  
 192  
 Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
 50 55 60

aaa ttt agt tct gat gaa gtt gat ctt ctt ctt cgt ctt cat aag ctt  
 240  
 Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu  
 65 70 75 80

cta gga aat agg tgg tcc ttg att gct ggt cga tta cct ggt cgg acc  
 288  
 Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
 85 90 95

gct aat gat gtc aag aac tac tgg aac acc cat ctg agt aag aag cat  
 336  
 Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
 100 105 110

gaa ccg tgt tgt aaa act aag ata aaa agg ata aat att ata acc cct  
 384  
 Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro  
 115 120 125

cct aat aca ccg gcc caa aaa gtt tgt gaa aat agt atc aca tgt aac  
 432  
 Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn  
 130 135 140

aaa gat gat gag aaa gat gat ttt gtg gat aat ttt atg gtt gga gat  
 480  
 Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp  
 145 150 155 160

aat ata tgg ttg gag cgt ttg cta gac gag ggc caa gag gta gat gtg  
 528  
 Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val  
 165 170 175

ctg gtt aca gaa gcg gcg gca aca gaa aag gag ggc act ttg gcg ttt  
 576



Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe  
180 185 190

gac gtt gag caa ctt tgg aat ttg ttc gat gga gag act gtg atc ttt  
624

Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe  
195 200 205

gat tag tgtttataaa cgtttgtgtt ctcttgtttg tgaggtttct ctatttaatt  
680

Asp

tagtatctat tttctaaatt aactaatatc ttatagtatt ttaggcaaac cttatgttct  
740

cgtttctgtg cggccgctct ag  
762

<210> 428 <211> 209 <212> PRT <213> Arabidopsis thaliana <400>  
428

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu  
1 5 10 15

Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys  
20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser  
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
50 55 60

Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu  
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
100 105 110

Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro  
115 120 125

Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn  
130 135 140

Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp  
145 150 155 160



Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val  
 165 170 175

Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe  
 180 185 190

Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe  
 195 200 205

Asp

<210> 429 <211> 741 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(741) <223> G2422

<400> 429

atg ggc gaa tca ccc aaa ggg ttg aga aaa ggt aca tgg act act gaa  
 48

Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu  
 1 5 10 15

gaa gat att ctc ttg agg caa tgc att gat aag tat gga gaa ggc aaa  
 96

Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys  
 20 25 30

tgg cat cga gtt cct tta aga act ggt ctc aat cgg tgc cga aag agt  
 144

Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser  
 35 40 45

tgt aga ctt aga tgg ttg aat tat ttg aag cca agt att aag aga gga  
 192

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
 50 55 60

aaa ctc tgc tcc gat gaa gtt gat ctt gtt ctt cgc ctt cat aaa ctt  
 240

Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu  
 65 70 75 80

cta gga aat agg tgg tcc ttg atc gct ggt aga ttg cct ggt cgg act  
 288

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
 85 90 95

gct aat gat gtc aag aat tac tgg aac act cat ttg agt aag aag cac  
 336

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
 100 105 110

gat gaa cga tgc tgt aag acg aag atg ata aac aaa aac att act tct  
 384

Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser  
 115 120 125



cat cct act tca tgc gcc caa aaa atc gat gtt tta aag cct cgg cct  
432

His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro  
130 135 140

cga tcc ttc tcc gat aaa aat agt tgc aac gat gtc aat atc ttg cca  
480

Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro  
145 150 155 160

aaa gtt gac gtt gtt cct tta cat ctt gga ctc aac aac aat tat gtt  
528

Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val  
165 170 175

tgt gaa agt agt att aca tgt aac aaa gat gag caa aaa gat aag ctt  
576

Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu  
180 185 190

att aat att aat cta ttg gat gga gat aat atg tgg tgg gaa agt tta  
624

Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu  
195 200 205

ctg gag gca gat gtg ttg ggt cca gaa gct acg gaa aca gca aag ggt  
672

Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly  
210 215 220

gtg acc tta ccg ctt gac ttt gag caa att tgg gct cgg ttt gat gaa  
720

Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu  
225 230 235 240

gag act tta gaa ctg aat tag  
741

Glu Thr Leu Glu Leu Asn  
245

<210> 430 <211> 246 <212> PRT <213> Arabidopsis thaliana <400>  
430

Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu  
1 5 10 15

Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys  
20 25 30

Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser  
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly  
50 55 60



Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu  
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr  
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His  
100 105 110

Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser  
115 120 125

His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro  
130 135 140

Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro  
145 150 155 160

Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val  
165 170 175

Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu  
180 185 190

Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu  
195 200 205

Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly  
210 215 220

Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu  
225 230 235 240

Glu Thr Leu Glu Leu Asn  
245

<210> 431 <211> 972 <212> DNA <213> Arabidopsis thaliana <220>  
<221> CDS <222> (1)..(972) <223> G2423

<400> 431  
atg gat gaa aaa gga aga agc ttg aag aac aac aac atg gaa gac gag  
48  
Met Asp Glu Lys Gly Arg Ser Leu Lys Asn Asn Asn Met Glu Asp Glu  
1 5 10 15

atg gac cta aag aga ggt ccg tgg act gct gaa gaa gat ttt aag etc  
96  
Met Asp Leu Lys Arg Gly Pro Trp Thr Ala Glu Glu Asp Phe Lys Leu  
20 25 30



atg aat tac att gct act aat gga gaa ggt cgc tgg aac tct ctt tct  
 144  
 Met Asn Tyr Ile Ala Thr Asn Gly Glu Gly Arg Trp Asn Ser Leu Ser  
 35 40 45  
 cgt tgc gcc ggc ctc caa cgc acc ggt aaa agc tgt aga cta agg tgg  
 192  
 Arg Cys Ala Gly Leu Gln Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp  
 50 55 60  
 tta aac tat ctc cgc cct gac gtc cgc cgt gga aac att aca ctt gaa  
 240  
 Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu Glu  
 65 70 75 80  
 gaa caa ctc ttg atc ctc gaa ctt cat tcc cgt tgg gga aat aga tgg  
 288  
 Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg Trp  
 85 90 95  
 tca aaa atc gca caa tat tta ccg gga aga acg gac aac gag atc aag  
 336  
 Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys  
 100 105 110  
 aac tac tgg agg acg cgg gtg caa aag cat gcg aaa cag ttg aaa tgt  
 384  
 Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys Cys  
 115 120 125  
 gat gtg aat agc caa caa ttc aaa gac aca atg aag tac ttg tgg atg  
 432  
 Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp Met  
 130 135 140  
 cct cga cta gtc gag agg att cag tca gcc tcg gcc tca tcc gca gca  
 480  
 Pro Arg Leu Val Glu Arg Ile Gln Ser Ala Ser Ala Ser Ser Ala Ala  
 145 150 155 160  
 gca gcc acc acc aca acc acc acc acc aca gga tca gcc ggc acg tca  
 528  
 Ala Ala Thr Thr Thr Thr Thr Thr Thr Gly Ser Ala Gly Thr Ser  
 165 170 175  
 tct tgc atc aca acc tct aac aat caa ttc atg aat tac gac tac aac  
 576  
 Ser Cys Ile Thr Thr Ser Asn Asn Gln Phe Met Asn Tyr Asp Tyr Asn  
 180 185 190  
 aac aac aac atg gga caa cag ttt ggt gta atg agc aac aat gat tat  
 624  
 Asn Asn Asn Met Gly Gln Gln Phe Gly Val Met Ser Asn Asn Asp Tyr  
 195 200 205  
 atc acg cct gaa aat tcc agc gtg gca gtg tct ccg gcg tca gac tta  
 672  
 Ile Thr Pro Glu Asn Ser Ser Val Ala Val Ser Pro Ala Ser Asp Leu  
 210 215 220



acg gag tac tac agc gct cca aac cct aac ccg gaa tac tat tcg ggt  
720

Thr Glu Tyr Tyr Ser Ala Pro Asn Pro Asn Pro Glu Tyr Tyr Ser Gly  
225 230 235 240

caa atg ggg aat agt tat tat cca gat cag aat tta gtg agt tca caa  
768

Gln Met Gly Asn Ser Tyr Tyr Pro Asp Gln Asn Leu Val Ser Ser Gln  
245 250 255

tta tta ccg gat aat tat ttc gac tat agt gga tta tta gac gaa gat  
816

Leu Leu Pro Asp Asn Tyr Phe Asp Tyr Ser Gly Leu Leu Asp Glu Asp  
260 265 270

cta acg gct atg caa gag cag agt aac ctc agc tgg ttt gaa aac att  
864

Leu Thr Ala Met Gln Glu Gln Ser Asn Leu Ser Trp Phe Glu Asn Ile  
275 280 285

aat ggt gct gct tct tct tca gac agt tta tgg aac att gga gaa act  
912

Asn Gly Ala Ala Ser Ser Ser Asp Ser Leu Trp Asn Ile Gly Glu Thr  
290 295 300

gat gaa gaa ttc tgg ttc tta cag cag caa caa cag ttc aac aat aat  
960

Asp Glu Glu Phe Trp Phe Leu Gln Gln Gln Gln Gln Phe Asn Asn Asn  
305 310 315 320

ggt agc ttc tga

972

Gly Ser Phe

<210> 432 <211> 323 <212> PRT <213> Arabidopsis thaliana <400>  
432

Met Asp Glu Lys Gly Arg Ser Leu Lys Asn Asn Asn Met Glu Asp Glu  
1 5 10 15

Met Asp Leu Lys Arg Gly Pro Trp Thr Ala Glu Glu Asp Phe Lys Leu  
20 25 30

Met Asn Tyr Ile Ala Thr Asn Gly Glu Gly Arg Trp Asn Ser Leu Ser  
35 40 45

Arg Cys Ala Gly Leu Gln Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp  
50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu Glu  
65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg Trp  
85 90 95



Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys  
 100 105 110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys Cys  
 115 120 125

Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp Met  
 130 135 140

Pro Arg Leu Val Glu Arg Ile Gln Ser Ala Ser Ala Ser Ser Ala Ala  
 145 150 155 160

Ala Ala Thr Thr Thr Thr Thr Thr Thr Gly Ser Ala Gly Thr Ser  
 165 170 175

Ser Cys Ile Thr Thr Ser Asn Asn Gln Phe Met Asn Tyr Asp Tyr Asn  
 180 185 190

Asn Asn Asn Met Gly Gln Gln Phe Gly Val Met Ser Asn Asn Asp Tyr  
 195 200 205

Ile Thr Pro Glu Asn Ser Ser Val Ala Val Ser Pro Ala Ser Asp Leu  
 210 215 220

Thr Glu Tyr Tyr Ser Ala Pro Asn Pro Asn Pro Glu Tyr Tyr Ser Gly  
 225 230 235 240

Gln Met Gly Asn Ser Tyr Tyr Pro Asp Gln Asn Leu Val Ser Ser Gln  
 245 250 255

Leu Leu Pro Asp Asn Tyr Phe Asp Tyr Ser Gly Leu Leu Asp Glu Asp  
 260 265 270

Leu Thr Ala Met Gln Glu Gln Ser Asn Leu Ser Trp Phe Glu Asn Ile  
 275 280 285

Asn Gly Ala Ala Ser Ser Ser Asp Ser Leu Trp Asn Ile Gly Glu Thr  
 290 295 300

Asp Glu Glu Phe Trp Phe Leu Gln Gln Gln Gln Gln Phe Asn Asn Asn  
 305 310 315 320

Gly Ser Phe



<210> 433 <211> 849 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (1)..(849) <223> G2467

<400> 433

atg gac ccg tgc tca agc tcc aga gca cgg tca atg cca ccg ccg gtg  
 48

Met Asp Pro Ser Ser Ser Ser Arg Ala Arg Ser Met Pro Pro Pro Val  
 1 5 10 15

cct atg gag gga ttg cag gaa gca ggg cct tct cct ttt cta aca aag  
 96

Pro Met Glu Gly Leu Gln Glu Ala Gly Pro Ser Pro Phe Leu Thr Lys  
 20 25 30

acg ttc gag atg gtt ggt gat cca aac aca aac cac att gtg tct tgg  
 144

Thr Phe Glu Met Val Gly Asp Pro Asn Thr Asn His Ile Val Ser Trp  
 35 40 45

aac agg gga ggc atc agt ttt gtc gtg tgg gat cca cat tcc ttc tgc  
 192

Asn Arg Gly Gly Ile Ser Phe Val Val Trp Asp Pro His Ser Phe Ser  
 50 55 60

gcc act att ctg cct cta tac ttc aag cac aac aac ttc tcc agc ttt  
 240

Ala Thr Ile Leu Pro Leu Tyr Phe Lys His Asn Asn Phe Ser Ser Phe  
 65 70 75 80

gtc aga caa ctt aac act tat gga ttc aga aag atc gag gca gag aga  
 288

Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu Arg  
 85 90 95

tgg gag ttt atg aat gaa ggt ttc ttg atg ggt cag agg gac ctt ctc  
 336

Trp Glu Phe Met Asn Glu Gly Phe Leu Met Gly Gln Arg Asp Leu Leu  
 100 105 110

aaa agc atc aag cga cga acc tcc tct tct tcc cct cct tgc ctt aac  
 384

Lys Ser Ile Lys Arg Arg Thr Ser Ser Ser Ser Pro Pro Ser Leu Asn  
 115 120 125

tac tct cag tct cag ccc gag gct cat gac cca ggc gtc gag ctt ccg  
 432

Tyr Ser Gln Ser Gln Pro Glu Ala His Asp Pro Gly Val Glu Leu Pro  
 130 135 140

cag ctc cga gaa gag agg cat gtc cta atg atg gag atc tgc acg ctc  
 480

Gln Leu Arg Glu Glu Arg His Val Leu Met Met Glu Ile Ser Thr Leu  
 145 150 155 160

aga cag gag gag caa aga gcg aga ggc tac gtc caa gcc atg gag cag  
 528

Arg Gln Glu Glu Gln Arg Ala Arg Gly Tyr Val Gln Ala Met Glu Gln  
 165 170 175



agg att aat gga gca gag aag aaa cag agg cat atg atg tcc ttc ttg  
576

Arg Ile Asn Gly Ala Glu Lys Lys Gln Arg His Met Met Ser Phe Leu  
180 185 190

agg cgt gcg gtg gag aat cct tcc ctt ctg cag cag att ttc gag cag  
624

Arg Arg Ala Val Glu Asn Pro Ser Leu Leu Gln Gln Ile Phe Glu Gln  
195 200 205

aag aga gac cga gag gag gcc gcg atg att gat cag gct ggc ttg atc  
672

Lys Arg Asp Arg Glu Glu Ala Ala Met Ile Asp Gln Ala Gly Leu Ile  
210 215 220

aaa atg gaa gag gtg gag cac ctg tcg gag ctg gag gct ctg gcg ctt  
720

Lys Met Glu Glu Val Glu His Leu Ser Glu Leu Glu Ala Leu Ala Leu  
225 230 235 240

gag atg caa gga tat gga cgg caa cgg act gat ggt gtg gag agg gag  
768

Glu Met Gln Gly Tyr Gly Arg Gln Arg Thr Asp Gly Val Glu Arg Glu  
245 250 255

ctt gac gac ggg ttt tgg gaa gag tta ctc atg aac aat gaa aac tcc  
816

Leu Asp Asp Gly Phe Trp Glu Glu Leu Leu Met Asn Asn Glu Asn Ser  
260 265 270

gac gaa gaa gag gcg aat gtg aag caa gat tag  
849

Asp Glu Glu Glu Ala Asn Val Lys Gln Asp  
275 280

<210> 434 <211> 282 <212> PRT <213> Arabidopsis thaliana <400>  
434

Met Asp Pro Ser Ser Ser Ser Arg Ala Arg Ser Met Pro Pro Pro Val  
1 5 10 15

Pro Met Glu Gly Leu Gln Glu Ala Gly Pro Ser Pro Phe Leu Thr Lys  
20 25 30

Thr Phe Glu Met Val Gly Asp Pro Asn Thr Asn His Ile Val Ser Trp  
35 40 45

Asn Arg Gly Gly Ile Ser Phe Val Val Trp Asp Pro His Ser Phe Ser  
50 55 60

Ala Thr Ile Leu Pro Leu Tyr Phe Lys His Asn Asn Phe Ser Ser Phe  
65 70 75 80

Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu Arg  
85 90 95



Trp Glu Phe Met Asn Glu Gly Phe Leu Met Gly Gln Arg Asp Leu Leu  
 100 105 110

Lys Ser Ile Lys Arg Arg Thr Ser Ser Ser Ser Pro Pro Ser Leu Asn  
 115 120 125

Tyr Ser Gln Ser Gln Pro Glu Ala His Asp Pro Gly Val Glu Leu Pro  
 130 135 140

Gln Leu Arg Glu Glu Arg His Val Leu Met Met Glu Ile Ser Thr Leu  
 145 150 155 160

Arg Gln Glu Glu Gln Arg Ala Arg Gly Tyr Val Gln Ala Met Glu Gln  
 165 170 175

Arg Ile Asn Gly Ala Glu Lys Lys Gln Arg His Met Met Ser Phe Leu  
 180 185 190

Arg Arg Ala Val Glu Asn Pro Ser Leu Leu Gln Gln Ile Phe Glu Gln  
 195 200 205

Lys Arg Asp Arg Glu Glu Ala Ala Met Ile Asp Gln Ala Gly Leu Ile  
 210 215 220

Lys Met Glu Glu Val Glu His Leu Ser Glu Leu Glu Ala Leu Ala Leu  
 225 230 235 240

Glu Met Gln Gly Tyr Gly Arg Gln Arg Thr Asp Gly Val Glu Arg Glu  
 245 250 255

Leu Asp Asp Gly Phe Trp Glu Glu Leu Leu Met Asn Asn Glu Asn Ser  
 260 265 270

Asp Glu Glu Glu Ala Asn Val Lys Gln Asp  
 275 280

<210> 435 <211> 690 <212> DNA <213> Arabidopsis thaliana <220>  
 <221> CDS <222> (112)..(690) <223> G2514

<400> 435  
 aaaacttctt catcttcttt aattagtttg ccacctcgca cgtgtgacaa atccttcttc  
 60

gccacgtgtg aaaacccttc tccggcttgc tactaatata cgactaatag t atg aat  
 117

Met Asn  
 1



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agt tca atg gct tct gcc ggc tta ggt agc cgg aga aag gat ccg gtg
165
Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp Pro Val
      5              10              15

tac aga gga atc cgg tgc cga agt ggg aaa tgg gtc tcc gag att cgt
213
Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg
      20              25              30

gag ccg agg aaa acc acg aga atc tgg ctt gga act tac ccc atg gca
261
Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Met Ala
      35              40              45              50

gag atg gca gca gcc gcc tat gat gtg gct gct atg gct ctt aaa gga
309
Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu Lys Gly
      55              60              65

aga gaa gct gtc ttg aac ttc cct gga tcc gtc ggg tca tac ccg gtt
357
Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr Pro Val
      70              75              80

cct gaa tca aca tcc gca gca gat ata cga gcc gct gcg gca gcc gca
405
Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala Ala Ala
      85              90              95

gca gca atg aag gga tgt gag gaa ggg gag gag gag aaa aag gca aag
453
Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys Ala Lys
      100              105              110

gag aag aag agt agt agt tcg aag tcg aga gcg cgt gag tgc cac gta
501
Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys His Val
      115              120              125              130

gat aat gat gtt gga tct tcg tcg tgg tgt ggg aca gag ttc atg gac
549
Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe Met Asp
      135              140              145

gaa gaa gaa gtc ttg aat atg cct aat ctg ctg gct aat atg gca gaa
597
Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met Ala Glu
      150              155              160

ggg atg atg gtt gcg ccg ccg tcg tgg atg ggt tct ccg ccg tcg gat
645
Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro Ser Asp
      165              170              175

gac tct ccg gag aat tca aat gat gag gac ttg tgg ggc tat tga
690
Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr
      180              185              190

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436

Met Asn Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp  
1 5 10 15

Pro Val Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu  
20 25 30

Ile Arg Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro  
35 40 45

Met Ala Glu Met Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu  
50 55 60

Lys Gly Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr  
65 70 75 80

Pro Val Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala  
85 90 95

Ala Ala Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys  
100 105 110

Ala Lys Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys  
115 120 125

His Val Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe  
130 135 140

Met Asp Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met  
145 150 155 160

Ala Glu Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro  
165 170 175

Ser Asp Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr  
180 185 190

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<400> 437

atg gac caa gaa caa aca cca cat agc cca acc cgc cat agt cgc tca  
48

Met Asp Gln Glu Gln Thr Pro His Ser Pro Thr Arg His Ser Arg Ser  
1 5 10 15



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ccc cca tcc tcc gcc tcc ggt tcc acc tca gca gaa ccg gtt cgg tcc
96
Pro Pro Ser Ser Ala Ser Gly Ser Thr Ser Ala Glu Pro Val Arg Ser
      20      25      30

cga tgg tca cct aaa ccg gaa caa ata ctc ata ctt gag tcg atc ttc
144
Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser Ile Phe
      35      40      45

cac agt ggt atg gtt aac cct ccc aaa gaa gag acg gta agg ata aga
192
His Ser Gly Met Val Asn Pro Pro Lys Glu Glu Thr Val Arg Ile Arg
      50      55      60

aag atg ctc gag aaa ttt ggc gcg gtg gga gat gca aat gtc ttc tat
240
Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala Asn Val Phe Tyr
      65      70      75      80

tgg ttt caa aac ccg ccg tca agg tcc cgt ccg aga cag cga cag cta
288
Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg Gln Leu
      85      90      95

cag gct gca gct gca gca gcg gac gca acc acc aac act tct agc tct
336
Gln Ala Ala Ala Ala Ala Ala Asp Ala Thr Thr Asn Thr Ser Ser Ser
      100      105      110

tct tct tct tat ggt ggt gga tgt gat aat caa agc aat agt ggc atg
384
Ser Ser Ser Tyr Gly Gly Gly Cys Asp Asn Gln Ser Asn Ser Gly Met
      115      120      125

gag aat ctc tta aca atg tct ggc caa atg agt tac cat gaa gct act
432
Glu Asn Leu Leu Thr Met Ser Gly Gln Met Ser Tyr His Glu Ala Thr
      130      135      140

cat cat cat tat caa aat cat agc tca aat gtc aca tcg att ttg tgc
480
His His His Tyr Gln Asn His Ser Ser Asn Val Thr Ser Ile Leu Cys
      145      150      155      160

cca tct gat caa aac tcc aat ttt caa tac caa caa ggg gct ata acg
528
Pro Ser Asp Gln Asn Ser Asn Phe Gln Tyr Gln Gln Gly Ala Ile Thr
      165      170      175

gtg ttt ata aac gga gtt ccg aca gaa gtg acg aga gga gga ata gac
576
Val Phe Ile Asn Gly Val Pro Thr Glu Val Thr Arg Gly Gly Ile Asp
      180      185      190

atg aaa gca acg ttt gga gaa gat ttg gtt ttg gtg cat tcc tca ggt
624
Met Lys Ala Thr Phe Gly Glu Asp Leu Val Leu Val His Ser Ser Gly
      195      200      205

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gtt cct ctt cct act gat gag ttt ggt ttt ttg atg cat agc tta caa  
672

Val Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln  
210 215 220

cat ggt gaa gct tat ttc ctg gtt cca aga cag aca tga actggcttta  
721

His Gly Glu Ala Tyr Phe Leu Val Pro Arg Gln Thr  
225 230 235

ctcgtatgtg tgggtgatgca acagatgtct tgtttttcta ccttggactt tattgcaacg  
781

gtccttccat tttttctttt cttttcgagt ctatcgtata atcaaagttt cttctattgg  
841

ttttttttta aaaaatttta ttttgcaatt tattttataa agatgaagtc aaaagctctt  
901

gtacgacgaa gatattctagg ttgtatcaat ttagttattt agatgtaaaa tacgtatgta  
961

taattgattt gcaataaaat ctctgtctag gga  
994

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438

Met Asp Gln Glu Gln Thr Pro His Ser Pro Thr Arg His Ser Arg Ser  
1 5 10 15

Pro Pro Ser Ser Ala Ser Gly Ser Thr Ser Ala Glu Pro Val Arg Ser  
20 25 30

Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser Ile Phe  
35 40 45

His Ser Gly Met Val Asn Pro Pro Lys Glu Glu Thr Val Arg Ile Arg  
50 55 60

Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala Asn Val Phe Tyr  
65 70 75 80

Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg Gln Leu  
85 90 95

Gln Ala Ala Ala Ala Ala Asp Ala Thr Thr Asn Thr Ser Ser Ser  
100 105 110

Ser Ser Ser Tyr Gly Gly Gly Cys Asp Asn Gln Ser Asn Ser Gly Met  
115 120 125



Glu Asn Leu Leu Thr Met Ser Gly Gln Met Ser Tyr His Glu Ala Thr  
 130 135 140

His His His Tyr Gln Asn His Ser Ser Asn Val Thr Ser Ile Leu Cys  
 145 150 155 160

Pro Ser Asp Gln Asn Ser Asn Phe Gln Tyr Gln Gln Gly Ala Ile Thr  
 165 170 175

Val Phe Ile Asn Gly Val Pro Thr Glu Val Thr Arg Gly Gly Ile Asp  
 180 185 190

Met Lys Ala Thr Phe Gly Glu Asp Leu Val Leu Val His Ser Ser Gly  
 195 200 205

Val Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln  
 210 215 220

His Gly Glu Ala Tyr Phe Leu Val Pro Arg Gln Thr  
 225 230 235

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 48  
 Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro  
 1 5 10 15

ttc cat gct aga gat ttc caa tta cat ctt caa caa caa caa caa cat  
 96  
 Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln His  
 20 25 30

caa caa caa cat caa caa caa caa caa caa cag ttc ttt ctc cac cat  
 144  
 Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Phe Phe Leu His His  
 35 40 45

cat cag caa cca caa aga aac ctt gat caa gat cac gag cag caa gga  
 192  
 His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly  
 50 55 60

ggg tca ata ttg aat aga tct atc aag atg gat cgc gaa gag aca agc  
 240  
 Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser  
 65 70 75 80

gat aac atg gac aac atc gct aat acc aac agc ggt agc gaa ggt aaa  
 288  
 Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys  
 85 90 95



gag atg agt tta cac gga gga gaa gga gga agc ggt ggt gga gga agt  
 336  
 Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser  
 100 105 110

gga gaa cag atg aca aga agg cca aga gga aga cca gca gga tcc aag  
 384  
 Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys  
 115 120 125

aac aaa cct aaa gct cca ata atc ata aca aga gac agc gca aac gcg  
 432  
 Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala  
 130 135 140

ctt cga act cac gtc atg gag ata gga gac gga tgt gac ata gtt gac  
 480  
 Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp  
 145 150 155 160

tgt atg gct acg ttc gct aga cgc cgc caa aga ggc gtt tgc gtt atg  
 528  
 Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met  
 165 170 175

agc ggt aca gga agc gtt act aac gtc act ata cgt cag cct gga tcg  
 576  
 Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser  
 180 185 190

cca cct ggc tcg gtg gtt agc ctt cac ggc cgg ttt gaa atc ctc tct  
 624  
 Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser  
 195 200 205

ctt tcg gga tct ttc ttg cct ccg cct gcg ccg cct gca gcc acc gga  
 672  
 Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly  
 210 215 220

cta agc gtt tac cta gcc gga gga caa ggg cag gtc gtt gga ggt agt  
 720  
 Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser  
 225 230 235 240

gtg gtg gga cct ttg ttg tgt tcg ggt cct gtg gtg gtt atg gcg gct  
 768  
 Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala  
 245 250 255

tct ttt agc aat gcg gcg tac gaa agg ctg cct ttg gaa gaa gat gag  
 816  
 Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu  
 260 265 270

atg cag acg cca gtt caa gga ggc ggt gga gga gga ggt ggt ggt  
 864  
 Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 275 280 285



gga atg gga tct ccc ccg atg atg gga`cag caa caa gct atg gca gct  
 912  
 Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala  
 290 295 300

atg gcg gcg gct caa gga cta cca ccg aat ctt ctt ggt tcg gtt cag  
 960  
 Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln  
 305 310 315 320

ttg cca ccg cca caa cag aat gat cag cag tat tgg tct acg ggt cgg  
 1008  
 Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg  
 325 330 335

cca ccg tat tga  
 1020  
 Pro Pro Tyr

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 440

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro  
 1 5 10 15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln His  
 20 25 30

Gln Gln Gln His Gln Gln Gln Gln Gln Gln Phe Phe Leu His His  
 35 40 45

His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly  
 50 55 60

Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser  
 65 70 75 80

Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys  
 85 90 95

Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser  
 100 105 110

Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys  
 115 120 125

Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala  
 130 135 140

Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp



145                      150                      155                      160  
 Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met  
                          165                                      170                                      175  
 Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser  
                          180                                      185                                      190  
 Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser  
                          195                                      200                                      205  
 Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly  
                          210                                      215                                      220  
 Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser  
                          225                                      230                                      235                                      240  
 Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala  
    245                                      250                                      255  
 Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu  
    260                                      265                                      270  
 Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
    275                                      280                                      285  
 Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala  
    290                                      295                                      300  
 Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln  
    305                                      310                                      315                                      320  
 Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg  
    325                                      330                                      335  
 Pro Pro Tyr

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 <221> CDS <222> (188)..(880) <223> G2659

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cactctaagc ttattttcgt ataaattata gtatagtcac attcttttag gacagaaccc  
 120



accgaaagaa agctccaaac ccaacaaaaa gggaggcggc ggagaagcaa acaacagcaa  
180

caaaaaa atg cag cca gag gtt tca gat caa ata ttt tat gcc ttc ctc  
229

Met Gln Pro Glu Val Ser Asp Gln Ile Phe Tyr Ala Phe Leu  
1 5 10

acc gga gga tta tgt gcc tcg tct act tcc acc acc gtg acg tcg tcg  
277

Thr Gly Gly Leu Cys Ala Ser Ser Thr Ser Thr Thr Val Thr Ser Ser  
15 20 25 30

tct gac cct ttt gcc acg gtt tat gaa gac aaa gct ctt gct tct ctg  
325

Ser Asp Pro Phe Ala Thr Val Tyr Glu Asp Lys Ala Leu Ala Ser Leu  
35 40 45

agg aac cat aaa gag gct gag cga aag aga aga gca aga atc aat tcc  
373

Arg Asn His Lys Glu Ala Glu Arg Lys Arg Arg Ala Arg Ile Asn Ser  
50 55 60

cat ctc aac aag ctc cgc aag tta ctc tct tgt aac tcc aag aca gac  
421

His Leu Asn Lys Leu Arg Lys Leu Leu Ser Cys Asn Ser Lys Thr Asp  
65 70 75

aaa tcc aca cta cta gca aaa gtg gtt caa cga gtc aaa gaa cta aaa  
469

Lys Ser Thr Leu Leu Ala Lys Val Val Gln Arg Val Lys Glu Leu Lys  
80 85 90

caa caa acc cta gaa atc acc gac gaa aca ata ccg tcg gag act gac  
517

Gln Gln Thr Leu Glu Ile Thr Asp Glu Thr Ile Pro Ser Glu Thr Asp  
95 100 105 110

gaa atc agt gta ctc aac att gag gac tgt tcc aga ggc gac gat cga  
565

Glu Ile Ser Val Leu Asn Ile Glu Asp Cys Ser Arg Gly Asp Asp Arg  
115 120 125

cgg ata atc ttt aag gta tcg ttt tgc tgc gag gac cgg cca gag ctc  
613

Arg Ile Ile Phe Lys Val Ser Phe Cys Cys Glu Asp Arg Pro Glu Leu  
130 135 140

ttg aaa gat ctc atg gag aca ctc aaa tct ctt cag atg gaa act ctc  
661

Leu Lys Asp Leu Met Glu Thr Leu Lys Ser Leu Gln Met Glu Thr Leu  
145 150 155

ttt gcc gac atg aca aca gtc ggt ggt cga aca aga aac gtt ctc gtt  
709

Phe Ala Asp Met Thr Thr Val Gly Gly Arg Thr Arg Asn Val Leu Val  
160 165 170

gtg gcc gct gac aaa gag cat cac ggc gtc cag tcg gtg aat ttt cta  
757

Val Ala Ala Asp Lys Glu His His Gly Val Gln Ser Val Asn Phe Leu



175                      180                      185                      190  
 cag aac gca ctc aag tct tta ctc gaa cgg tca agc aag tcg gtg atg  
 805  
 Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Val Met  
                     195                      200                      205  
 gtg gga cat ggt ggt ggt ggt ggg gaa gaa agg tta aaa cga cgt cgt  
 853  
 Val Gly His Gly Gly Gly Gly Gly Glu Glu Arg Leu Lys Arg Arg Arg  
                     210                      215                      220  
 gcg ctg gat cac atc ata atg gtc tga  
 880  
 Ala Leu Asp His Ile Ile Met Val  
                     225                      230  
  
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 Gly Leu Cys Ala Ser Ser Thr Ser Thr Thr Val Thr Ser Ser Ser Asp  
                     20                      25                      30  
  
 Pro Phe Ala Thr Val Tyr Glu Asp Lys Ala Leu Ala Ser Leu Arg Asn  
                     35                      40                      45  
  
 His Lys Glu Ala Glu Arg Lys Arg Arg Ala Arg Ile Asn Ser His Leu  
                     50                      55                      60  
  
 Asn Lys Leu Arg Lys Leu Leu Ser Cys Asn Ser Lys Thr Asp Lys Ser  
 65                      70                      75                      80  
  
 Thr Leu Leu Ala Lys Val Val Gln Arg Val Lys Glu Leu Lys Gln Gln  
                     85                      90                      95  
  
 Thr Leu Glu Ile Thr Asp Glu Thr Ile Pro Ser Glu Thr Asp Glu Ile  
                     100                      105                      110  
  
 Ser Val Leu Asn Ile Glu Asp Cys Ser Arg Gly Asp Asp Arg Arg Ile  
                     115                      120                      125  
  
 Ile Phe Lys Val Ser Phe Cys Cys Glu Asp Arg Pro Glu Leu Leu Lys  
                     130                      135                      140  
  
 Asp Leu Met Glu Thr Leu Lys Ser Leu Gln Met Glu Thr Leu Phe Ala  
 145                      150                      155                      160



Asp Met Thr Thr Val Gly Gly Arg Thr Arg Asn Val Leu Val Val Ala  
165 170 175

Ala Asp Lys Glu His His Gly Val Gln Ser Val Asn Phe Leu Gln Asn  
180 185 190

Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Val Met Val Gly  
195 200 205

His Gly Gly Gly Gly Gly Glu Glu Arg Leu Lys Arg Arg Arg Ala Leu  
210 215 220

Asp His Ile Ile Met Val  
225 230

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<221> CDS <222> (46)..(837) <223> G2701

<400> 443  
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57

Met Glu Thr Leu  
1

cat cca ttc tct cac cta cct atc tct gac cac cgg ttc gtt gtt caa  
105  
His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe Val Val Gln  
5 10 15 20

gag atg gtg agc tta cac agc tcg agt agc ggt agc tgg act aaa gaa  
153  
Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser Trp Thr Lys Glu  
25 30 35

gag aac aag atg ttc gaa cga gct ctt gcg ata tac gct gaa gac tcg  
201  
Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala Glu Asp Ser  
40 45 50

cct gat cgc tgg ttt aaa gtt gct tcc atg atc cct gga aag act gtt  
249  
Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly Lys Thr Val  
55 60 65

ttt gat gtt atg aag caa tat agt aag ctt gaa gaa gac gtt ttc gat  
297  
Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp Val Phe Asp  
70 75 80

att gaa gca gga cgt gtt ccc att cct ggt tat cct gca gct tct tct  
345  
Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala Ala Ser Ser  
85 90 95 100

ccc ttg ggg ttt gac acg gac atg tgt cgt aaa cgg cct agt gga gct  
393



Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro Ser Gly Ala  
 105 110 115  
 aga gga tct gat caa gat cga aag aaa gga .gtc cct tgg aca gag gaa  
 441  
 Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp Thr Glu Glu  
 120 125 130  
 gaa cac agg aga ttc ttg tta ggc ctt ctc aag tac ggt aaa gga gat  
 489  
 Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp  
 135 140 145  
 tgg aga aac ata tcg aga aac ttc gtg gtg tca aag acg cca acg caa  
 537  
 Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr Pro Thr Gln  
 150 155 160  
 gtg gcg agc cac gcc caa aag tat tac cag aga cag ctc tcc gga gcc  
 585  
 Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala  
 165 170 175 180  
 aag gac aaa cgc agg cca agt atc cat gac atc aca acc ggc aat ctt  
 633  
 Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Gly Asn Leu  
 185 190 195  
 ctc aat gcc aat ctc aac cgt tcc ttt tcc gat cat aga gat att ctc  
 681  
 Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His Arg Asp Ile Leu  
 200 205 210  
 cct gat tta ggg ttt atc gat aag gat gat acg gag gag gga gta ata  
 729  
 Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu Glu Gly Val Ile  
 215 220 225  
 ttt atg ggt cag aat ctc tct tca gaa aat ctg ttt tct cca tca cca  
 777  
 Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe Ser Pro Ser Pro  
 230 235 240  
 act tca ttc gaa gct gcc att aac ttc gcc gga gaa aat gtc ttc agt  
 825  
 Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu Asn Val Phe Ser  
 245 250 255 260  
 gcc gga gct taa ggcaacatag aatccccaaa ctcagcggc  
 866  
 Ala Gly Ala

<210> 444 <211> 263 <212> PRT <213> Arabidopsis thaliana <400>  
 444

Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg  
 1 5 10 15



Phe Val Val Gln Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser  
 20 25 30  
 Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr  
 35 40 45  
 Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro  
 50 55 60  
 Gly Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu  
 65 70 75 80  
 Asp Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro  
 85 90 95  
 Ala Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg  
 100 105 110  
 Pro Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro  
 115 120 125  
 Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr  
 130 135 140  
 Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys  
 145 150 155 160  
 Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln  
 165 170 175  
 Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr  
 180 185 190  
 Thr Gly Asn Leu Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His  
 195 200 205  
 Arg Asp Ile Leu Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu  
 210 215 220  
 Glu Gly Val Ile Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe  
 225 230 235 240  
 Ser Pro Ser Pro Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu  
 245 250 255  
 Asn Val Phe Ser Ala Gly Ala



260

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<400> 445

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 48

Met Gly Glu Glu Val Gln Met Ser Asp Tyr Asp Val Ser Gly Asp Gly  
 1 5 10 15

gat agg gtt tct gaa tgg gag atg gga tta cca agc gac gaa gat cta  
 96

Asp Arg Val Ser Glu Trp Glu Met Gly Leu Pro Ser Asp Glu Asp Leu  
 20 25 30

gca tct ctt tct tac tct ctg att cca ccg aat ttg gcg atg gcg ttt  
 144

Ala Ser Leu Ser Tyr Ser Leu Ile Pro Pro Asn Leu Ala Met Ala Phe  
 35 40 45

agt atc aca ccg gag aga agc cgt acg att cag gat gtg aat cgt gca  
 192

Ser Ile Thr Pro Glu Arg Ser Arg Thr Ile Gln Asp Val Asn Arg Ala  
 50 55 60

tcg gag acg acg ctc tcg tcg cta cgt ggt gga tct tca ggt cca aat  
 240

Ser Glu Thr Thr Leu Ser Ser Leu Arg Gly Gly Ser Ser Gly Pro Asn  
 65 70 75 80

acc tcg tcg tcg aat aat aac gtg gag gag gaa gat cga gtt gga tct  
 288

Thr Ser Ser Ser Asn Asn Asn Val Glu Glu Glu Asp Arg Val Gly Ser  
 85 90 95

agc agt cct gga tcg gat tcg aag aag caa aag aca tca aac ggt gat  
 336

Ser Ser Pro Gly Ser Asp Ser Lys Lys Gln Lys Thr Ser Asn Gly Asp  
 100 105 110

gga gat gac ggt ggc ggt gtg gat ccg gat tcg gcg atg gcg gcg gaa  
 384

Gly Asp Asp Gly Gly Gly Val Asp Pro Asp Ser Ala Met Ala Ala Glu  
 115 120 125

gaa gga gat tca gga act gaa gat cta tct ggg aaa aca ctt aaa cga  
 432

Glu Gly Asp Ser Gly Thr Glu Asp Leu Ser Gly Lys Thr Leu Lys Arg  
 130 135 140

ccg cgt tta gtg tgg aca ccg cag cta cac aag aga ttc gtt gac gtt  
 480

Pro Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val  
 145 150 155 160

gta gct cac tta ggg atc aaa aac gct gtt ccg aag acg att atg cag  
 528

Val Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln  
 165 170 175



ctg atg aac gtt gaa gga tta act cgt gag aac gtt gcg tct cat ctt  
 576  
 Leu Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu  
 180 185 190  
 caa aag tat agg ctt tac ctc aaa agg atg cag gga ttg act aat gaa  
 624  
 Gln Lys Tyr Arg Leu Tyr Leu Lys Arg Met Gln Gly Leu Thr Asn Glu  
 195 200 205  
 ggt ccc tct gct tcg gat aag ctc ttc tct tca aca cct gtt cct cca  
 672  
 Gly Pro Ser Ala Ser Asp Lys Leu Phe Ser Ser Thr Pro Val Pro Pro  
 210 215 220  
 cag agc ttc caa gat atc ggt ggc ggt ggc ggt agc agc ggt aat gtt  
 720  
 Gln Ser Phe Gln Asp Ile Gly Gly Gly Gly Gly Ser Ser Gly Asn Val  
 225 230 235 240  
 gga gtg ccg att ccg ggg gcg tat gga acg caa cag atg atg cag atg  
 768  
 Gly Val Pro Ile Pro Gly Ala Tyr Gly Thr Gln Gln Met Met Gln Met  
 245 250 255  
 cca gtt tat gca cat cat atg ggt atg caa gga tat cat cat caa aat  
 816  
 Pro Val Tyr Ala His His Met Gly Met Gln Gly Tyr His His Gln Asn  
 260 265 270  
 cat aat cat gat cct tat cat cag aat cat cgt cat cat cat gga gct  
 864  
 His Asn His Asp Pro Tyr His Gln Asn His Arg His His His Gly Ala  
 275 280 285  
 ggt gga aat ggt gcg ttt gag tca aat cct tat atg atg cag cag aat  
 912  
 Gly Gly Asn Gly Ala Phe Glu Ser Asn Pro Tyr Met Met Gln Gln Asn  
 290 295 300  
 aag ttt gga tcc atg gct tct tat cct tct gtt gga ggt gga agc gca  
 960  
 Lys Phe Gly Ser Met Ala Ser Tyr Pro Ser Val Gly Gly Gly Ser Ala  
 305 310 315 320  
 aat gag aat taa  
 972  
 Asn Glu Asn

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Met Gly Glu Glu Val Gln Met Ser Asp Tyr Asp Val Ser Gly Asp Gly  
 1 5 10 15

Asp Arg Val Ser Glu Trp Glu Met Gly Leu Pro Ser Asp Glu Asp Leu  
 20 25 30



Ala Ser Leu Ser Tyr Ser Leu Ile Pro Pro Asn Leu Ala Met Ala Phe  
           35                                  40                                  45

Ser Ile Thr Pro Glu Arg Ser Arg Thr Ile Gln Asp Val Asn Arg Ala  
           50                                  55                                  60

Ser Glu Thr Thr Leu Ser Ser Leu Arg Gly Gly Ser Ser Gly Pro Asn  
           65                                  70                                  75                                  80

Thr Ser Ser Ser Asn Asn Asn Val Glu Glu Glu Asp Arg Val Gly Ser  
                                   85                                  90                                  95

Ser Ser Pro Gly Ser Asp Ser Lys Lys Gln Lys Thr Ser Asn Gly Asp  
                                   100                                  105                                  110

Gly Asp Asp Gly Gly Gly Val Asp Pro Asp Ser Ala Met Ala Ala Glu  
           115                                  120                                  125

Glu Gly Asp Ser Gly Thr Glu Asp Leu Ser Gly Lys Thr Leu Lys Arg  
           130                                  135                                  140

Pro Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val  
           145                                  150                                  155                                  160

Val Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln  
                                   165                                  170                                  175

Leu Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu  
                                   180                                  185                                  190

Gln Lys Tyr Arg Leu Tyr Leu Lys Arg Met Gln Gly Leu Thr Asn Glu  
           195                                  200                                  205

Gly Pro Ser Ala Ser Asp Lys Leu Phe Ser Ser Thr Pro Val Pro Pro  
           210                                  215                                  220

Gln Ser Phe Gln Asp Ile Gly Gly Gly Gly Gly Ser Ser Gly Asn Val  
           225                                  230                                  235                                  240

Gly Val Pro Ile Pro Gly Ala Tyr Gly Thr Gln Gln Met Met Gln Met  
                                   245                                  250                                  255

Pro Val Tyr Ala His His Met Gly Met Gln Gly Tyr His His Gln Asn  
           260                                  265                                  270



His Asn His Asp Pro Tyr His Gln Asn His Arg His His His Gly Ala  
 275 280 285

Gly Gly Asn Gly Ala Phe Glu Ser Asn Pro Tyr Met Met Gln Gln Asn  
 290 295 300

Lys Phe Gly Ser Met Ala Ser Tyr Pro Ser Val Gly Gly Gly Ser Ala  
 305 310 315 320

Asn Glu Asn

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 Met Asp Gln Lys Ser Lys Thr Ile Gly Glu Gln Trp Trp Arg Ser Asn  
 1 5 10 15

cca acg ttt aaa ccg cct gaa acg cca tta gat tct atg gag ttt ttg  
 96  
 Pro Thr Phe Lys Pro Pro Glu Thr Pro Leu Asp Ser Met Glu Phe Leu  
 20 25 30

tca cgt act tgg agt gct tcc gct act gaa gtt tca aga gct gtc gtc  
 144  
 Ser Arg Thr Trp Ser Ala Ser Ala Thr Glu Val Ser Arg Ala Val Val  
 35 40 45

gcg tct cca ccg act tct caa ccg ccg caa atg cgt ttc tcg gag atc  
 192  
 Ala Ser Pro Pro Thr Ser Gln Pro Pro Gln Met Arg Phe Ser Glu Ile  
 50 55 60

caa aac ggt tct tct gac gtc act ttg gtg ccg gaa gat gaa gaa aac  
 240  
 Gln Asn Gly Ser Ser Asp Val Thr Leu Val Pro Glu Asp Glu Glu Asn  
 65 70 75 80

ggc atc gtt ctt gga aat act ttt tct ttt gct tct tca gaa act tct  
 288  
 Gly Ile Val Leu Gly Asn Thr Phe Ser Phe Ala Ser Ser Glu Thr Ser  
 85 90 95

tta atg gtc atg gaa cgt atc atg gct cag tca ccg gag att tca tcg  
 336  
 Leu Met Val Met Glu Arg Ile Met Ala Gln Ser Pro Glu Ile Ser Ser  
 100 105 110

cca cga aca tca ggg aga ctt tct cat agc tca ttc acc gac agt cct  
 384  
 Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Phe Thr Asp Ser Pro  
 115 120 125



ccg atc tct ccc tcc gac atc gac gac ttt aag caa ttc tac cgt gtg  
 432  
 Pro Ile Ser Pro Ser Asp Ile Asp Asp Phe Lys Gln Phe Tyr Arg Val  
 130 135 140

agc cct tcc ttt aac ggc cac ata cgt ggt tca tca gcc att ccc ggc  
 480  
 Ser Pro Ser Phe Asn Gly His Ile Arg Gly Ser Ser Ala Ile Pro Gly  
 145 150 155 160

acc gcc gga ggg tct aaa act gtt ggt cgt tgg cta aag gac cgg cga  
 528  
 Thr Ala Gly Gly Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg  
 165 170 175

gag aag aag aga gaa gag acg cgt gca caa aat gca cag ctt cac gcg  
 576  
 Glu Lys Lys Arg Glu Glu Thr Arg Ala Gln Asn Ala Gln Leu His Ala  
 180 185 190

gct gta tct gta gct gga gtg gct gcc gcg gtg gct gct atc gct gca  
 624  
 Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala  
 195 200 205

gcc act gcc tct cag tcg agt tct gga act gac gag caa gtg gcc aaa  
 672  
 Ala Thr Ala Ser Gln Ser Ser Ser Gly Thr Asp Glu Gln Val Ala Lys  
 210 215 220

aat gac tcc gcg gtg gct tct gcc gcg act ttg gtg gcg gcg aag tgt  
 720  
 Asn Asp Ser Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Lys Cys  
 225 230 235 240

gtg gaa gct gca gag att atg gga gct gat cgt gag cac ttg gcc tcc  
 768  
 Val Glu Ala Ala Glu Ile Met Gly Ala Asp Arg Glu His Leu Ala Ser  
 245 250 255

gtt gtt agt tct gcg gtt aac gtt cgt tct gcc gga gat atc atg act  
 816  
 Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr  
 260 265 270

ttg acc gcc gct gct gcc aca gct ttg aga gga gct gca caa tta aag  
 864  
 Leu Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Ala Ala Gln Leu Lys  
 275 280 285

gca aga gca ttg aag gag gta tgg aac att gcg gct gtg att cct gta  
 912  
 Ala Arg Ala Leu Lys Glu Val Trp Asn Ile Ala Ala Val Ile Pro Val  
 290 295 300

gat aag ggt aca cca aaa ggc ggt ggt ggt ggt tat aga ggt ggc gag  
 960  
 Asp Lys Gly Thr Pro Lys Gly Gly Gly Gly Gly Tyr Arg Gly Gly Glu  
 305 310 315 320



tta gcc cct gta gat aat ttt ctt ggg att tgc agt aaa gaa ttg cta  
1008

Leu Ala Pro Val Asp Asn Phe Leu Gly Ile Cys Ser Lys Glu Leu Leu  
325 330 335

gct aaa ggt tgc gaa ttg ctt aaa cgc acc cgc aaa ggt gat ctt cat  
1056

Ala Lys Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His  
340 345 350

tgg aaa gtt gtt tcg atc tac att aat aga aca aag cag gta ata ttg  
1104

Trp Lys Val Val Ser Ile Tyr Ile Asn Arg Thr Lys Gln Val Ile Leu  
355 360 365

aag act aag agc aaa cat gtt gct ggg acc atc aca aag aag aaa aag  
1152

Lys Thr Lys Ser Lys His Val Ala Gly Thr Ile Thr Lys Lys Lys Lys  
370 375 380

aat gtg gtg gtg gga ttg gtt aag gga tta ccg gcg tgg cct ggc cgg  
1200

Asn Val Val Val Gly Leu Val Lys Gly Leu Pro Ala Trp Pro Gly Arg  
385 390 395 400

gaa atg ctc gag ggt gga gag aat ttg agg tat ttc ggg ctg aag acg  
1248

Glu Met Leu Glu Gly Gly Glu Asn Leu Arg Tyr Phe Gly Leu Lys Thr  
405 410 415

gtg gag aaa aga gtg att gaa ttc gag tgc aaa agc caa agg gaa tat  
1296

Val Glu Lys Arg Val Ile Glu Phe Glu Cys Lys Ser Gln Arg Glu Tyr  
420 425 430

gat ctt tgg aca caa ggt gtt tcc atg ctt ctt tcc att gct tct gat  
1344

Asp Leu Trp Thr Gln Gly Val Ser Met Leu Leu Ser Ile Ala Ser Asp  
435 440 445

agg aaa cat aaa tgt tga  
1362

Arg Lys His Lys Cys  
450

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448

Met Asp Gln Lys Ser Lys Thr Ile Gly Glu Gln Trp Trp Arg Ser Asn  
1 5 10 15

Pro Thr Phe Lys Pro Pro Glu Thr Pro Leu Asp Ser Met Glu Phe Leu  
20 25 30

Ser Arg Thr Trp Ser Ala Ser Ala Thr Glu Val Ser Arg Ala Val Val  
35 40 45



Ala Ser Pro Pro Thr Ser Gln Pro Pro Gln Met Arg Phe Ser Glu Ile  
 50 55 60

Gln Asn Gly Ser Ser Asp Val Thr Leu Val Pro Glu Asp Glu Glu Asn  
 65 70 75 80

Gly Ile Val Leu Gly Asn Thr Phe Ser Phe Ala Ser Ser Glu Thr Ser  
 85 90 95

Leu Met Val Met Glu Arg Ile Met Ala Gln Ser Pro Glu Ile Ser Ser  
 100 105 110

Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Phe Thr Asp Ser Pro  
 115 120 125

Pro Ile Ser Pro Ser Asp Ile Asp Asp Phe Lys Gln Phe Tyr Arg Val  
 130 135 140

Ser Pro Ser Phe Asn Gly His Ile Arg Gly Ser Ser Ala Ile Pro Gly  
 145 150 155 160

Thr Ala Gly Gly Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg  
 165 170 175

Glu Lys Lys Arg Glu Glu Thr Arg Ala Gln Asn Ala Gln Leu His Ala  
 180 185 190

Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala  
 195 200 205

Ala Thr Ala Ser Gln Ser Ser Ser Gly Thr Asp Glu Gln Val Ala Lys  
 210 215 220

Asn Asp Ser Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Lys Cys  
 225 230 235 240

Val Glu Ala Ala Glu Ile Met Gly Ala Asp Arg Glu His Leu Ala Ser  
 245 250 255

Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr  
 260 265 270

Leu Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Ala Ala Gln Leu Lys  
 275 280 285

Ala Arg Ala Leu Lys Glu Val Trp Asn Ile Ala Ala Val Ile Pro Val



290                      295                      300  
 Asp Lys Gly Thr Pro Lys Gly Gly Gly Gly Gly Tyr Arg Gly Gly Glu  
 305                      310                      315                      320  
 Leu Ala Pro Val Asp Asn Phe Leu Gly Ile Cys Ser Lys Glu Leu Leu  
                     325                      330                      335  
 Ala Lys Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His  
                     340                      345                      350  
 Trp Lys Val Val Ser Ile Tyr Ile Asn Arg Thr Lys Gln Val Ile Leu  
                     355                      360                      365  
 Lys Thr Lys Ser Lys His Val Ala Gly Thr Ile Thr Lys Lys Lys Lys  
                     370                      375                      380  
 Asn Val Val Val Gly Leu Val Lys Gly Leu Pro Ala Trp Pro Gly Arg  
 385                      390                      395                      400  
 Glu Met Leu Glu Gly Gly Glu Asn Leu Arg Tyr Phe Gly Leu Lys Thr  
                     405                      410                      415  
 Val Glu Lys Arg Val Ile Glu Phe Glu Cys Lys Ser Gln Arg Glu Tyr  
                     420                      425                      430  
 Asp Leu Trp Thr Gln Gly Val Ser Met Leu Leu Ser Ile Ala Ser Asp  
                     435                      440                      445  
 Arg Lys His Lys Cys  
                     450

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 <221> CDS <222> (1)..(495) <223> G2839

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 48  
 Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala  
 1                      5                      10                      15  
 aaa tgt ttg atg ttg tta tca aga gtt gga gaa tgc ggc gga gga gga  
 96  
 Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly  
                     20                      25                      30  
 gag aaa cga gtt ttc cga tgc aag act tgt ctt aaa gag ttt tcg tcg  
 144  
 Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser  
                     35                      40                      45



ttt caa gct ttg gga ggt cat cgt gca agc cac aag aaa ctc att aac  
 192  
 Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn  
 50 55 60  
 agt agc gat cca tca ctt ctt gga tcc ttg tct aac aag aaa act aaa  
 240  
 Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys  
 65 70 75 80  
 acg gcg acg tct cat cct tgt ccg ata tgt ggc gtg gag ttt ccg atg  
 288  
 Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met  
 85 90 95  
 ggg caa gct ctt ggt ggt cac atg agg aga cat agg agt gag aaa gcc  
 336  
 Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala  
 100 105 110  
 tca cca ggc acg ttg gtt aca cgt tct ttt tta ccg gag acg acg acg  
 384  
 Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr  
 115 120 125  
 gtg acg act ttg aaa aaa tcg agt agt ggg aag aga gtg gct tgt ttg  
 432  
 Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu  
 130 135 140  
 gac tta gat tcg atg gag agt tta gtc aat tgg aag ttg gag ttg gga  
 480  
 Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly  
 145 150 155 160  
 aga acg att tct tga  
 495  
 Arg Thr Ile Ser

<210> 450 <211> 164 <212> PRT <213> Arabidopsis thaliana <400>  
 450

Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala  
 1 5 10 15

Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly  
 20 25 30

Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser  
 35 40 45

Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn  
 50 55 60



Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys  
65 70 75 80

Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met  
85 90 95

Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala  
100 105 110

Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr  
115 120 125

Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu  
130 135 140

Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly  
145 150 155 160

Arg Thr Ile Ser

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<221> CDS <222> (184)..(2493) <223> G3010

<400> 451  
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60

tccctctttac tcaaggttct tctttgtcat cttgttgccg aatccacaaa gaggagaata  
120

aagattcgac ctttattaga tattaacgac tctggatttt tgggtttttg gagttggatc  
180

cac atg ggt tct tat ccg gat gga ttc cct gga tcc atg gac gag ttg  
228

Met Gly Ser Tyr Pro Asp Gly Phe Pro Gly Ser Met Asp Glu Leu  
1 5 10 15

gat ttc aat aag gac ttt gat ttg cct ccc tcc tca aac caa acc tta  
276

Asp Phe Asn Lys Asp Phe Asp Leu Pro Pro Ser Ser Asn Gln Thr Leu  
20 25 30

ggt tta gct aat ggg ttc tat tta gat gac tta gat ttc tca tcc ttg  
324

Gly Leu Ala Asn Gly Phe Tyr Leu Asp Asp Leu Asp Phe Ser Ser Leu  
35 40 45

gat cct cca gag gca tat ccc tcc cag aac aac aac aac aac atc  
372

Asp Pro Pro Glu Ala Tyr Pro Ser Gln Asn Asn Asn Asn Asn Ile  
50 55 60



aac aac aaa gct gta gca gga gat ctg tta tca tct tca tct gat gac  
 420  
 Asn Asn Lys Ala Val Ala Gly Asp Leu Leu Ser Ser Ser Ser Asp Asp  
 65 70 75  
 gct gat ttc tct gat tct gtt ttg aag tat ata agc caa gtt ctt atg  
 468  
 Ala Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile Ser Gln Val Leu Met  
 80 85 90 95  
 gaa gag gat atg gaa gag aag cct tgt atg ttt cat gac gct ttg gct  
 516  
 Glu Glu Asp Met Glu Glu Lys Pro Cys Met Phe His Asp Ala Leu Ala  
 100 105 110  
 ctt caa gct gct gag aaa tct ctc tat gag gct ctt ggt gag aaa tac  
 564  
 Leu Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala Leu Gly Glu Lys Tyr  
 115 120 125  
 cct tct tcg tct tct gct tct tct gtg gat cat cct gag aga ttg gct  
 612  
 Pro Ser Ser Ser Ser Ala Ser Ser Val Asp His Pro Glu Arg Leu Ala  
 130 135 140  
 agt gat agc cct gac ggt tct tgt tca ggt ggt gct ttt agt gat tac  
 660  
 Ser Asp Ser Pro Asp Gly Ser Cys Ser Gly Gly Ala Phe Ser Asp Tyr  
 145 150 155  
 gct agc acc act acc act act tcc tct gat tct cac tgg agt gtt gat  
 708  
 Ala Ser Thr Thr Thr Thr Thr Ser Ser Asp Ser His Trp Ser Val Asp  
 160 165 170 175  
 ggt ttg gag aat aga cct tct tgg tta cat aca cct atg ccg agt aat  
 756  
 Gly Leu Glu Asn Arg Pro Ser Trp Leu His Thr Pro Met Pro Ser Asn  
 180 185 190  
 ttt gtt ttc cag tct act tct agg tcc aac agt gtc acc ggt ggt ggt  
 804  
 Phe Val Phe Gln Ser Thr Ser Arg Ser Asn Ser Val Thr Gly Gly Gly  
 195 200 205  
 ggt ggt ggt aat agt gcg gtt tac ggt tca ggt ttt ggc gat gat ttg  
 852  
 Gly Gly Gly Asn Ser Ala Val Tyr Gly Ser Gly Phe Gly Asp Asp Leu  
 210 215 220  
 gtt tcg aat atg ttt aaa gat gat gaa ttg gct atg cag ttc aag aaa  
 900  
 Val Ser Asn Met Phe Lys Asp Asp Glu Leu Ala Met Gln Phe Lys Lys  
 225 230 235  
 ggg gtt gag gaa gct agt aag ttc ctt cct aag tct tct cag ctc ttt  
 948  
 Gly Val Glu Glu Ala Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Phe  
 240 245 250 255



att gat gtg gat agt tac atc cct atg aat tct ggt tcc aag gaa aat  
 996  
 Ile Asp Val Asp Ser Tyr Ile Pro Met Asn Ser Gly Ser Lys Glu Asn  
 260 265 270

ggt tct gag gtt ttt gtt aag acg gag aag aaa gat gag aca gag cat  
 1044  
 Gly Ser Glu Val Phe Val Lys Thr Glu Lys Lys Asp Glu Thr Glu His  
 275 280 285

cat cat cat cat agc tat gct cct cct ccc aac aga tta act ggt aag  
 1092  
 His His His His Ser Tyr Ala Pro Pro Pro Asn Arg Leu Thr Gly Lys  
 290 295 300

aaa agc cat tgg cgc gac gaa gat gaa gat ttc gtt gaa gaa aga agt  
 1140  
 Lys Ser His Trp Arg Asp Glu Asp Glu Asp Phe Val Glu Glu Arg Ser  
 305 310 315

aac aag caa tca gct gtt tat gtt gag gaa agc gag ctt tct gaa atg  
 1188  
 Asn Lys Gln Ser Ala Val Tyr Val Glu Glu Ser Glu Leu Ser Glu Met  
 320 325 330 335

ttt gat aag atc ttg gta tgt ggc cct ggg aaa cct gta tgc att ctt  
 1236  
 Phe Asp Lys Ile Leu Val Cys Gly Pro Gly Lys Pro Val Cys Ile Leu  
 340 345 350

aac cag aac ttt cct aca gaa tcc gct aaa gtc gtg acc gca cag tca  
 1284  
 Asn Gln Asn Phe Pro Thr Glu Ser Ala Lys Val Val Thr Ala Gln Ser  
 355 360 365

aat gga gca aag att cgt ggg aag aaa tca act tct act agt cat agt  
 1332  
 Asn Gly Ala Lys Ile Arg Gly Lys Lys Ser Thr Ser Thr Ser His Ser  
 370 375 380

aac gat tct aag aaa gaa act gct gat ttg agg act ctt ttg gtg tta  
 1380  
 Asn Asp Ser Lys Lys Glu Thr Ala Asp Leu Arg Thr Leu Leu Val Leu  
 385 390 395

tgt gca caa gct gta tca gtg gat gat cgt aga acc gcc aac gaa atg  
 1428  
 Cys Ala Gln Ala Val Ser Val Asp Asp Arg Arg Thr Ala Asn Glu Met  
 400 405 410 415

cta agg cag ata cga gag cat tct tcg cct cta ggc aat ggt tca gag  
 1476  
 Leu Arg Gln Ile Arg Glu His Ser Ser Pro Leu Gly Asn Gly Ser Glu  
 420 425 430

cgg ttg gct cat tat ttt gca aat agt ctt gaa gca cgc tta gct ggg  
 1524  
 Arg Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala Arg Leu Ala Gly  
 435 440 445



acc ggt aca cag atc tac acc gct tta tct tcg aag aaa acg tct gca  
1572

Thr Gly Thr Gln Ile Tyr Thr Ala Leu Ser Ser Lys Lys Thr Ser Ala  
450 455 460

gca gac atg ttg aag gct tac cag aca tac atg tcg gtc tgc cct ttc  
1620

Ala Asp Met Leu Lys Ala Tyr Gln Thr Tyr Met Ser Val Cys Pro Phe  
465 470 475

aag aaa gct gct atc ata ttt gct aac cac agc atg atg cgt ttc act  
1668

Lys Lys Ala Ala Ile Ile Phe Ala Asn His Ser Met Met Arg Phe Thr  
480 485 490 495

gca aac gcc aac acg atc cac ata ata gat ttc gga ata tct tac ggt  
1716

Ala Asn Ala Asn Thr Ile His Ile Ile Asp Phe Gly Ile Ser Tyr Gly  
500 505 510

ttt cag tgg cct gct ctg att cat cgc ctc tcg ctc agc aga cct ggt  
1764

Phe Gln Trp Pro Ala Leu Ile His Arg Leu Ser Leu Ser Arg Pro Gly  
515 520 525

ggt tcg cct aag ctt cga att acc ggt ata gag ctt cct cag cgc ggt  
1812

Gly Ser Pro Lys Leu Arg Ile Thr Gly Ile Glu Leu Pro Gln Arg Gly  
530 535 540

ttt aga cca gcg gaa gag ttc agg aga cag gtc atc gct tgg ctc gat  
1860

Phe Arg Pro Ala Glu Glu Phe Arg Arg Gln Val Ile Ala Trp Leu Asp  
545 550 555

act gtc agc gac aca atg ttc cgt ttg agt aca acg caa ttg ctc aga  
1908

Thr Val Ser Asp Thr Met Phe Arg Leu Ser Thr Thr Gln Leu Leu Arg  
560 565 570 575

aat ggg gaa acg atc caa gtc gaa gac tta aag ctt cga caa gga gag  
1956

Asn Gly Glu Thr Ile Gln Val Glu Asp Leu Lys Leu Arg Gln Gly Glu  
580 585 590

tat gtg gtt gtg aac tct ttg ttc cgt ttc agg aac ctt cta gat gag  
2004

Tyr Val Val Val Asn Ser Leu Phe Arg Phe Arg Asn Leu Leu Asp Glu  
595 600 605

acc gtt ctg gta aac agc ccg aga gat gca gtt ttg aag ctg ata aga  
2052

Thr Val Leu Val Asn Ser Pro Arg Asp Ala Val Leu Lys Leu Ile Arg  
610 615 620

aaa ata aac ccg aat gtc ttc att cca gcg atc tta agc ggg aat tac  
2100

Lys Ile Asn Pro Asn Val Phe Ile Pro Ala Ile Leu Ser Gly Asn Tyr  
625 630 635



aac gcg cca ttc ttt gtc acg agg ttc aga gaa gcg ttg ttt cat tac  
 2148  
 Asn Ala Pro Phe Phe Val Thr Arg Phe Arg Glu Ala Leu Phe His Tyr  
 640 645 650 655  
 tcg gct gtg ttt gat atg tgt gac tcg aag cta gct agg gaa gac gag  
 2196  
 Ser Ala Val Phe Asp Met Cys Asp Ser Lys Leu Ala Arg Glu Asp Glu  
 660 665 670  
 atg agg ctg atg tat gag aaa gag ttt tat ggg aga gag att gtg aat  
 2244  
 Met Arg Leu Met Tyr Glu Lys Glu Phe Tyr Gly Arg Glu Ile Val Asn  
 675 680 685  
 gtt gtg gct tgt gaa gga aca gag aga gtg gag aga cca gag aca tat  
 2292  
 Val Val Ala Cys Glu Gly Thr Glu Arg Val Glu Arg Pro Glu Thr Tyr  
 690 695 700  
 aag cag tgg cag gcg aga ctg atc cga gcc gga ttt aga cag ctt ccg  
 2340  
 Lys Gln Trp Gln Ala Arg Leu Ile Arg Ala Gly Phe Arg Gln Leu Pro  
 705 710 715  
 ctt gag aag gaa ctg atg cag aat ctg aag ttg aaa atc gaa aac ggg  
 2388  
 Leu Glu Lys Glu Leu Met Gln Asn Leu Lys Leu Lys Ile Glu Asn Gly  
 720 725 730 735  
 tac gat aaa aac ttc gat gtt gat caa aac ggt aac tgg tta ctt caa  
 2436  
 Tyr Asp Lys Asn Phe Asp Val Asp Gln Asn Gly Asn Trp Leu Leu Gln  
 740 745 750  
 ggg tgg aaa ggt aga atc gtg tat gct tca tct cta tgg gtt cct tcg  
 2484  
 Gly Trp Lys Gly Arg Ile Val Tyr Ala Ser Ser Leu Trp Val Pro Ser  
 755 760 765  
 tct tca tag atgttggttc ttacgttcta agcgactggg atttatgtag  
 2533  
 Ser Ser  
 ggcttttctg ttgatagtct ctgcacca caagtggtt aagttcagag ttagggttct  
 2593  
 tgaacactag aatgttggtta tattatgctt gtgacatagc gtgtgtaaga gtgtagccta  
 2653  
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 2693  
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 20 25 30

Leu Ala Asn Gly Phe Tyr Leu Asp Asp Leu Asp Phe Ser Ser Leu Asp  
 35 40 45

Pro Pro Glu Ala Tyr Pro Ser Gln Asn Asn Asn Asn Asn Ile Asn  
 50 55 60

Asn Lys Ala Val Ala Gly Asp Leu Leu Ser Ser Ser Ser Asp Asp Ala  
 65 70 75 80

Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile Ser Gln Val Leu Met Glu  
 85 90 95

Glu Asp Met Glu Glu Lys Pro Cys Met Phe His Asp Ala Leu Ala Leu  
 100 105 110

Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala Leu Gly Glu Lys Tyr Pro  
 115 120 125

Ser Ser Ser Ser Ala Ser Ser Val Asp His Pro Glu Arg Leu Ala Ser  
 130 135 140

Asp Ser Pro Asp Gly Ser Cys Ser Gly Gly Ala Phe Ser Asp Tyr Ala  
 145 150 155 160

Ser Thr Thr Thr Thr Thr Ser Ser Asp Ser His Trp Ser Val Asp Gly  
 165 170 175

Leu Glu Asn Arg Pro Ser Trp Leu His Thr Pro Met Pro Ser Asn Phe  
 180 185 190

Val Phe Gln Ser Thr Ser Arg Ser Asn Ser Val Thr Gly Gly Gly Gly  
 195 200 205

Gly Gly Asn Ser Ala Val Tyr Gly Ser Gly Phe Gly Asp Asp Leu Val  
 210 215 220

Ser Asn Met Phe Lys Asp Asp Glu Leu Ala Met Gln Phe Lys Lys Gly  
 225 230 235 240

Val Glu Glu Ala Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Phe Ile  
 245 250 255



Asp Val Asp Ser Tyr Ile Pro Met Asn Ser Gly Ser Lys Glu Asn Gly  
 260 265 270

Ser Glu Val Phe Val Lys Thr Glu Lys Lys Asp Glu Thr Glu His His  
 275 280 285

His His His Ser Tyr Ala Pro Pro Pro Asn Arg Leu Thr Gly Lys Lys  
 290 295 300

Ser His Trp Arg Asp Glu Asp Glu Asp Phe Val Glu Glu Arg Ser Asn  
 305 310 315 320

Lys Gln Ser Ala Val Tyr Val Glu Glu Ser Glu Leu Ser Glu Met Phe  
 325 330 335

Asp Lys Ile Leu Val Cys Gly Pro Gly Lys Pro Val Cys Ile Leu Asn  
 340 345 350

Gln Asn Phe Pro Thr Glu Ser Ala Lys Val Val Thr Ala Gln Ser Asn  
 355 360 365

Gly Ala Lys Ile Arg Gly Lys Lys Ser Thr Ser Thr Ser His Ser Asn  
 370 375 380

Asp Ser Lys Lys Glu Thr Ala Asp Leu Arg Thr Leu Leu Val Leu Cys  
 385 390 395 400

Ala Gln Ala Val Ser Val Asp Asp Arg Arg Thr Ala Asn Glu Met Leu  
 405 410 415

Arg Gln Ile Arg Glu His Ser Ser Pro Leu Gly Asn Gly Ser Glu Arg  
 420 425 430

Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala Arg Leu Ala Gly Thr  
 435 440 445

Gly Thr Gln Ile Tyr Thr Ala Leu Ser Ser Lys Lys Thr Ser Ala Ala  
 450 455 460

Asp Met Leu Lys Ala Tyr Gln Thr Tyr Met Ser Val Cys Pro Phe Lys  
 465 470 475 480

Lys Ala Ala Ile Ile Phe Ala Asn His Ser Met Met Arg Phe Thr Ala  
 485 490 495

Asn Ala Asn Thr Ile His Ile Ile Asp Phe Gly Ile Ser Tyr Gly Phe



500	505	510
Gln Trp Pro Ala Leu Ile His Arg Leu Ser Leu Ser Arg Pro Gly Gly		
515	520	525
Ser Pro Lys Leu Arg Ile Thr Gly Ile Glu Leu Pro Gln Arg Gly Phe		
530	535	540
Arg Pro Ala Glu Glu Phe Arg Arg Gln Val Ile Ala Trp Leu Asp Thr		
545	550	555
		560
Val Ser Asp Thr Met Phe Arg Leu Ser Thr Thr Gln Leu Leu Arg Asn		
	565	570
		575
Gly Glu Thr Ile Gln Val Glu Asp Leu Lys Leu Arg Gln Gly Glu Tyr		
	580	585
		590
Val Val Val Asn Ser Leu Phe Arg Phe Arg Asn Leu Leu Asp Glu Thr		
	595	600
		605
Val Leu Val Asn Ser Pro Arg Asp Ala Val Leu Lys Leu Ile Arg Lys		
	610	615
		620
Ile Asn Pro Asn Val Phe Ile Pro Ala Ile Leu Ser Gly Asn Tyr Asn		
	625	630
		635
		640
Ala Pro Phe Phe Val Thr Arg Phe Arg Glu Ala Leu Phe His Tyr Ser		
	645	650
		655
Ala Val Phe Asp Met Cys Asp Ser Lys Leu Ala Arg Glu Asp Glu Met		
	660	665
		670
Arg Leu Met Tyr Glu Lys Glu Phe Tyr Gly Arg Glu Ile Val Asn Val		
	675	680
		685
Val Ala Cys Glu Gly Thr Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys		
	690	695
		700
Gln Trp Gln Ala Arg Leu Ile Arg Ala Gly Phe Arg Gln Leu Pro Leu		
	705	710
		715
		720
Glu Lys Glu Leu Met Gln Asn Leu Lys Leu Lys Ile Glu Asn Gly Tyr		
	725	730
		735
Asp Lys Asn Phe Asp Val Asp Gln Asn Gly Asn Trp Leu Leu Gln Gly		
	740	745
		750



Trp Lys Gly Arg Ile Val Tyr Ala Ser Ser Leu Trp Val Pro Ser Ser  
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Ser

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 1 5 10 15  
 tct tct gat cct ttc ctc tcc tct tca gaa aat ggg gtc acc acc aca  
 96  
 Ser Ser Asp Pro Phe Leu Ser Ser Ser Glu Asn Gly Val Thr Thr Thr  
 20 25 30  
 aac aca tcc act cag aag agg aaa aga aga cct gca ggt acc cca gat  
 144  
 Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp  
 35 40 45  
 cca gat gca gaa gtt gtg tct tta tca cca aga act ctt ctt gaa tca  
 192  
 Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser  
 50 55 60  
 gac aga tac ata tgt gag atc tgt aac caa ggg ttt caa aga gac cag  
 240  
 Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln  
 65 70 75 80  
 aat ctc cag atg cat aga aga cgt cac aaa gtt cca tgg aag ctt ctt  
 288  
 Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu  
 85 90 95  
 aaa aga gac aac aac ata gag gtg aag aaa cga gtc tat gtt tgc cct  
 336  
 Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro  
 100 105 110  
 gaa ccc act tgc ctt cac cat aat cct tgt cat gct ctg gga gat ctt  
 384  
 Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu  
 115 120 125  
 gtc ggc atc aaa aaa cat ttc aga aga aaa cat agt aac cat aag caa  
 432  
 Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln  
 130 135 140  
 tgg gtt tgt gag aga tgc tct aaa ggt tat gct gtt caa tct gat tac  
 480



Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr  
 145 150 155 160  
 aaa gct cat ctc aaa act tgt ggt act aga gga cat tct tgt gac tgt  
 528  
 Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys  
 165 170 175  
 ggt cgt gtc ttc tcc agg gtg gag agt ttt att gaa cat caa gat aat  
 576  
 Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn  
 180 185 190  
 tgt tcc gca cgg aga gtt cac cgt gaa ccg cct cga cca cca caa acc  
 624  
 Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr  
 195 200 205  
 gcg gta aca gtc ccg gca tgc tct tct aga acc gcc tca acc gtc agc  
 672  
 Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser  
 210 215 220  
 act ccg tct agt gaa acc aat tac ggc ggt aca gtt gcg gtt acg act  
 720  
 Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr  
 225 230 235 240  
 cct caa cct cta gaa ggc cgt cca att cat cag aga atc tca tct tca  
 768  
 Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser  
 245 250 255  
 att ctc acc aac tca tca aac aat ctc aac ctc gaa ctc caa ctt ctt  
 816  
 Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu  
 260 265 270  
 cca tta tcg tcg aat caa aac cct aat caa gaa aac caa caa caa aaa  
 864  
 Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys  
 275 280 285  
 gtt aaa gaa cca tct cat cat cat aat cat aat cat gat acc aca aac  
 912  
 Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn  
 290 295 300  
 tta aac ctc tcc att gca cca tca tca tca tat caa cat tac aac aac  
 960  
 Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn  
 305 310 315 320  
 ttt gat cgt ata aaa gag att atg gcg agc gag caa att atg aag ata  
 1008  
 Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile  
 325 330 335  
 gcg atg aag gag aaa gct tac gct gag gaa gct aaa aga gaa gcc aag  
 1056  
 Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys



340 345 350  
 agg caa cga gag ata gcg gaa aac gag ttt gca aat gcc aaa aag att  
 1104  
 Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile  
 355 360 365  
 agg caa aaa gca caa gct gaa ctc gag aga gct aag ttt tta aag gaa  
 1152  
 Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu  
 370 375 380  
 caa tct atg aag aag ata agt tca acg atc atg cag gtc act tgt caa  
 1200  
 Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln  
 385 390 395 400  
 aca tgt aaa gga cag ttt caa gca gtt gcg gtt ccg gcg gct acg gct  
 1248  
 Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala  
 405 410 415  
 gat gag acg tct ctt gtc gtg agt tac atg tcg tca gcg aat act gac  
 1296  
 Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp  
 420 425 430  
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 1320  
 Gly Glu Leu Glu Asn Gly Phe  
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 20 25 30  
 Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp  
 35 40 45  
 Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser  
 50 55 60  
 Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln  
 65 70 75 80  
 Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu  
 85 90 95  
 Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro



100	105	110
Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu		
115	120	125
Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln		
130	135	140
Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr		
145	150	155
Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys		
165	170	175
Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn		
180	185	190
Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr		
195	200	205
Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser		
210	215	220
Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr		
225	230	235
Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser		
245	250	255
Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu		
260	265	270
Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys		
275	280	285
Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn		
290	295	300
Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn		
305	310	315
Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile		
325	330	335
Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys		
340	345	350



Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile  
 355 360 365

Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu  
 370 375 380

Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln  
 385 390 395 400

Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala  
 405 410 415

Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp  
 420 425 430

Gly Glu Leu Glu Asn Gly Phe  
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gagaacaaga agagtccagg gccaatgagc ctgagggtat caaatcagtg attgatgaca  
 120

tctacatttt tgaagacgac cctgtggttg ataggttcaa taggtttggc acggag atg  
 179

Met  
 1

tct gcc atg gtc tcg gcc ttg aca cag gtg gtt tct gct cgc tct cag  
 227

Ser Ala Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser Gln  
 5 10 15

act gag gct gaa ggt gct cac tct cag act gag gct gaa ggt gct cac  
 275

Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala His  
 20 25 30

tct tct tcc tct tcg gct gga cat aaa aga gga tgg ctt gga atc gat  
 323

Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile Asp  
 35 40 45

tct gct cct att ccc tca tca ttt gct cgt gta gac tct tca cat aat  
 371

Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His Asn  
 50 55 60 65



ccg atc gaa gaa tcc atg agc aag gca ttt cca gag gaa gca agg gag  
 419  
 Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg Glu  
 70 75 80

aaa aaa agg agg tac aga gga gta agg cag aga cca tgg ggc aaa tgg  
 467  
 Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp  
 85 90 95

gca gct gag ata cgt gat cca cat aga gcc gct agg gtt tgg ctc ggg  
 515  
 Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu Gly  
 100 105 110

acg ttt gat aca gcg gag gcc gcg gct aga gcc tac gac gag gct gca  
 563  
 Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala Ala  
 115 120 125

ctc cgg ttc cgt gga aat aaa gca aag cta aat ttc cca gag gat gta  
 611  
 Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp Val  
 130 135 140 145

agg att ctt cct cct ccc cct cct ctt ctt cgt tca cca gct gac acg  
 659  
 Arg Ile Leu Pro Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp Thr  
 150 155 160

gtg gcg aat aaa gca gaa gag gat ctg ata aat tat tgg agt tat aca  
 707  
 Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr Thr  
 165 170 175

aag ttg ttg caa agt tca ggc caa cgg tca ttt ctc gag cga gga caa  
 755  
 Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly Gln  
 180 185 190

gaa gag agt agt aac ata ttt gaa cat tca cca atg gaa caa cct ctg  
 803  
 Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro Leu  
 195 200 205

cct cct tca agt tct ggt cca agt tcc tct aat ttt cct gca cct tct  
 851  
 Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro Ser  
 210 215 220 225

cta cct aat aca tag tttcactttt attaaagctc tacaaataca attaaataca  
 906  
 Leu Pro Asn Thr

tagctaaatg aaaatgattt tcttgctctgt ataccttctt aagtgctaaa caatatattg  
 966

tactctttgt tttccttaac taaaaaaaaa aaaaaaaaaa aaa  
 1009



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Gln Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala  
20 25 30

His Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile  
35 40 45

Asp Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His  
50 55 60

Asn Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg  
65 70 75 80

Glu Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys  
85 90 95

Trp Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu  
100 105 110

Gly Thr Phe Asp Thr Ala Glu Ala Ala Arg Ala Tyr Asp Glu Ala  
115 120 125

Ala Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp  
130 135 140

Val Arg Ile Leu Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp  
145 150 155 160

Thr Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr  
165 170 175

Thr Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly  
180 185 190

Gln Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro  
195 200 205

Leu Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro  
210 215 220

Ser Leu Pro Asn Thr



225

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<400> 457

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 48

Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Met Val Lys Lys Gly Pro  
 1 5 10 15

tgg acg gcg gag gaa gac aag aaa ctg ata aac ttt atc ttg acc aac  
 96

Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn  
 20 25 30

ggc cac tgt tgc tgg agg gct ttg ccg aag ctg gcc ggt ctc cgt cgc  
 144

Gly His Cys Cys Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Arg Arg  
 35 40 45

tgt ggg aag agc tgc cgt cta cgg tgg acc aat tat ctc cga cct gac  
 192

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp  
 50 55 60

ttg aag aga ggt ctt ctc tcc gac gcc gag gaa cag ctt gtc atc gac  
 240

Leu Lys Arg Gly Leu Leu Ser Asp Ala Glu Glu Gln Leu Val Ile Asp  
 65 70 75 80

ctt cat gct ctt ctc ggc aac aga tgg tcc aag atc gct gca aga tta  
 288

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Lys Ile Ala Ala Arg Leu  
 85 90 95

cca gga aga aca gac aac gaa ata aaa aat cat tgg aat act cat atc  
 336

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile  
 100 105 110

aag aag aag ctc ctt aag atg gaa atc gat cct tcg acc cat caa cct  
 384

Lys Lys Lys Leu Leu Lys Met Glu Ile Asp Pro Ser Thr His Gln Pro  
 115 120 125

tta aac aaa gta ttt acc gat aca aac tta gtc gat aaa tct gaa act  
 432

Leu Asn Lys Val Phe Thr Asp Thr Asn Leu Val Asp Lys Ser Glu Thr  
 130 135 140

tca tcg aaa gcc gac aat gta aat gat aat aaa atc gta gag atc gat  
 480

Ser Ser Lys Ala Asp Asn Val Asn Asp Asn Lys Ile Val Glu Ile Asp  
 145 150 155 160

ggg aca acg aca aat aca ata gat gat agc att atc act cat caa aat  
 528

Gly Thr Thr Thr Asn Thr Ile Asp Asp Ser Ile Ile Thr His Gln Asn  
 165 170 175



agt tca aat gat gat tat gaa tta ctt ggt gat ata att cat aat tat  
576

Ser Ser Asn Asp Asp Tyr Glu Leu Leu Gly Asp Ile Ile His Asn Tyr  
180 185 190

gga gat tta ttt aat att cta tgg acc aac gat gaa cct cct cta gtc  
624

Gly Asp Leu Phe Asn Ile Leu Trp Thr Asn Asp Glu Pro Pro Leu Val  
195 200 205

gat gat gca tca tgg agc aat cat aac gtt ggt att gga gga aca gct  
672

Asp Asp Ala Ser Trp Ser Asn His Asn Val Gly Ile Gly Gly Thr Ala  
210 215 220

gca gtt gca gcc tca gac aag aac aac act gct gcc gag gaa gat ttc  
720

Ala Val Ala Ala Ser Asp Lys Asn Asn Thr Ala Ala Glu Glu Asp Phe  
225 230 235 240

ccg gaa aga tca ttt gaa aaa cag aac ggc gaa agt tgg atg ttc ttg  
768

Pro Glu Arg Ser Phe Glu Lys Gln Asn Gly Glu Ser Trp Met Phe Leu  
245 250 255

gat tat tgc caa gaa ttt ggt gtt gaa gat ttt ggg ttc gag tgt tac  
816

Asp Tyr Cys Gln Glu Phe Gly Val Glu Asp Phe Gly Phe Glu Cys Tyr  
260 265 270

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Gly His Cys Cys Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Arg Arg  
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp  
50 55 60

Leu Lys Arg Gly Leu Leu Ser Asp Ala Glu Glu Gln Leu Val Ile Asp  
65 70 75 80

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Lys Ile Ala Ala Arg Leu



85 90 95  
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile  
 100 105 110  
 Lys Lys Lys Leu Leu Lys Met Glu Ile Asp Pro Ser Thr His Gln Pro  
 115 120 125  
 Leu Asn Lys Val Phe Thr Asp Thr Asn Leu Val Asp Lys Ser Glu Thr  
 130 135 140  
 Ser Ser Lys Ala Asp Asn Val Asn Asp Asn Lys Ile Val Glu Ile Asp  
 145 150 155 160  
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 Ser Ser Asn Asp Asp Tyr Glu Leu Leu Gly Asp Ile Ile His Asn Tyr  
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 Gly Asp Leu Phe Asn Ile Leu Trp Thr Asn Asp Glu Pro Pro Leu Val  
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 Asp Asp Ala Ser Trp Ser Asn His Asn Val Gly Ile Gly Gly Thr Ala  
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 Pro Glu Arg Ser Phe Glu Lys Gln Asn Gly Glu Ser Trp Met Phe Leu  
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atcgattaaa ttcacctcag ggttttttga tttctgaaag aagttaatct tcttcgaagg  
240

cgattgcaaa agagtgcctc gctgtgaatt tccactgag atg caa tca aaa ccg  
294

Met Gln Ser Lys Pro  
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342

Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His His Ala Val Gln Gln  
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390

Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn Asn Ser Phe Gly Val  
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438

Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser Asn Ser Ser Ser Leu  
40 45 50

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486

Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val His Ser Ala Ser Glu  
55 60 65

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534

Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr Trp Lys Asp Ser Gln  
70 75 80 85

gct gca act tcc tct cgt tca gat aat cac gga atg gaa gga aat gac  
582

Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly Met Glu Gly Asn Asp  
90 95 100

cca gcg ctc tct atc cgt aac atg cat gat cag cca ctt gta caa cca  
630

Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln Pro Leu Val Gln Pro  
105 110 115

cca gag ctt gtt gga cac tat atc gct tgt gtc cca aac cca tat cag  
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Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val Pro Asn Pro Tyr Gln  
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726

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774

Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu Arg Thr Ala Leu Pro  
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 Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly Arg Asp Arg Glu Arg  
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 aat gag acc ctg aat tct tct ggt gca cca taa taaaaaaagc caaagctctg  
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 Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro  
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Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser  
 35 40 45

Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val  
 50 55 60

His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr  
 65 70 75 80

Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly  
 85 90 95

Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln  
 100 105 110

Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val  
 115 120 125

Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr  
 130 135 140

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 145 150 155 160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn  
 165 170 175

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 180 185 190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His  
 195 200 205

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Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly  
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 116

Met Ala Phe  
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gat ctc cac cat ggc tca gct tca gat acg cat tca tca gaa ctt ccg  
 164

Asp Leu His His Gly Ser Ala Ser Asp Thr His Ser Ser Glu Leu Pro  
 5 10 15

tcg ttt tct ctc cca cct tat cct cag atg ata atg gaa gcg att gag  
 212

Ser Phe Ser Leu Pro Pro Tyr Pro Gln Met Ile Met Glu Ala Ile Glu  
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tcc ttg aac gat aag aac ggc tgc aac aaa acg acg att gct aag cac  
 260

Ser Leu Asn Asp Lys Asn Gly Cys Asn Lys Thr Thr Ile Ala Lys His  
 40 45 50

atc gag tcg act caa caa act cta ccg ccg tca cac atg acg ctg ctc  
 308

Ile Glu Ser Thr Gln Gln Thr Leu Pro Pro Ser His Met Thr Leu Leu  
 55 60 65

agc tac cat ctc aac cag atg aag aaa acc ggt cag cta atc atg gtg  
 356

Ser Tyr His Leu Asn Gln Met Lys Lys Thr Gly Gln Leu Ile Met Val  
 70 75 80

aag aac aat tat atg aaa cca gat cca gat gct cct cct aag cgt ggt  
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Lys Asn Asn Tyr Met Lys Pro Asp Pro Asp Ala Pro Pro Lys Arg Gly  
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cgt ggc cgt cct ccg aag cag aag act cag gcc gaa tct gac gcc gct  
 452

Arg Gly Arg Pro Pro Lys Gln Lys Thr Gln Ala Glu Ser Asp Ala Ala  
 100 105 110 115

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Ala Ala Ala Val Val Ala Ala Thr Val Val Ser Thr Asp Pro Pro Arg  
 120 125 130

tct cgt ggc cgt cca ccg aag ccg aaa gat cca tcg gag cct ccc cag  
 548

Ser Arg Gly Arg Pro Pro Lys Pro Lys Asp Pro Ser Glu Pro Pro Gln  
 135 140 145

gag aag gtc att acc gga tct gga agg cca cga gga cga cca ccg aag  
 596

Glu Lys Val Ile Thr Gly Ser Gly Arg Pro Arg Gly Arg Pro Pro Lys  
 150 155 160



aga ccg aga aca gat tcg gag acg gtt gct gcg ccg gaa ccg gca gct  
644

Arg Pro Arg Thr Asp Ser Glu Thr Val Ala Ala Pro Glu Pro Ala Ala  
165 170 175

cag gcg aca ggt gag cgt agg gga cgt ggg aga cct ccg aag gtg aag  
692

Gln Ala Thr Gly Glu Arg Arg Gly Arg Gly Arg Pro Pro Lys Val Lys  
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742

Pro Thr Val Val Ala Pro Val Gly Cys  
200

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862

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35 40 45

Ala Lys His Ile Glu Ser Thr Gln Gln Thr Leu Pro Pro Ser His Met  
50 55 60

Thr Leu Leu Ser Tyr His Leu Asn Gln Met Lys Lys Thr Gly Gln Leu  
65 70 75 80

Ile Met Val Lys Asn Asn Tyr Met Lys Pro Asp Pro Asp Ala Pro Pro  
85 90 95

Lys Arg Gly Arg Gly Arg Pro Pro Lys Gln Lys Thr Gln Ala Glu Ser  
100 105 110



Asp Ala Ala Ala Ala Val Val Ala Ala Thr Val Val Ser Thr Asp  
 115 120 125

Pro Pro Arg Ser Arg Gly Arg Pro Pro Lys Pro Lys Asp Pro Ser Glu  
 130 135 140

Pro Pro Gln Glu Lys Val Ile Thr Gly Ser Gly Arg Pro Arg Gly Arg  
 145 150 155 160

Pro Pro Lys Arg Pro Arg Thr Asp Ser Glu Thr Val Ala Ala Pro Glu  
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 Ala Val Ser Ala Asp Leu Ser Phe Gly Ala Pro Leu Tyr Val Val Glu  
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 Ser Met Cys Met Arg Cys Gln Glu Asn Gly Thr Thr Arg Phe Leu Leu  
 35 40 45

acc tta att cct cac ttc aga aag gtc tta ata tct gca ttt gaa tgt  
 192  
 Thr Leu Ile Pro His Phe Arg Lys Val Leu Ile Ser Ala Phe Glu Cys  
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 65 70 75 80

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 288  
 Gln Pro Arg Gly Cys Cys Tyr Asn Leu Glu Val Leu Ala Gly Asp Val  
 85 90 95



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 Lys Ile Phe Asp Arg Gln Val Val Lys Ser Glu Ser Ala Thr Ile Lys  
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 115 120 125

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 432  
 Leu Ser Thr Val Glu Gly Ile Leu Ala Arg Ala Ala Asp Glu Leu Ser  
 130 135 140

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 528  
 Ile Asp Gln Phe Leu Ser Lys Leu Arg Ala Cys Ala Lys Ala Glu Thr  
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 180 185 190

aac cca cat gct cca tca cca gat ccc tct cta acc atc aaa ttc tat  
 624  
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 195 200 205

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 210 215 220

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 225 230 235 240

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 Phe Pro Ser Thr Cys Gly Ala Cys Thr Glu Pro Cys Glu Thr Arg Met  
 245 250 255

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 260 265 270

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 Thr Cys Asp Ser Cys Gly Tyr Arg Asn Ser Glu Leu Lys Pro Gly Gly  
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912

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290 295 300

aca gac ctt agc cga gat gtt atc aag tcg gac act gca gga gtg ata  
960

Thr Asp Leu Ser Arg Asp Val Ile Lys Ser Asp Thr Ala Gly Val Ile  
305 310 315 320

atc cca gaa ctt gat ctg gag cta gct ggt ggt aca ctt ggt gga atg  
1008

Ile Pro Glu Leu Asp Leu Glu Leu Ala Gly Gly Thr Leu Gly Gly Met  
325 330 335

gta aca aca gtt gaa ggg ttg gtt aca cag atc aga gaa agc cta gcg  
1056

Val Thr Thr Val Glu Gly Leu Val Thr Gln Ile Arg Glu Ser Leu Ala  
340 345 350

aga gtt cac gga ttc act ttt ggt gat agt atg gaa gag agt aag ttg  
1104

Arg Val His Gly Phe Thr Phe Gly Asp Ser Met Glu Glu Ser Lys Leu  
355 360 365

aac aaa tgg aga gaa ttt gga gcc agg ctc act aag ctc cta agc ttt  
1152

Asn Lys Trp Arg Glu Phe Gly Ala Arg Leu Thr Lys Leu Leu Ser Phe  
370 375 380

gaa cag ccg tgg aca ttg att ctt gat gat gaa tta gca aat tcc ttt  
1200

Glu Gln Pro Trp Thr Leu Ile Leu Asp Asp Glu Leu Ala Asn Ser Phe  
385 390 395 400

att gca cca gta aca gat gat atc aaa gat gac cat cag ctc aca ttt  
1248

Ile Ala Pro Val Thr Asp Asp Ile Lys Asp Asp His Gln Leu Thr Phe  
405 410 415

gaa gag tac gag agg tca tgg gat caa aac gag gag ttg ggt ctc aac  
1296

Glu Glu Tyr Glu Arg Ser Trp Asp Gln Asn Glu Glu Leu Gly Leu Asn  
420 425 430

gac ata gat act tct tca gct gat gct gct tat gaa tcc aca gag acg  
1344

Asp Ile Asp Thr Ser Ser Ala Asp Ala Ala Tyr Glu Ser Thr Glu Thr  
435 440 445

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1359

Thr Lys Leu Pro

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Thr Leu Ile Pro His Phe Arg Lys Val Leu Ile Ser Ala Phe Glu Cys  
                   50                                  55                                  60

Pro His Cys Gly Glu Arg Asn Asn Glu Val Gln Phe Ala Gly Glu Ile  
                   65                                  70                                  75                                  80

Gln Pro Arg Gly Cys Cys Tyr Asn Leu Glu Val Leu Ala Gly Asp Val  
                                   85                                  90                                  95

Lys Ile Phe Asp Arg Gln Val Val Lys Ser Glu Ser Ala Thr Ile Lys  
                   100                                  105                                  110

Ile Pro Glu Leu Asp Phe Glu Ile Pro Pro Glu Ala Gln Arg Gly Ser  
                   115                                  120                                  125

Leu Ser Thr Val Glu Gly Ile Leu Ala Arg Ala Ala Asp Glu Leu Ser  
                   130                                  135                                  140

Ala Leu Gln Glu Glu Arg Lys Lys Val Asp Pro Lys Thr Ala Glu Ala  
                   145                                  150                                  155                                  160

Ile Asp Gln Phe Leu Ser Lys Leu Arg Ala Cys Ala Lys Ala Glu Thr  
                                   165                                  170                                  175

Ser Phe Thr Phe Ile Leu Asp Asp Pro Ala Gly Asn Ser Phe Ile Glu  
                   180                                  185                                  190

Asn Pro His Ala Pro Ser Pro Asp Pro Ser Leu Thr Ile Lys Phe Tyr  
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Ser Gln Ala Gly Gln Ser Glu Gly Ser Leu Gly Ala Pro Val Met Thr  
                   225                                  230                                  235                                  240

Phe Pro Ser Thr Cys Gly Ala Cys Thr Glu Pro Cys Glu Thr Arg Met  
                                   245                                  250                                  255



Phe Lys Ile Glu Ile Pro Tyr Phe Gln Glu Val Ile Val Met Ala Ser  
 260 265 270

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 275 280 285

Ala Ile Pro Glu Lys Gly Lys Lys Ile Thr Leu Ser Val Arg Asn Ile  
 290 295 300

Thr Asp Leu Ser Arg Asp Val Ile Lys Ser Asp Thr Ala Gly Val Ile  
 305 310 315 320

Ile Pro Glu Leu Asp Leu Glu Leu Ala Gly Gly Thr Leu Gly Gly Met  
 325 330 335

Val Thr Thr Val Glu Gly Leu Val Thr Gln Ile Arg Glu Ser Leu Ala  
 340 345 350

Arg Val His Gly Phe Thr Phe Gly Asp Ser Met Glu Glu Ser Lys Leu  
 355 360 365

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 370 375 380

Glu Gln Pro Trp Thr Leu Ile Leu Asp Asp Glu Leu Ala Asn Ser Phe  
 385 390 395 400

Ile Ala Pro Val Thr Asp Asp Ile Lys Asp Asp His Gln Leu Thr Phe  
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Glu Glu Tyr Glu Arg Ser Trp Asp Gln Asn Glu Glu Leu Gly Leu Asn  
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Asp Ile Asp Thr Ser Ser Ala Asp Ala Ala Tyr Glu Ser Thr Glu Thr  
 435 440 445

Thr Lys Leu Pro  
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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

<b>A. CLASSIFICATION OF SUBJECT MATTER</b>												
IPC(7) : A01H 5/00; C12P 21/00; C12N 15/82												
US CL : 435/69.1; 800/279, 281, 289, 290, 300, 301												
According to International Patent Classification (IPC) or to both national classification and IPC												
<b>B. FIELDS SEARCHED</b>												
Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/69.1; 800/279, 281, 289, 290, 300, 301												
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched												
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EAST, and SEQUENCE search of SEQ ID NOs: 1, 2, 3 and 4												
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>												
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.										
Y	KRANZ, H.D. et al. Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana. The Plant Journal. 1998, Vol 16, No. 2, pages 263-276, see entire document.	1-5,7-22										
X	ALLEN, M.D. et al. A novel mode of DNA recognition by a beta-sheet revealed by the solution structure of the GCC-box binding domain in complex with DNA. The EMBO Journal. 1998, Vol. 17, No. 18, pages 5484-5496, in particular page 5493, left column, section under Materials and Methods.	4,5										
Y	SMALLE, J. et al. The trihelix DNA-binding motif in higher plants is not restricted to the transcription factors GT-1 and GT-2. Proc. Natl. Acad. Sci. USA. 1998, Vol. 95, pages 3318-3322, see entire document, in particular Fig. 1A on page 3319.	1-3,7-22										
X		4,5										
Y		1-3,7-22										
X,P	Database NCBI on WEST, AN BE522812. WHITE, J.A. et al. 'A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil'. Plant Physiol. 124,(4), 1582-1594. NCBI-Genbank (National Library of Medicine, Bethesda, MD), submitted 19 March 2001.	4										
Y,P		1-3,5,7-22										
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.												
* Special categories of cited documents: <table border="0"> <tr> <td>"A" document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E" earlier application or patent published on or after the international filing date</td> <td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O" document referring to an oral disclosure, use, exhibition or other means</td> <td>"&amp;" document member of the same patent family</td> </tr> <tr> <td>"P" document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	"P" document published prior to the international filing date but later than the priority date claimed	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention											
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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art											
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"P" document published prior to the international filing date but later than the priority date claimed												
Date of the actual completion of the international search 27 November 2001 (27.11.2001)		Date of mailing of the international search report 16 JAN 2002										
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230		Authorized officer David H Kruse Telephone No. 703-308-0196										



# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

## C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	OHME-TAKAGI, M. et al. Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive element. The Plant Cell.	4,5
—		
Y	February 1995, Vol. 7, pages 173-182, see entire document.	1-3,7-22
A	ELOMAA, P. et al. Transformation of antisense constructs of the chalcone synthase gene superfamily into Gerbera hybrida: differential effect on the expression of family members. Molecular Breeding 1996, Vol. 2, pages 41-50, see entire document.	1-5,7-22
A	QUATTROCCHIO, F. et al. Analysis of bHLH and MYB domain proteins: species-specific regulatory differences are caused by divergent evolution of target anthocyanin genes. The Plant Journal. 1998, Vol. 13, No. 4, pages 475-488, see entire document.	1-5,7-22



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

### Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claim Nos.: 52-70  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:  
Please See Continuation Sheet
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: Please See Continuation Sheet
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☒  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

### Continuation of Box I Reason 2:

Claims 52-60 constitute unsearchable subject matter under PCT Rule 39.1(iii) as a process of thought or a business method and claims 61-70 constitute unsearchable subject matter under PCT Rule 39.1(v) a mere presentation of information.

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Groups 1-232, claim(s) 1-5, 7-22 and 44-47 (Group 1 is claims 1-5, 7-22 and 44-47 and SEQ ID NOS: 1 & 2, Group 2 is claims 1-5, 7-22 and 44-47 and SEQ ID NOS: 3 & 4, etc), drawn to an isolated or recombinant polynucleotide, transgenic plants comprising said polynucleotide and a method of making said transgenic plant.

Groups 233-465, claim(s) 6 and 34-43 (Group 233 is claims 6 and 34-43 and SEQ ID NOS: 1 & 2, Group 234 is claims 6 and 34-43 and SEQ ID NOS: 3 & 4, etc), drawn to an isolated or recombinant polypeptide.

Groups 466-698, claim(s) 23-33 (Group 466 is claims 23-33 and SEQ ID NOS: 1 & 2, Group 467 is claims 23-33 and SEQ ID NOS: 3 & 4, etc), drawn to a method comprising expressing an antisense nucleic acid in a transformed plant and the plant produced by said method.

Groups 699-931, claim(s) 48-51 (Group 699 is claims 48-51 and SEQ ID NOS: 1 & 2, Group 700 is claims 48-51 and SEQ ID NOS: 3 & 4, etc), drawn to a computer readable medium.

The inventions listed as Groups 1-931 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The isolated polynucleotide is anticipated by the prior art because Applicant's SEQ ID NO: 66 is 99% identical to the MYB12 disclosed by Kranz *et al* (1998, The Plant Journal, 16(2):263-278). Because Applicant has claimed an isolated polynucleotide encoding a polypeptide having at least anywhere from 31-95% sequence identity outside of a conserved domain of the polypeptide of SEQ ID NO: 66 and an isolated polypeptide having at least 31-95% sequence identity over the entire length of the polypeptide of SEQ ID NO: 66, the claimed invention has been anticipated by the prior art and thus Unity of Invention is lacking as required under PCT Rule 13.1 and it lacks a special technical feature as required under PCT Rule 13.2.

2. Claims 52-60 constitute unsearchable subject matter under PCT Rule 39.1(iii) as a process of thought or a business method and Claims 61-70 constitute unsearchable subject matter under PCT Rule 39.1(v) as mere presentation of information.

### Continuation of Box II Item 3:

1-5, 7-22, 44-45 and SEQ ID NOs. 1, 2, 3, 4

Claims 46 and 47 were not searched because no additional fees were paid for the inventions to which the claims are directed.